

PLANT GENES INVOLVED IN DEFENSE AGAINST PATHOGENS

Cross-Reference to Related Applications

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26, 2001, and U.S. application Serial No. 60/273,879, filed on March 7, 2001 under
35 U.S.C. § 119(e).

Field of the Invention

The present invention generally relates to the field of plant molecular
biology, and more specifically to the regulation of gene expression in plants in
response to pathogen exposure.

Background of the Invention

Plants are capable of activating a large array of defense mechanisms in
response to pathogen attack, some of which are preexisting and others are inducible.
Pathogens must specialize to circumvent the defense mechanisms of the host,
20 especially those biotrophic pathogens that derive their nutrition from an intimate
association with living plant cells. If the pathogen can cause disease, the interaction
is said to be compatible, but if the plant is resistant, the interaction is said to be
incompatible. A crucial factor determining the success of these mechanisms is the
speed of their activation. Consequently, there is considerable interest in
25 understanding how plants recognize pathogen attack and control expression of
defense mechanisms.

Some potential pathogens trigger a very rapid resistance response called
gene-for-gene resistance. This occurs when the pathogen carries an avirulence (*avr*)
gene that triggers specific recognition by a corresponding host resistance (*R*) gene.
30 *R* gene specificity is generally quite narrow, in most cases only pathogens carrying a
particular *avr* gene are recognized. Recognition is thought to be mediated by ligand-

receptor binding. *R* genes have been studied extensively in recent years. For a review of *R* genes, see Ellis et al. (1998); Jones et al. (1997); and Ronald (1998).

One of the defense mechanisms triggered by gene-for-gene resistance is programmed cell death at the infection site. This is called the hypersensitive response, or HR. Pathogens that induce the HR, or cause cell death by other means, activate a systemic resistance response called systemic acquired resistance (SAR). During SAR, levels of salicylic acid (SA) rise throughout the plant, defense genes such as pathogenesis related (PR) genes are expressed, and the plant becomes more resistant to pathogen attack. SA is a crucial component of this response. Plants that cannot accumulate SA due to the presence of a transgene that encodes an SA-degrading enzyme (*nahG*), develop a HR in response to challenge by avirulent pathogens, but do not exhibit systemic expression of defense genes and do not develop resistance to subsequent pathogen attack (Ryals et al., 1996). The nature of the systemic signal that triggers SAR is a subject of debate (Shulaev et al., 1995; Vernooji et al., 1994). SA clearly moves from the site of the HR to other parts of the plant, but if this is the signal, it must be effective at extremely low concentration (Willits et al., 1998).

SAR is quite similar to some reactions that occur locally in response to attack by virulent (those that cause disease) or avirulent (those that trigger gene-for-gene resistance) pathogens. In general, activation of defense gene expression occurs more slowly in response to virulent pathogens than in response to avirulent pathogens. Some pathogens trigger expression of defense genes through a different signaling pathway that requires components of the jasmonic acid (JA) and ethylene signaling pathways (Creelman et al., 1997).

One approach to understanding the signal transduction networks that control defense mechanisms is to use genetic methods to identify signaling components and determine their roles within the network. Considerable progress has been made using this approach in *Arabidopsis*-pathogen model systems.

R gene signal transduction

Genes such as *NDR1* and *EDS1*, as well as *DND1* and the lesion-mimic genes, likely act in signal transduction pathways downstream from *R-avr*

recognition. *NDR1* and *EDS1* are required for gene-for-gene mediated resistance to avirulent strains of the bacterial pathogen *Pseudomonas syringae* and the oomycete pathogen *Peronospora parasitica*. Curiously, *ndr1* mutants are susceptible to one set of avirulent pathogens, whereas *eds1* mutants are susceptible to a non-overlapping set (Aarts et al., 1998). The five cloned *R* genes that require *EDS1* all belong to the subset of the nucleotide binding site-leucine rich repeat (NBS-LRR) class of *R* genes that contain sequences similar to the cytoplasmic domains of *Drosophila* Toll and mammalian interleukin 1 transmembrane receptors (TIR-NBS-LRR). The two genes that require *NDR1* belong to the leucine-zipper (LZ-NBS-LRR) subclass of NBS-LRR genes. There is another LZ-NBS-LRR gene, *RPP8*, that does not require *EDS1* or *NDR1*, so the correlation between *R* gene structure and requirement for *EDS1* or *NDR1* is not perfect. Nevertheless, these results show that *R* genes differ in their requirements for downstream factors and that these differences are correlated with *R* gene structural type.

NDR1 encodes a protein with two predicted transmembrane domains (Century et al. 1997). RPM1, which requires *NDR1* to mediate resistance, is membrane-associated, despite the fact that its primary sequence does not include any likely membrane-integral stretches (Boyee et al., 1998). It is possible that part of the function of *NDR1* is to hold *R* proteins close to the membrane. *EDS1* encodes a protein with blocks of homology to triacyl glycerol lipases (Falk et al., 1999). The significance of this homology is not known, but it is tempting to speculate that *EDS1* is involved in synthesis or degradation of a signal molecule. *EDS1* expression is inducible by SA and pathogen infection, suggesting that *EDS1* may be involved in signal amplification (Falk et al., 1999).

It has been extremely difficult to isolate mutations in genes other than the *R* genes that are required for gene-for-gene resistance. A selection procedure was devised (McNellis et al., 1998) on the basis of precisely controlled inducible expression of the *avr* gene *avrRpt2* in plants carrying the corresponding resistance gene *RPS2*. Expression of *avrRpt2* in this background is lethal, as it triggers a systemic HR. It is now possible to select for mutants with subtle defects in gene-

for-gene signaling by requiring growth on a concentration of inducer slightly higher than the lethal dose.

Putative plant receptor proteins encoded by *RPP* genes (recognition of *P. parasitica*) mediate specific recognition of *Peronospora* isolates and trigger defense reactions. Recently, McDowell et al. (2000) reported that two members of this class, *RPP7* and *RPP8* (the latter of which encodes a LZ-NBS-LRR type R protein) were not significantly suppressed by mutations in either *EDS1* or *NDR1*, and that *RPP7* resistance was also not compromised by mutations in *EIN2*, *JAR1* or *COI1*, which affect ethylene or jasmonic acid signaling, or in *coil/npr1* or *coil/NahG* backgrounds. The authors suggested that *RPP7* initiates resistance through a novel signaling pathway that is independent of salicylic acid accumulation or jasmonic acid response components.

SA-dependent signaling

SA levels increase locally in response to pathogen attack, and systemically in response to the SAR-inducing signal. SA is necessary and sufficient for activation of PR gene expression and enhanced disease resistance. Physiological analyses and characterization of certain lesion-mimic mutants strongly suggest that there is a positive autoregulatory loop affecting SA concentrations (Shirasu et al., 1997; Hunt et al., 1997; Weymann et al., 1995). Several mutants with defects in SA signaling have been characterized. These include *npr1*, in which expression of PR genes in response to SA is blocked; *cpr1*, *cpr5*, and *cpr6*, which constitutively express PR genes; the *npr1* suppressor *ssi1*; *pad4*, which has a defect in SA accumulation; and *eds5*, which has a defect in *PR1* expression.

Expression of the defense genes *PR1*, *BG2*, and *PR5* in response to SA treatment requires a gene called *NPR1* or *NIM1*. Mutations in *npr1* abolish SAR, and cause enhanced susceptibility to infection by various pathogens (Cao et al., 1994; Delaney et al., 1995; Glazebrook et al., 1996; Shah et al., 1997). *NPR1* appears to be a positive regulator of PR gene expression that acts downstream from SA. *NPR1* encodes a novel protein that contains ankyrin repeats (which are often involved in protein-protein interactions (Cao et al., 1997; Ryals et al., 1997), and that is localized to the nucleus in the presence of SA (Dong et al., 1998).

Consequently, it is unlikely that NPR1 acts as a transcription factor to directly control *PR* gene expression, but its nuclear localization suggests that it may interact with such transcription factors.

PAD4 appears to act upstream from SA. In *pad4* plants infected with a virulent *P. syringae* strain, SA levels, synthesis of the antimicrobial compound camalexin, and *PR1* expression are all reduced (Zhou et al., 1998). SA is necessary, but not sufficient, for activation of camalexin synthesis (Zhou et al., 1998; Zhao et al., 1996). The camalexin defect in *pad4* plants is reversible by exogenous SA (Zhou et al., 1998). Mutations in *pad4* do not affect SA levels, camalexin synthesis, or *PR1* when plants are infected with an avirulent *P. syringae* strain (Zhou et al., 1998). Taken together, these results suggest that PAD4 is required for signal amplification to activate the SA pathway in response to pathogens that do not elicit a strong defense response (Zhou et al., 1998).

JA-dependent signaling

JA signaling affects diverse processes including fruit ripening, pollen development, root growth, and response to wounding (Creelman et al., 1997). The *jar1* and *coil* mutants fail to respond to JA (Feys et al., 1994; Staswick et al., 1992). *COI1* has been cloned, and found to encode protein containing leucine-rich repeats and a degenerate F-box motif (Xie et al., 1998). These features are characteristic of proteins that function in complexes that ubiquitinate protein targeted for degradation.

In the past few years it has become apparent that JA plays an important role in regulation of pathogen defenses. For example, the induction of the defensin gene *PDF1.2* after inoculation of *Arabidopsis* with the avirulent pathogen *Alternaria brassicicola* does not require SA or NPR1, but does require ethylene and JA signaling (Penninck et al., 1996).

SA signaling and JA signaling pathways are interconnected in complicated ways. Studies in other systems have shown that SA signaling and JA signaling are mutually inhibitory (Creelman et al., 1997; Harms et al., 1998). However, synthesis of camalexin in response to *P. syringae* infection is blocked in *nahG* (Zhou et al.,

1998; Zhao et al., 1996) and *coi1* (Glazebrook, 1999) plants, strongly suggesting that camalexin synthesis requires both SA and JA signaling.

Induced systemic resistance (ISR)

Some rhizosphere-associated bacteria promote disease resistance (van Loon et al., 1998). This phenomenon, called ISR, has been studied using *Pseudomonas fluorescens* strain WCS417r to colonize *Arabidopsis* roots (Pieterse et al., 1996). Colonized plants are more resistant to infection by the fungal pathogen *Fusarium oxysporum* f sp *raphani* and *P. syringae* (Pieterse et al., 1996). ISR occurs in *nahG* plants, indicating that it is not a SA-dependent phenomenon (Pieterse et al., 1996). Rather, ISR appears to be JA- and ethylene-dependent. The observation that ethylene can induce ISR in *jar1* mutants led to the hypothesis that ISR requires a JA signal followed by an ethylene signal (Pieterse et al., 1998). No changes in gene expression associated with ISR have been detected (Pieterse et al., 1998), suggesting that it is different from activation of *PDF1.2* expression by *A. brassicicola*.

Curiously, ISR requires *NPR1* (Pieterse et al., 1996). This was unexpected in light of the fact that *NPR1* was previously known to be involved only in SA-dependent processes and ISR is SA-independent. If the SA-dependent signal is received, *NPR1* mediates a resistance response characterized by *PR1* expression, whereas if the ISR signal is received, *NPR1* mediates a different resistance response. It is difficult to imagine how this could occur, unless *NPR1* is interacting with different 'adapter' molecules to mediate the different signals. The ankyrin repeats found in *NPR1* could function in protein-protein interactions between *NPR1* and adapter proteins. Identification of proteins that interact with *NPR1*, and characterization of plants with loss-of-function mutations affecting those proteins, would be very helpful for understanding how *NPR1* acts in each pathway. It would also be worthwhile to determine if the *ssi1* or *cpr6* mutations suppress the ISR defect of *npr1* mutants.

Relevance to disease resistance

Characterization of the effects of various mutations on resistance to different pathogens has revealed that there is considerable variation in the extent to which pathogens are affected by defense mechanisms. SAR is known to confer resistance

to a wide array of pathogens, including bacteria, fungi, oomycetes, and viruses. JA signaling is important for limiting the growth of certain fungal pathogens. In *Arabidopsis*, the SA pathway mutants *npr1* and *pad4* show enhanced susceptibility to *P. syringae* and *P. parasitica* (Cao et al., 1994; Delaney et al., 1995; Shah et al., 1997; Zhou et al., 1998; Glazebrook et al., 1997).

Overexpression of rate-limiting defense response regulators may cause the signaling network to respond faster or more strongly to pathogen attack, thereby improving resistance. For example, overexpression of *NPR1* caused increased resistance to *P. syringae* and *P. parasitica* in a dosage dependent manner (Cao et al., 1998). Moreover, *NPR1*-overexpression had no obvious deleterious effects on plant growth, in contrast to mutations that lead to constitutive overexpression of defense responses, which generally cause dwarfism.

Promoters for gene expression of plant pathogen defense genes

Promoters (and other regulatory components) from bacteria, viruses, fungi and plants have been used to control gene expression in plant cells. Numerous plant transformation experiments using DNA constructs comprising various promoter sequences fused to various foreign genes (for example, bacterial marker genes) have led to the identification of useful promoter sequences. It has been demonstrated that sequences up to 500-1,000 bases in most instances are sufficient to allow for the regulated expression of foreign genes. However, it has also been shown that sequences much longer than 1 kb may have useful features which permit high levels of gene expression in transgenic plants. The expression of genes encoding proteins that are useful for protecting plants from pathogen attack may have deleterious effects on plant growth if expressed constitutively. Consequently, it is desirable to have promoter sequences that control expression of these gene(s) in such a way that expression is absent or very low in the absence of pathogens, and high in the presence of pathogens.

Thus, what is needed is the identification of plant genes useful to confer resistance to a pathogen(s) and plant promoters, the expression of which is altered in response to pathogen attack.

Summary of the Invention

The invention generally provides an isolated nucleic acid molecule (polynucleotide) comprising a plant nucleotide sequence obtained or isolatable from a gene, the expression of which is altered, either increased or decreased, in response to pathogen infection. In one embodiment, the plant nucleotide sequence comprises an open reading frame, while in another embodiment, the plant nucleotide sequence comprises a promoter. A promoter sequence of the invention directs transcription of a linked nucleic acid segment, e.g., a linked plant DNA comprising an open reading frame for a structural or regulatory gene, in a host cell, such as a plant cell, in response to pathogen infection of that cell. As used herein, a "pathogen" includes bacteria, fungi, oomycetes, viruses, nematodes and insects, e.g., aphids (see Hammond-Kosack and Jones, 1997). Moreover, the expression of a plant nucleotide sequence of the invention comprising a promoter may be altered in response to one or more species of bacteria, nematode, fungi, oomycete, virus, or insect. Likewise, the expression of a plant nucleotide sequence of the invention comprising an open reading frame may be useful to confer tolerance or resistance of a plant to one or more species of bacteria, nematode, fungi, oomycete, virus or insect.

The nucleotide sequence preferably is obtained or isolatable from plant DNA. In particular, the nucleotide sequence is obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-953 and 2137-2661 or a fragment (portion) thereof which encodes a partial length polypeptide having substantially the same activity of the full-length polypeptide, a rice gene comprising one of SEQ ID NOs: 2000-2129 and 2662-6813, or a *Chenopodium* gene comprising one of SEQ ID NOs: 1954-1966.

The present invention also provides an isolated nucleic acid molecule comprising a plant nucleotide sequence that directs transcription of a linked nucleic acid segment in a host cell, e.g., a plant cell. The nucleotide sequence preferably is

obtained or isolatable from plant genomic DNA. In particular, the nucleotide sequence is obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising any one of SEQ ID NOs:1-953 and 2137-2661, a rice gene comprising one of SEQ ID NOs:2000-2129 and 2662-6813, or a *Chenopodium* gene comprising any one of SEQ ID NOs:1954-1966, the expression of which is increased or decreased in response to pathogen infection. Preferred promoters comprise DNA obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising a promoter according to SEQ ID NOs:1001-1095 and 2137-2661, a rice gene comprising a promoter according to SEQ IN NOs:4738-6813, or a fragment thereof (i.e., promoters isolatable from any one of SEQ ID NOs:1001-1095, 2137-2661 and 4738-6813) which increases or decreases transcription of a linked nucleic acid segment in response to pathogen infection.

The invention also provides uses for an isolated nucleic acid molecule, e.g., DNA or RNA, comprising a plant nucleotide sequence comprising an open reading frame encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis*, *Chenopodium* or rice gene comprising an open reading frame comprising any one of SEQ ID NOs:1-953, 1954-1966, 2000-2129, 2662-4737 or the complement thereof. For example, these open reading frames may be useful to prepare plants that over- or under-express the encoded product or to prepare knockout plants.

The promoters and open reading frames of the invention can be identified by any method. For example, they can be identified by employing an array of nucleic acid samples, e.g., each sample having a plurality of oligonucleotides, and each plurality corresponding to a different plant gene, on a solid substrate, e.g., a DNA chip, and probes corresponding to nucleic acid which is up- or down-regulated in response to pathogen infection in one or more ecotypes or species of plant relative to a control (e.g., a water control, nucleic acid from an uninfected plant or nucleic acid from a mutant plant). Thus, genes that are upregulated or downregulated in response to pathogen infection can be systematically identified.

As described herein, GeneChip® technology was utilized to discover a plurality of genes, the expression of which is altered after pathogen infection. The *Arabidopsis* oligonucleotide probe array consists of probes from about 8,100 unique *Arabidopsis* genes, which covers approximately one third of the genome. This genome array permits a broader, more complete and less biased analysis of gene expression. Using labeled cRNA probes, expression levels were determined by laser scanning and genes generally selected for expression levels that were > 2 fold over the control.

For example, using this approach, 953 genes were identified, the expression of which was altered after infection of wild-type *Arabidopsis* plants with a pathogen (SEQ ID NOs:1-953). In addition, 745 genes were identified, the expression which was increased after infection of wild-type *Arabidopsis* with *Pseudomonas syringae* (SEQ ID NOs: 2-6, 8-13, 16, 18, 22-23, 25, 28-29, 31-32, 35-37, 39-43, 45-47, 49-50, 52, 54-55, 57-58, 60-66, 70-72, 74, 76-77, 79, 81, 83, 85, 87-90, 92, 94, 97, 100-107, 111-115, 117-125, 127-135, 138-140, 142-153, 156-158, 160, 162-165, 168-170, 173-181, 183-184, 186-188, 190-198, 200-201, 203-211, 214-215, 218-224, 227-232, 234-249, 251-262, 264, 266-268, 270, 272-275, 277-281, 283, 286-294, 297-298, 302, 304-306, 308-326, 328-339, 341, 344-345, 347, 350-351, 353-358, 361-371, 373-377, 379-386, 388-390, 392, 394-400, 402-406, 408-410, 412-417, 419-427, 429-433, 435-443, 445-452, 454-457, 459-460, 462-464, 466-470, 473-475, 478-479, 481-482, 484-187, 489-494, 496-498, 500-501, 503-506, 508, 510, 512-515, 517-523, 526, 528-529, 531-538, 540, 544-548, 550-558, 560, 563-568,

570, 572-577, 579-580, 582-585, 588-594, 596, 598-600, 602-603, 605-606, 608-612, 614-617, 619-624, 626-630, 632-639, 642, 644, 646-651, 653-657, 659-665, 667-671, 673-678, 681-689, 691-693, 695-713, 715-717, 719, 721-727, 729-733, 736-738, 740, 742, 744, 746, 748-752, 755-756, 758-760, 762-769, 771, 774, 776-781, 783-788, 790-796, 798-799, 802, 804-808, 810-815, 817-831, 833-848, 850-855, 857-869, 871-880, 882-900, 903-907, 909, 911-915, 918-920, 922-925, 927, 929, 931-938, 940, 943-945, 947, and 950-953). Of the 745 genes, the expression of 530 of those genes was altered in at least one mutant *Arabidopsis* after infection with *Pseudomonas syringae* (SEQ ID NOs: 2, 4-6, 11-13, 18, 22-23, 28, 31, 36, 39-43, 45, 47, 49-50, 52, 54-55, 57-58, 60-61, 63-66, 71-72, 74, 77, 81, 83, 85, 87-89, 92, 97, 100-107, 111-112, 114-115, 117-120, 122, 125, 127-128, 134, 128-140, 143-144, 148-151, 153, 156-157, 160, 165, 168-170, 173-174, 176-180, 183, 187-188, 191, 193-194, 197-198, 200, 203-210, 214, 219-224, 227, 230-232, 235-237, 239-240, 243-246, 248-249, 251-254, 256-258, 261, 264, 266-268, 270, 272-275, 277-278, 280, 283, 286-287, 290-293, 297, 302, 305-306, 308-310, 312-316, 321-326, 328-331, 333, 336-339, 341, 345, 351, 353, 355-358, 361-363, 365-366, 368-371, 373, 375, 377, 379-381, 384-385, 388-390, 392, 394-400, 402-406, 410, 412, 415-416, 419-420, 422-425, 429-433, 435-439, 441-443, 445-452, 454, 459-460, 463, 466, 468-470, 473, 481-482, 485-486, 489, 491-494, 497-498, 500-501, 503, 505-506, 508, 510, 513-515, 517, 520-521, 523, 528-529, 531, 533-538, 540, 545-548, 550-551, 553-554, 556-558, 560, 566-567, 575, 580, 582-584, 588-593, 596, 598-600, 602-603, 605-606, 608-610, 612, 614, 616, 620-622, 627-629, 633-634, 636-639, 644, 646, 648-651, 654-657, 659, 661-663, 667, 669, 673-674, 677, 682, 684-687, 689, 691-693, 697, 699, 701, 703-708, 713, 717, 719, 721-727, 730-733, 736, 740, 744, 746, 749-752, 755-756, 758-760, 762-764, 766-769, 774, 776-778, 780-781, 786, 788, 791-796, 799, 802, 804-808, 810-812, 815, 818-821, 823-825, 827-829, 831, 833-836, 838-843, 845, 847-848, 852-853, 855, 858, 860-869, 871-874, 876, 878-880, 884-887, 889, 892-894, 896-900, 904-907, 911-915, 918-920, 922-924, 931, 933, 938, 943-945, 947, and 950-952). Of the 530, 81 encode regulatory factors (SEQ ID NOs: 39, 52, 60, 63, 81, 83, 106, 107, 115, 117, 118, 168, 174, 176, 179, 204, 207, 208, 220, 221, 248, 258, 268, 275, 280, 309, 323, 326, 329, 351, 419,

422, 429, 430, 432, 459, 460, 468, 469, 473, 500, 505, 506, 508, 529, 531, 533, 535, 538, 545, 553, 602, 606, 608, 610, 614, 616, 634, 654, 655, 684, 686, 687, 691, 717, 751, 752, 766, 777, 815, 831, 834, 835, 839, 841, 847, 876, 884, 906, 920, and 924).

As also described herein, 333 genes were identified that are useful to confer improved resistance to plants to bacterial infection (SEQ ID NOs: 12-13, 18, 23, 36, 39-40, 43, 45, 50, 52, 57-58, 60-61, 64, 71-72, 81, 87-89, 97, 100, 102-105, 107, 111-112, 115, 119-120, 122, 125, 127-128, 140, 144, 148-150, 153, 165, 168-169, 176-177, 179, 183, 188, 191, 193-194, 197-198, 203-206, 208-209, 214, 219-222, 227, 230, 232, 237, 244-246, 248-249, 251-253, 258, 261, 264, 266, 268, 273-275, 283, 287, 290, 293, 297, 302, 305-306, 308, 312-315, 321-322, 324, 326, 330, 333, 338, 341, 345, 353, 356-358, 362-363, 366, 369, 371, 375, 377, 380, 384-385, 389, 392, 394-395, 398-399, 402-404, 406, 410, 415, 419, 422, 425, 429-430, 433, 435-439, 443, 445-452, 454, 463, 466, 468-470, 473, 486, 489, 491-492, 4894, 498, 500-501, 503, 508, 513-514, 517, 529, 533-538, 548, 550, 553-554, 4556-558, 566, 575, 580, 582-583, 590-591, 593, 600, 602, 609-610, 612, 614, 620-622, 627-629, 637-638, 644, 649, 654-657, 659, 663, 667, 669, 673-674, 677, 684-685, 689, 691-693, 699, 703-705, 708, 719, 721, 724-726, 730-732, 744, 746, 749-750, 752, 755-756, 758, 760, 762-764, 767, 769, 774, 780-781, 786, 788, 791-792, 794-796, 799, 804-808, 810-812, 815, 818-819, 823, 828-829, 833, 840841, 843, 847, 852-853, 858, 860, 862-865, 867-868, 872-874, 876, 885-887, 889, 892-894, 896-900, 904-905, 907, 911-914, 918-920, 922-924, 931, 933, 938, 947, 950, and 952).

Further, 296 genes were identified that are useful to confer improved resistance to plants to fungal infection (SEQ ID NOs: 2, 4, 6, 11-13, 18, 22-23, 31, 41-43, 49-50, 54, 57-58, 61, 64-66, 71-72, 74, 77, 85, 87, 89, 92, 97, 101, 103, 106-107, 112, 114, 117-119, 125, 128, 134, 138, 143, 149, 151, 156-157, 165, 169-170, 174, 176-180, 187-188, 191, 193, 206, 208, 219-220, 222, 224, 231, 236, 239, 243-245, 251-254, 256-257, 267, 272, 287, 290, 292, 297, 302, 312-313, 315-316, 321-322, 324-325, 328, 330, 345, 351, 353, 355-357, 362-363, 366, 368-371, 373, 375, 379, 381, 384, 388-390, 392, 395-400, 405, 410, 415-416, 419, 422, 424, 431-432, 435-436, 438-439, 447, 459-460, 470, 473, 481-482, 489, 491, 493-494, 500-501, 505-506, 513-514, 517, 520-521, 523, 528-529, 531, 535, 537-538, 540, 545-548,

551, 553-554, 557-558, 566, 575, 580, 582, 584, 589, 591, 593, 596, 598-599, 603, 605, 608-609, 612, 628, 633-634, 636-637, 639, 646, 648, 650-651, 656, 661, 663, 667, 674, 685-687, 689, 691, 693, 697, 699, 701, 705, 707, 713, 723-724, 726, 736, 740, 749, 751-752, 756, 758-759, 764, 766-768, 774, 776, 778, 780, 792-796, 799, 802, 806, 810-812, 818, 820-821, 825, 827-829, 833-836, 838-839, 841-843, 848, 855, 860-861, 866, 868-869, 871, 873-874, 876, 878-880, 889, 892, 898-900, 904-905, 907, 915, 918, 922, 924, 933, 943-945, 947, and 951).

In addition, 288 genes were identified that are useful to confer improved resistance to plants to infection with more than one pathogen, e.g., pathogens that include bacteria, oomycetes and viruses (SEQ ID NOs: 12-13, 18, 23, 36, 39-40, 43, 45, 50, 52, 57-58, 60-61, 64, 71-72, 81, 87-88, 100, 102-105, 107, 111-112, 115, 119-120, 122, 125, 127-128, 140, 148-150, 153, 168-169, 176-177, 188, 191, 193-194, 197-198, 203-206, 209, 219-222, 227, 232, 237, 244-246, 248-249, 251-253, 258, 261, 264, 266, 268, 273-275, 283, 287, 290, 293, 297, 302, 305-306, 308, 312-315, 324, 326, 330, 333, 341, 345, 353, 356, 358, 366, 371, 375, 377, 380, 385, 389, 392, 394, 398, 402-404, 406, 410, 415, 419, 425, 429-430, 433, 435-438, 443, 445-447, 449-452, 454, 463, 466, 468-470, 473, 486, 489, 492, 494, 498, 500-501, 503, 508, 513-514, 517, 533-538, 548, 550, 553-554, 57-558, 566, 575, 582-583, 590-591, 593, 600, 602, 609-610, 612, 620-622, 627-629, 637-638, 644, 649, 654-657, 659, 667, 669, 673, 677, 684, 689, 692-693, 703-705, 719, 721, 724-726, 730-732, 744, 746, 749-750, 752, 755-756, 760, 762-764, 767, 769, 774, 780-781, 786, 788, 791-792, 795-796, 805-808, 810-812, 815, 818-819, 823, 828, 833, 840-841, 843, 852-853, 858, 860, 862-865, 867-868, 872-874, 876, 887, 889, 893-894, 896-898, 900, 905, 907, 911-914, 918-920, 922-923, 931, 933, 938, 947, 950, and 952).

Using the same approach described above, 25 genes were identified (SEQ ID NOs: 1, 15, 19, 20, 24, 26, 27, 34, 38, 51, 56, 59, 67-69, 99, 116, 155, 159, 182, 212, 284, 372, 444, and 789), the expression of which was decreased at 6 hours in an *avr2* plant. Also identified were 33 genes (SEQ ID NOs: 17, 70, 76, 81, 84, 109, 123, 144, 160, 230, 265, 268, 269, 271, 323, 333, 385, 427, 428, 430, 457, 505, 569, 597, 602, 606, 616, 708, 730, 741, 812, 862, and 942), the expression of which was elevated in an incompatible or a compatible interaction in four *Arabidopsis* ecotypes

infected with bacteria. Eight of the genes were upregulated by 3 hours in an incompatible interaction, 18 of the genes were upregulated by 6 hours, but not at 3 hours, in an incompatible interaction, and 6 of the genes were upregulated in a compatible interaction.

5 Further identified were 33 genes, the expression of which was induced early after infection (SEQ ID NOs:17, 21, 80, 81, 156, 174, 176, 221, 227, 296, 302, 303, 306, 333, 340, 360, 500, 505, 524, 575, 601, 602, 614, 628, 687, 733, 782, 811, 835, 862, 900, 905, and 912), 10 genes, the expression of which was decreased early after infection (SEQ ID NOs:30, 73, 282, 541, 640, 679, 761, 870, 917, and 930), and 135
10 genes, 107 of which were induced at 3 and/or 6 hours after infection, and 28 of which were decreased after infection (SEQ ID NOs:7, 21, 33, 44, 46, 60, 82, 86, 91, 93, 106, 110, 119, 122, 130, 131, 136, 141, 154, 161, 166-168, 171, 176, 185, 189, 199, 200, 202, 203, 213, 225, 227, 248, 261, 262, 266, 274, 285, 300, 301, 302, 320, 326, 341, 345, 348, 349, 360, 366, 378, 406, 409, 422, 425, 434, 441, 443, 446, 449,
15 454, 461, 471, 475, 476, 483, 485, 499, 500, 511, 512, 516, 527, 530, 533, 543, 545, 549, 550, 552, 567, 575, 578, 586, 590, 608, 611, 615, 618, 625, 631, 643, 656, 658, 659, 666, 668, 671, 680, 690, 694, 704, 706, 711, 714, 718, 721, 728, 734, 738, 757, 770, 772, 791, 807, 811, 813, 816, 827, 857, 864, 868, 875, 881, 893, 901, 905, 908, 912, 916, 939, 941, 951, and 952).

20 In a similar approach, 48 genes that were upregulated in response to infection, e.g., bacterial or fungal infection, as well as 46 of the corresponding promoter containing regions, were identified. Thirty-six of the genes were upregulated in response to bacterial, e.g., *Pseudomonas*, infection (the promoters for genes corresponding to SEQ ID NOs: 104-106, 119, 123, 129, 131, 151-152, 183,
25 191, 198, 200, 227, 249, 274, 302, 358, 415, 481, 547, 566, 582, 628, 633, 639, 656, 673, 793, 818, 827, 864, 874, 880, and 904-905), while 23 of the genes were upregulated in response to fungal, e.g., *Botrytis*, infection (SEQ ID NOs: 18, 71, 119, 123, 129, 151, 191, 244, 245, 302, 545, 547, 562, 566, 637, 653, 747, 756, 774, 793, 842, 864, and 905). Twenty-five of the genes were upregulated only in
30 response to bacterial, e.g., *Pseudomonas*, infection (the promoters for genes corresponding to SEQ ID NOs: 104-106, 131, 152, 183, 198, 200, 227, 249, 274,

358, 415, 481, 582, 628, 633, 639, 656, 673, 818, 827, 874, 880, and 904 are provided in SEQ ID NOs:1001-1025), 10 of the genes were upregulated only in response to fungal, e.g., *Botrytis*, infection (the promoters for genes corresponding to SEQ ID NOs:18, 71, 244, 245, 545, 562, 637, 653, 747, 756, 774, and 842 are provided in SEQ ID NOs:1026-1035), and 11 genes were upregulated in response to both bacterial and fungal infection (the promoters for genes corresponding to SEQ ID NOs:119, 123, 129, 151, 191, 302, 547, 566, 793, 864, and 905 are provided in SEQ ID NOs:1036-1046).

As also described hereinbelow, 129 *Arabidopsis* genes (SEQ ID NOs: 3, 51, 54, 60, 61, 66, 75, 76, 78, 88, 95, 96, 101, 106, 108, 123, 126, 128, 129, 131, 137, 145-147, 150, 158, 169, 170, 172, 173, 197, 200, 216, 219, 224, 230, 233, 237, 249, 250, 263, 274, 275, 276, 299, 307, 323, 333, 342, 346, 359, 382, 383, 387, 391, 393, 401, 411, 415, 427, 442, 455, 459, 466, 477, 481, 485, 487, 502, 511, 515, 525, 534, 539, 542, 560, 571, 577, 579, 584, 587, 595, 600, 627, 638, 645, 654, 659, 668, 681, 688, 695, 696, 706, 708, 730, 742, 753, 775, 785, 786, 791, 797, 800, 801, 809, 817, 819, 820, 823, 827, 847, 856, 875, 885, 896, 902, 910, 921, 922, 923, 925, 926, 928, 946, and 952) were identified that were upregulated in response to viral infection, and 46 *Arabidopsis* genes were identified that were downregulated in response to viral infection (SEQ ID NOs: 14, 48, 53, 98, 217, 226, 295, 327, 343, 352, 369, 404, 407, 418, 453, 458, 465, 472, 480, 488, 495, 507, 509, 513, 514, 559, 561, 581, 604, 607, 613, 641, 652, 672, 720, 735, 739, 743, 745, 754, 773, 803, 832, 849, 948, and 949).

Also provided are nucleic acid molecules comprising a nucleotide sequence comprising an open reading frame expressed in response to pathogen infection comprising SEQ ID NOs:209, 216, 262, 267, 317, 386, 425, 440 and 800. These sequences are useful to over- or under-express the encoded product, or prepare knock-out plants which have an altered response to pathogen infection.

The invention therefore provides a method in which the open reading frame of a plant pathogen resistance gene, e.g., a gene that is associated with a response to pathogen infection, which is altered in a plant in response to infection is identified and isolated. A transgene comprising the isolated open reading frame may be

introduced to and expressed in a transgenic plant, e.g., prior to infection, e.g., constitutively, or early and/or rapidly after infection, or in regulatable (inducible) fashion, e.g., after exposure to a chemical or using a promoter that is upregulated after infection, so as to confer resistance to that transgenic plant to the pathogen
5 relative to a corresponding plant which does not have the transgene. The expression of the transgene is preferably at higher than normal levels, and under the regulation of a promoter that allows very fast and high induction in response to the presence of a pathogen or under cycling promoters (e.g., circadian clock regulated promoters), such that the encoded gene product(s) is maintained at sufficiently high levels to
10 provide enhanced resistance or tolerance. The invention further provides a method in which a gene in a plant which is downregulated in response to infection, is disrupted or the expression of that gene is further downregulated, e.g., using antisense expression, so as to result in a plant that has enhanced resistance to infection, and which disruption or downregulation preferably has little or no
15 detrimental effect(s) on the host plant.

As also described herein, it was found that the early incompatible response was similar to the late compatible response, suggesting that early expression of plant pathogen-resistance genes is important for resistance. Also, various plant strains were found to respond differently to the same pathogen, but there was also an
20 identifiable global pattern of response. Thus, the comparison of the expression patterns in incompatible and compatible interactions in one or more ecotypes can lead to identifying subsets of key responding genes and clusters of genes that are key (early) responders. In addition, the observed global expression pattern indicated that the least resistant strain tested (Ws) had a low basal level of pathogen-upregulated
25 genes and a high level of pathogen-downregulated genes compared to the most resistant strain (Ler). Thus, plant strains that are more resistant to pathogens have a gene expression phenotype in which genes that are upregulated in response to infection are already expressed at a higher than normal basal level, and those genes that are downregulated are expressed at a lower than normal basal level.

30 Thus, further provided herein is a method to identify at least one gene involved in plant (dicot or monocot) resistance or response to infection by at least

one pathogen, e.g., a bacterium, fungus or virus, which method involves determining or detecting plant gene expression in an incompatible interaction and identifying at least one gene whose expression is significantly altered, e.g., upregulated or downregulated in response to infection, in the incompatible interaction relative to expression of the at least one gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to infection by a pathogen, or in a corresponding compatible interaction. Also provided is a method to identify at least one gene involved in plant (dicot or monocot) resistance or response to infection by at least one pathogen, e.g., bacterium, fungus or virus, which method involves determining or detecting plant gene expression in a compatible interaction; and identifying at least one gene whose expression is significantly altered, e.g., upregulated or downregulated in response to infection, in the compatible interaction relative to expression of the at least one gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to infection by a pathogen, or in a corresponding incompatible interaction. A compatible interaction can be, for example, between a plant having a resistance gene and a pathogen lacking a corresponding avirulence gene, a plant lacking a resistance gene to a pathogen having a corresponding avirulence gene, or a plant lacking a resistance gene and a pathogen lacking a corresponding avirulence gene. For example, the gene identified by such a method can encode a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising one of SEQ ID NOs: 50, 139, 609, 2699, 3311, 3463, 3584, 3791, 4210, 4451 or 4595, or has an open reading frame comprising one of SEQ ID NOs: 50, 139, 609, 2699, 3311, 3463, 3584, 3791, 4210, 4451 or 4595. In such a method, gene expression can be detected or determined using, for example, a gene chip, a cDNA array, cDNA-AFLP or differential display PCR. Such a method can further involve isolating the at least one gene or a portion thereof which includes the open reading frame or promoter for the gene.

Further provided is a method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation that decreases jasmonic acid or ethylene-dependent signaling, which

method involves contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of

5 oligonucleotides corresponding to at least a portion of one plant gene; and comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having the mutation and infected with the pathogen, so as to identify a gene, the expression of which is

10 altered by pathogen infection in a wild-type plant relative to the mutant plant. Also provided herein is a method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation in a gene that interferes with salicylic acid dependent signaling, which method involves contacting a plurality of isolated nucleic acid samples on a solid

15 substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and comparing complex formation in a) with complex formation between a second

20 plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having a mutation and infected with the pathogen, so as to identify a gene, the expression of which is altered by pathogen infection in a wild-type plant relative to the mutant plant. Also provided herein is a method to identify at least one gene, the expression of which is

25 altered by pathogen infection in a wild-type plant relative to a plant having a mutation that results in enhanced susceptibility to bacterial infection, which method involves contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to

30 form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and comparing complex

formation in a) with complex formation between a second plurality of isolated
 nucleic acid samples on a solid substrate with a second probe comprising nucleic
 acid corresponding to RNA from the plant having a mutation and infected with the
 pathogen, so as to identify a gene, the expression of which is altered by pathogen
 5 infection in a wild-type plant relative to the mutant plant. In addition, provided
 herein is a method to identify at least one gene, the expression of which is altered by
 infection with at least one virus, which method comprises contacting a plurality of
 isolated nucleic acid samples on a solid substrate each comprising isolated nucleic
 acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-
 10 type plant infected with a virus, so as to form a complex, wherein each sample
 comprises a plurality of oligonucleotides corresponding to at least a portion of one
 plant gene; and comparing complex formation in a) with complex formation
 between a second plurality of isolated nucleic acid samples on a solid substrate with
 a second probe comprising nucleic acid corresponding to RNA from an uninfected
 15 plant, so as to identify a gene, the expression of which is altered by virus infection.
 Also provided is a method to identify at least one gene, the expression of which is
 altered by infection with at least one pathogen, which involves contacting a plurality
 of isolated nucleic acid samples on a solid substrate each comprising isolated
 nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from
 20 an incompatible interaction so as to form a complex, wherein each sample
 comprises a plurality of oligonucleotides corresponding to at least a portion of one
 plant gene; and comparing complex formation in a) with complex formation
 between a second plurality of isolated nucleic acid samples on a solid substrate with
 a second probe comprising nucleic acid corresponding to RNA from a
 25 corresponding compatible interaction so as to identify a gene, the expression of
 which is altered by the pathogen. In any of the methods described herein, the probes
 can have nucleic acid, for example, from a dicot, a cereal plant, or a monocot.
 Further, the methods can additionally involve identifying the promoter for the at
 least one gene.
 30 The genes and promoters described hereinabove can be used to identify
 orthologous genes and their promoters which are also likely useful to enhance

resistance of plants to pathogens. Moreover, the orthologous promoters are useful to express linked open reading frames. In addition by aligning the promoters of these orthologs, novel *cis* elements can be identified that are useful to generate synthetic promoters.

5 Hence, the isolated nucleic acid molecules of the invention include the orthologs (homologs) of the *Arabidopsis*, *Chenopodium* and rice sequences disclosed herein, i.e., the corresponding nucleic acid molecules in organisms other than *Arabidopsis*, *Chenopodium* and rice, including, but not limited to, plants other than *Arabidopsis*, *Chenopodium* and rice, preferably cereal plants, e.g., corn, wheat,
10 rye, turfgrass, sorghum, millet, sugarcane, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, tobacco, sugarbeet, or rice. An ortholog is a gene from a different species that encodes a product having the same function as the product encoded by a gene from a reference organism. Databases such GenBank or one found at <http://bioserver.myongji.ac.kr/rjce.html> (for rice) may be employed to
15 identify sequences related to the *Arabidopsis* or *Chenopodium* sequences, e.g., orthologs in cereal crops such as rice. Alternatively, recombinant DNA techniques such as hybridization or PCR may be employed to identify sequences related to the *Arabidopsis* sequences. The encoded ortholog products likely have at least 70% sequence identity to each other. Hence, the invention includes an isolated nucleic
20 acid molecule comprising a nucleotide sequence encoding a polypeptide having at least 70% identity to a polypeptide encoded by one or more of the *Arabidopsis*, *Chenopodium* or rice sequences disclosed herein. For example, promoter sequences within the scope of the invention are those which direct expression of an open reading frame which encodes a polypeptide that is substantially similar to an
25 *Arabidopsis* polypeptide encoded by a gene comprising SEQ ID NOs:1-953.

 The genes and promoters described hereinabove can be used to identify orthologous genes and their promoters which are also likely expressed in a particular tissue and/or development manner. Moreover, the orthologous promoters are useful to express linked open reading frames. In addition, by aligning the promoters of
30 these orthologs, novel *cis* elements can be identified that are useful to generate synthetic promoters. Hence, the isolated nucleic acid molecules of the invention

include the orthologs of the *Arabidopsis* sequences disclosed herein, i.e., the corresponding nucleotide sequences in organisms other than *Arabidopsis*, including, but not limited to, plants other than *Arabidopsis*, preferably cereal plants, e.g., corn, wheat, rye, turfgrass, sorghum, millet, sugarcane, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, tobacco, sugarbeet, or rice. An orthologous gene is a gene from a different species that encodes a product having the same or similar function, e.g., catalyzing the same reaction as a product encoded by a gene from a reference organism. Thus, an ortholog includes polypeptides having less than, e.g., 65% amino acid sequence identity, but which ortholog encodes a polypeptide having the same or similar function. Databases such as GenBank or one found at <http://bioserver.myongji.ac.kr/rjce.html> (for rice) may be employed to identify sequences related to the *Arabidopsis* sequences, e.g., orthologs in cereal crops such as rice, wheat, sunflower or alfalfa. SEQ ID NOs: 6286, 4210 and for example, are the rice promoter and open reading frame for rice peroxidase, the ortholog of the *Arabidopsis* gene comprising SEQ ID NO: 50. SEQ ID NOs: 3311, 5387, 3791 and 5867 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO: 609; SEQ ID NOs: 2699, 4775, 3463, 5539, 3584, 5660, 4451, 6527, 4595 and 6671 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO: 139.

Preferably, the promoters of the invention include a consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, of any one of SEQ ID NOs: 1001-1095, 2137-2661, 4738-6813 or the promoter orthologs thereof, which include the minimal promoter region. Preferably, the nucleotide sequence that includes the promoter region includes at least one copy of a TATA box. Thus, the invention provides plant promoters, including orthologs of *Arabidopsis* promoters corresponding to genes comprising any one of SEQ ID NOs: 1-953. The present invention further provides a composition, an expression cassette or a recombinant vector containing the nucleic acid molecule of the invention, and host cells comprising the expression cassette or vector, e.g., comprising a plasmid. In particular, the present invention provides an expression cassette or a recombinant

vector comprising a promoter of the invention linked to a nucleic acid segment which, when present in a plant, plant cell or plant tissue, results in transcription of the linked nucleic acid segment.

In its broadest sense, the term "substantially similar" when used herein with respect to a nucleotide sequence means that the nucleotide sequence is part of a gene which encodes a polypeptide having substantially the same structure and function as a polypeptide encoded by a gene for the reference nucleotide sequence, e.g., the nucleotide sequence comprises a promoter from a gene that is the ortholog of the gene corresponding to the reference nucleotide sequence, as well as promoter sequences that are structurally related the promoter sequences particularly exemplified herein, i.e., the substantially similar promoter sequences hybridize to the complement of the promoter sequences exemplified herein under high or very high stringency conditions. The term "substantially similar" thus includes nucleotide sequences wherein the sequence has been modified, for example, to optimize expression in particular cells, as well as nucleotide sequences encoding a variant polypeptide comprising one or more amino acid substitutions relative to the (unmodified) polypeptide encoded by the reference sequence, which substitution(s) does not alter the activity of the variant polypeptide relative to the unmodified polypeptide. In its broadest sense, the term "substantially similar" when used herein with respect to polypeptide means that the polypeptide has substantially the same structure and function as the reference polypeptide. The percentage of amino acid sequence identity between the substantially similar and the reference polypeptide is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, up to at least 99%, wherein the reference polypeptide is a polypeptide encoded by an *Arabidopsis* gene comprising any one of SEQ ID NOs:1-953, a *Chenopodium* gene comprising any one of SEQ ID NOs:1954-1966, or a rice gene comprising any one of SEQ ID NOs:2000-2129 and 2662-4737. One indication that two polypeptides are substantially similar to each other, besides having substantially the same function, is

that an agent, e.g., an antibody, which specifically binds to one of the polypeptides, specifically binds to the other.

Sequence comparisons may be carried out using a Smith-Waterman sequence alignment algorithm (see e.g., Waterman (1995) or <http://www>

5 [.uto.usc.edu/software/seqaln/index.html](http://www.uto.usc.edu/software/seqaln/index.html)). The localS program, version 1.16, is preferably used with following parameters: match: 1, mismatch penalty: 0.33, open-gap penalty: 2, extended-gap penalty: 2. Further, a nucleotide sequence that is "substantially similar" to a reference nucleotide sequence hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM
10 EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM
15 EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

Hence, the present invention further provides an expression cassette or a vector containing the nucleic acid molecule comprising an open reading frame of the
20 invention operably linked to a promoter, or comprising a promoter of the invention operably linked to an open reading frame or portion thereof, and the vector may be a plasmid. Such cassettes or vectors, when present in a plant, plant cell or plant tissue result in transcription of the linked nucleic acid fragment in the plant. The expression cassettes or vectors of the invention may optionally include other
25 regulatory sequences, e.g., transcription terminator sequences, operator, repressor binding site, transcription factor binding site, and/or an enhancer and may be contained in a host cell. The expression cassette or vector may augment the genome of a transformed plant or may be maintained extrachromosomally. The expression cassette or vector may further have a Ti plasmid and be contained in an
30 *Agrobacterium tumefaciens* cell; it may be carried on a microparticle, wherein the microparticle is suitable for ballistic transformation of a plant cell; or it may be

contained in a plant cell or protoplast. Further, the expression cassette can be contained in a transformed plant or cells thereof and the plant may be a dicot or a monocot. In particular, the plant may be a cereal plant.

The invention also provides sense and anti-sense nucleic acid molecules corresponding to the open reading frames identified herein as well as their orthologs. Also provided are expression cassettes, e.g., recombinant vectors, and host cells, comprising the nucleic acid molecule of the invention, e.g., one which comprises a nucleotide sequence which encodes a polypeptide the expression of which is altered in response to pathogen infection.

The present invention further provides a method of augmenting a plant genome by contacting plant cells with a nucleic acid molecule of the invention, e.g., one isolatable or obtained from a plant gene encoding a polypeptide that is substantially similar to a polypeptide encoded by an *Arabidopsis*, *Chenopodium* or rice gene comprising a sequence comprising any one of SEQ ID NOs: 1-953, 1954-1966, 2000-2129 or 2662-4737 so as to yield transformed plant cells; and regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the nucleic acid molecule in the cells of the plant. The nucleic acid molecule may be present in the nucleus, chloroplast, mitochondria and/or plastid of the cells of the plant. The present invention also provides a transgenic plant prepared by this method, a seed from such a plant and progeny plants from such a plant including hybrids and inbreds. Preferred transgenic plants are transgenic maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice, wheat, rye, turfgrass, millet, sugarcane, tomato, or potato.

The invention also provides a method of plant breeding, e.g., to prepare a crossed fertile transgenic plant. The method comprises crossing a fertile transgenic plant comprising a particular nucleic acid molecule of the invention with itself or with a second plant, e.g., one lacking the particular nucleic acid molecule, to prepare the seed of a crossed fertile transgenic plant comprising the particular nucleic acid molecule. The seed is then planted to obtain a crossed fertile transgenic plant. The

plant may be a monocot or a dicot. In a particular embodiment, the plant is a cereal plant.

The crossed fertile transgenic plant may have the particular nucleic acid molecule inherited through a female parent or through a male parent. The second
5 plant may be an inbred plant. The crossed fertile transgenic may be a hybrid. Also included within the present invention are seeds of any of these crossed fertile transgenic plants.

The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the
10 parental lines, or selecting appropriate progeny plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of
15 plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic plants according to the invention can be used for the breeding of improved plant lines that for example
20 increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can be obtained that, due to their optimized genetic "equipment", yield harvested product of better quality than products that were not able to tolerate comparable adverse
25 developmental conditions.

The nucleic acid molecules of the invention, their encoded polypeptides and compositions thereof, are: for open reading frames, useful to provide resistance to pathogens to alter expression of a particular gene corresponding to the open reading frame by decreasing or eliminating expression of that plant gene or by
30 overexpressing a particular gene product, and as a diagnostic for the presence or absence of the pathogen by correlating the expression level or pattern of expression

of one or more of the nucleic acid molecules or polypeptides of the invention; and for promoters, useful to alter the expression of a linked open reading frame in response to pathogen infection. As one embodiment of the invention includes isolated nucleic acid molecules that have increased expression in response to

5 pathogen infection, the invention further provides compositions and methods for enhancing resistance to pathogen infection. The compositions of the invention include plant nucleic acid sequences and the amino acid sequences for the polypeptides or partial-length polypeptides encoded thereby which are described herein, or other plant nucleic acid sequences and the amino acid sequences for the

10 polypeptides or partial-length polypeptides encoded thereby which are operably linked to a promoters are useful to provide tolerance or resistance to a plant to a pathogen, preferably by preventing or inhibiting pathogen infection. Methods of the invention involve stably transforming a plant with one or more of at least a portion of these nucleotide sequences which confer tolerance or resistance operably linked

15 to a promoter capable of driving expression of that nucleotide sequence in a plant cell. By "portion" or "fragment", as it relates to a nucleic acid molecule, sequence or segment of the invention, when it is linked to other sequences for expression, is meant a sequence comprising at least 80 nucleotides, more preferably at least 150 nucleotides, and still more preferably at least 400 nucleotides. If not employed for

20 expressing, a "portion" or "fragment" means at least 9, preferably 12, more preferably 15, even more preferably at least 20, consecutive nucleotides, e.g., probes and primers (oligonucleotides), corresponding to the nucleotide sequence of the nucleic acid molecules of the invention. By "resistant" is meant a plant which exhibits substantially no phenotypic changes as a consequence of infection with the

25 pathogen. By "tolerant" is meant a plant which, although it may exhibit some phenotypic changes as a consequence of infection, does not have a substantially decreased reproductive capacity or substantially altered metabolism.

A method of combating a pathogen in an agricultural crop is also provided. The method comprises introducing to a plant, plant cell, or plant tissue an

30 expression cassette comprising a nucleic acid molecule of the invention comprising an open reading frame so as to yield a transformed differentiated plant, transformed

cell or transformed tissue. Transformed cells or tissue can be regenerated to provide a transformed differentiated plant. The transformed differentiated plant preferably expresses the nucleic acid molecule in an amount that confers resistance to the transformed plant to pathogen infection relative to a corresponding nontransformed plant. The present invention also provides a transformed plant prepared by the method, progeny and seed thereof. Examples of plant viruses which may be combated by the present invention include single stranded RNA viruses (with and without envelope), double stranded RNA viruses, and single and double stranded DNA viruses such as (but not limited to) tobacco mosaic virus, cucumber mosaic virus, turnip mosaic virus, turnip vein clearing virus, oilseed rape mosaic virus, tobacco rattle virus, pea enation mosaic virus, barley stripe mosaic virus, potato viruses X and Y, carnation latent virus, beet yellows virus, maize chlorotic virus, tobacco necrosis virus, turnip yellow mosaic virus, tomato bushy stunt virus, southern bean mosaic virus, barley yellow dwarf virus, tomato spotted wilt virus, lettuce necrotic yellows virus, wound tumor virus, maize streak virus, and cauliflower mosaic virus. Other pathogens within the scope of the invention include, but are not limited to, fungi such as *Cochliobolus carbonum*, *Phytophthora infestans*, *Phytophthora sojae*, *Colletesichum*, *Melampsora lini*, *cladosporium fulvum*, *Heminthosporium maydia*, *Peronospora parasitica*, *Puccinia sorghi*, and *Puccinia polysora*; bacteria such as *Phynchosporium secalis*, *Pseudomonas glycinea*, *Xanthomonas oryzae* and, *Fusarium oxyaporium*; and nematodes such as *Globodera rostochiensis*.

For example, the invention provides a nucleic acid molecule comprising a plant nucleotide sequence comprising at least a portion of a key effector gene(s) responsible for host resistance to particular pathogens. To provide resistance or tolerance to a pathogen in a plant, this sequence may be overexpressed individually, in the sense or antisense orientation, or in combination with other sequences to confer improved disease resistance or tolerance to a plant relative to a plant that does not comprise and/or express the sequence. The overexpression may be constitutive, or it may be preferable to express the effector gene(s) in a tissue-specific manner or from an inducible promoter including a promoter which is

responsive to external stimuli, such as chemical application, or to pathogen infection, e.g., so as to avoid possible deleterious effects on plant growth if the effector gene(s) was constitutively expressed. In one embodiment of the invention, the promoter employed may be one that is rapidly and transiently and/or highly transcribed after pathogen infection.

A transformed (transgenic) plant of the invention includes plants, for example, a plant the cells of which have an expression cassette of the invention, i.e., an expression cassette having a polynucleotide of the invention operatively linked to an open reading frame, or, the genome of which is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields, e.g., under conditions of pathogen infection, and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and probes.

For example, the invention includes a pathogen, e.g., virus, tolerant or resistant plant and seed thereof having stably integrated and expressed within its genome, a nucleic acid molecule of the invention. The normal fertile transformed (transgenic) plant may be selfed to yield a substantially homogenous line with respect to viral resistance or tolerance. Individuals of the line, or the progeny thereof, may be crossed with plants which optionally exhibit the trait. In a particular embodiment of the method, the selfing and selection steps are repeated at least five times in order to obtain the homogenous (isogenic) line. Thus, the invention also provides transgenic plants and the products of the transgenic plants.

The invention further includes a nucleotide sequence which is complementary to one (hereinafter "test" sequence) which hybridizes under low, moderate or stringent conditions with the nucleic acid molecules of the invention as well as RNA which is encoded by the nucleic acid molecule. When the hybridization is performed under stringent conditions, either the test or nucleic acid molecule of invention is preferably supported, e.g., on a membrane or DNA chip. Thus, either a denatured test or nucleic acid molecule of the invention is preferably

first bound to a support and hybridization is effected for a specified period of time at a temperature of, e.g., between 55 and 70°C, in double strength citrate buffered saline (SC) containing 0.1% SDS followed by rinsing of the support at the same temperature but with a buffer having a reduced SC concentration. Depending upon
5 the degree of stringency required such reduced concentration buffers are typically single strength SC containing 0.1% SDS, half strength SC containing 0.1% SDS and one-tenth strength SC containing 0.1% SDS.

The invention further provides a method to identify an open reading frame in the genome of a plant cell, the expression of which is altered by pathogen infection
10 of that cell. The method comprises contacting a solid substrate comprising a plurality of samples comprising isolated plant nucleic acid of a probe comprising plant nucleic acid, e.g., cRNA, isolated from a pathogen infected plant so as to form a complex. Each individual sample comprises one or more nucleic acid sequences (e.g., oligonucleotides) corresponding to at least a portion of a plant gene. The
15 method may be employed with nucleic acid samples and probes from any organism, e.g., any prokaryotic or eukaryotic organism. Preferably, the nucleic acid sample and probes are from a plant, such as a dicot or monocot. More preferably the nucleic acid samples and probes are from a cereal plant. Even more preferably the nucleic acids and probes are from a crop plant. A second plurality of samples on a
20 solid substrate, i.e., a DNA chip, each comprising a plurality of samples comprising isolated plant nucleic acid is contacted with a probe comprising plant nucleic acid isolated from an uninfected or infected control (mutant) plant so as to form a complex. Then complex formation between the samples and probes comprising nucleic acid from infected or control cells compared. For example, potato virus X,
25 tobacco mosaic virus, tobnavirus, cucumber mosaic virus and geminivirus are known to infect *Arabidopsis*. Thus, *Arabidopsis* genes, the expression of which is altered in response to infection by any of these viruses, can be identified. Regions that are 5' to the start codon for the gene can then be identified and/or isolated.

The invention further provides a method for identifying a plant cell infected
30 with a pathogen. The method comprises contacting nucleic acid obtained from a plant cell suspected of being infected with a pathogen with oligonucleotides

corresponding to a portion of a plurality of sequences selected from SEQ ID NOs: 1-953, 1954-1966, 2000-2129 or 2662-4737 under conditions effective to amplify those sequences. Then the presence of the amplified product is detected or determined. The presence of two or more amplified products, e.g., in an amount that
5 is different than the amount of the corresponding amplified products from an uninfected plant, each corresponding to two or more SEQ ID NOs: 1-953, 1954-1966, 2000-2129 or 2662-4737 is indicative of pathogen infection.

The invention further provides a method for identifying a plant cell infected with a pathogen. The method comprises contacting a protein sample obtained from
10 a plant cell suspected of being infected with a pathogen with an agent that specifically binds a polypeptide encoded by an open reading frame comprising SEQ ID NOs: 1-953, 1954-1966, 2000-2129 or 2662-4737 so as to form a complex. Then the presence or amount of complex formation is detected or determined.

The invention provides an additional method for identifying a plant cell
15 infected with a pathogen. The method comprises hybridizing a probe selected from SEQ ID NOs: 1-953, 1954-1966, 2000-2129 or 2662-4737 to nucleic acid obtained from a plant cell suspected of being infected with a pathogen. The amount of the probe hybridized to nucleic acid obtained from a cell suspected of being infected with a virus is compared to hybridization of the probe to nucleic acid isolated from
20 an uninfected cell. A change in the amount of at least two probes that hybridize to nucleic acid isolated from a cell suspected of being infected by a virus relative to hybridization of at least two probes to nucleic acid isolated from an uninfected cell is indicative of viral infection.

A method to shuffle the nucleic acids of the invention is provided. This
25 method involves fragmentation of a nucleic acid corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-953, 1954-1966, 2000-2129 or 2662-4737, the orthologs thereof, and the corresponding genes, followed by religation. This method allows for the production of polypeptides having altered activity relative to the native form of the polypeptide. Accordingly, the invention provides cells and
30 transgenic plants containing nucleic acid segments produced through shuffling that

encode polypeptides having altered activity relative to the corresponding native polypeptide.

A computer readable medium, e.g., a magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory, or bubble memory, containing the nucleic acid sequences of the invention as well as methods of use for the computer readable medium are provided. For example, a computer readable medium can contain a nucleic acid molecule that has at least 70% nucleic acid sequence identity to SEQ ID NOs: 50, 139, 609, 4210, 6286, 3311, 5387, 3791, 5867, 2699, 4775, 3463, 5539, 3584, 5660, 4451, 6527, 4595, 6671 or the complement thereof. This medium allows a nucleic acid segment corresponding to a nucleic acid sequence listed in SEQ ID NOs:1-953, 1001-1095, 1954-1966, 2000-2129 or 2662-4737 to be used as a reference sequence to search against databases. This medium also allows for computer-based manipulation of a nucleic acid sequence corresponding to a nucleic acid sequence listed in SEQ ID NOs :1-953, 1001-1095, 1954-1966, 2000-2129 or 2662-4737, and the corresponding gene and polypeptide encoded by the nucleic acid sequence.

The invention also provides a method for marker-assisted breeding to select for plants having altered resistance to a pathogen. The method involves contacting plant DNA or cDNA with a probe corresponding to a nucleic acid sequence listed in SEQ ID NOs. 1-953, 1954-1966, 2000-2129 or 2662-4737, the orthologs thereof, and the corresponding genes, or a portion thereof which hybridizes under moderate stringency conditions to a gene corresponding to one of of SEQ ID Nos. 1-953, 1954-1966, 2000-2129 or 2662-4737 so as to form a duplex and detecting or determining the presence or amount of the duplex. The amount or presence of the duplex is indicative of the presence of a gene, the expression of which alters the resistance of the plant to a pathogen.

Therefore, another embodiment of the present invention provides a method of using known inducers or inhibitors of genes identified as being important in plant-pathogen interactions to induce genes that are important in resistance, or to inhibit genes that are downregulated in resistance.

Thus, some of the isolated nucleic acid molecules of the invention are useful in a method of combating a pathogen in an agricultural crop. The method comprises introducing to a plant an expression cassette comprising a nucleic acid molecule of the invention so as to yield a transformed differentiated plant. The transformed differentiated plant expresses the nucleic acid molecule in an amount that confers resistance to the transformed plant to infection relative to a corresponding nontransformed plant.

Detailed Description of the Invention

I. Definitions

The term "gene" is used broadly to refer to any segment of nucleic acid associated with a biological function. Thus, genes include coding sequences and/or the regulatory sequences required for their expression. For example, gene refers to a nucleic acid fragment that expresses mRNA or functional RNA, or encodes a specific protein, and which includes regulatory sequences. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

The term "native" or "wild type" gene refers to a gene that is present in the genome of an untransformed cell, i.e., a cell not having a known mutation.

A "marker gene" encodes a selectable or screenable trait.

The term "chimeric gene" refers to any gene that contains 1) DNA sequences, including regulatory and coding sequences, that are not found together in nature, or 2) sequences encoding parts of proteins not naturally adjoined, or 3) parts of promoters that are not naturally adjoined. Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences that are derived from different sources, or comprise regulatory sequences and coding sequences derived from the same source, but arranged in a manner different from that found in nature.

A "transgene" refers to a gene that has been introduced into the genome by transformation and is stably maintained. Transgenes may include, for example,

genes that are either heterologous or homologous to the genes of a particular plant to be transformed. Additionally, transgenes may comprise native genes inserted into a non-native organism, or chimeric genes. The term "endogenous gene" refers to a native gene in its natural location in the genome of an organism. A "foreign" gene
5 refers to a gene not normally found in the host organism but that is introduced by gene transfer.

An "oligonucleotide" corresponding to a nucleotide sequence of the invention, e.g., for use in probing or amplification reactions, may be about 30 or fewer nucleotides in length (e.g., 9, 12, 15, 18, 20, 21 or 24, or any number between
10 9 and 30). Generally specific primers are upwards of 14 nucleotides in length. For optimum specificity and cost effectiveness, primers of 16 to 24 nucleotides in length may be preferred. Those skilled in the art are well versed in the design of primers for use processes such as PCR. If required, probing can be done with entire restriction fragments of the gene disclosed herein which may be 100's or even 1000's
15 of nucleotides in length.

The terms "protein," "peptide" and "polypeptide" are used interchangeably herein.

The nucleotide sequences of the invention can be introduced into any plant. The genes to be introduced can be conveniently used in expression cassettes for
20 introduction and expression in any plant of interest. Such expression cassettes will comprise the transcriptional initiation region of the invention linked to a nucleotide sequence of interest. Preferred promoters include constitutive, tissue-specific, developmental-specific, inducible and/or viral promoters. Such an expression cassette is provided with a plurality of restriction sites for insertion of the gene of
25 interest to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes. The cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of interest, and a transcriptional and translational termination region functional in plants. The termination region may be native with
30 the transcriptional initiation region, may be native with the DNA sequence of interest, or may be derived from another source. Convenient termination regions are

available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also, Guerineau et al., 1991; Proudfoot, 1991; Sanfacon et al., 1991; Mogen et al., 1990; Munroe et al., 1990; Ballas et al., 1989; Joshi et al., 1987.

5 "Coding sequence" refers to a DNA or RNA sequence that codes for a specific amino acid sequence and excludes the non-coding sequences. It may constitute an "uninterrupted coding sequence", i.e., lacking an intron, such as in a cDNA or it may include one or more introns bounded by appropriate splice junctions. An "intron" is a sequence of RNA which is contained in the primary
10 transcript but which is removed through cleavage and re-ligation of the RNA within the cell to create the mature mRNA that can be translated into a protein.

The terms "open reading frame" and "ORF" refer to the amino acid sequence encoded between translation initiation and termination codons of a coding sequence. The terms "initiation codon" and "termination codon" refer to a unit of three
15 adjacent nucleotides ('codon') in a coding sequence that specifies initiation and chain termination, respectively, of protein synthesis (mRNA translation).

A "functional RNA" refers to an antisense RNA, ribozyme, or other RNA that is not translated.

The term "RNA transcript" refers to the product resulting from RNA
20 polymerase catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complementary copy of the DNA sequence, it is referred to as the primary transcript or it may be a RNA sequence derived from posttranscriptional processing of the primary transcript and is referred to as the mature RNA. "Messenger RNA" (mRNA) refers to the RNA that is without introns and that can be translated into
25 protein by the cell. "cDNA" refers to a single- or a double-stranded DNA that is complementary to and derived from mRNA.

"Regulatory sequences" and "suitable regulatory sequences" each refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence
30 the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences include enhancers, promoters, translation leader

sequences, introns, and polyadenylation signal sequences. They include natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. As is noted above, the term "suitable regulatory sequences" is not limited to promoters.

5 "5' non-coding sequence" refers to a nucleotide sequence located 5' (upstream) to the coding sequence. It is present in the fully processed mRNA upstream of the initiation codon and may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency (Turner et al., 1995).

10 "3' non-coding sequence" refers to nucleotide sequences located 3' (downstream) to a coding sequence and include polyadenylation signal sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The use of different 3' non-coding sequences is exemplified by
15 Ingelbrecht et al., 1989.

 The term "translation leader sequence" refers to that DNA sequence portion of a gene between the promoter and coding sequence that is transcribed into RNA and is present in the fully processed mRNA upstream (5') of the translation start codon. The translation leader sequence may affect processing of the primary
20 transcript to mRNA, mRNA stability or translation efficiency.

 The term "mature" protein refers to a post-translationally processed polypeptide without its signal peptide. "Precursor" protein refers to the primary product of translation of an mRNA. "Signal peptide" refers to the amino terminal extension of a polypeptide, which is translated in conjunction with the polypeptide
25 forming a precursor peptide and which is required for its entrance into the secretory pathway. The term "signal sequence" refers to a nucleotide sequence that encodes the signal peptide.

 The term "intracellular localization sequence" refers to a nucleotide sequence that encodes an intracellular targeting signal. An "intracellular targeting
30 signal" is an amino acid sequence that is translated in conjunction with a protein and directs it to a particular sub-cellular compartment. "Endoplasmic reticulum (ER)

stop transit signal" refers to a carboxy-terminal extension of a polypeptide, which is translated in conjunction with the polypeptide and causes a protein that enters the secretory pathway to be retained in the ER. "ER stop transit sequence" refers to a nucleotide sequence that encodes the ER targeting signal. Other intracellular
5 targeting sequences encode targeting signals active in seeds and/or leaves and vacuolar targeting signals.

"Pathogen" as used herein includes but is not limited to bacteria, fungi, yeast, oomycetes and virus, e.g., American wheat striate mosaic virus mosaic (AWSMV), barley stripe mosaic virus (BSMV), barley yellow dwarf virus (BYDV),
10 Brome mosaic virus (BMV), cereal chlorotic mottle virus (CCMV), corn chlorotic vein banding virus (CCVBV), maize chlorotic mottle virus (MCMV), maize dwarf mosaic virus (MDMV), A or B, wheat streak mosaic virus (WSMV), cucumber mosaic virus (CMV), cynodon chlorotic streak virus (CCSV), Johnsongrass mosaic virus (JGMV), maize bushy stunt or mycoplasma-like organism (NJILO), maize
15 chlorotic dwarf virus (MCDV), maize chlorotic mottle virus (MCMV), maize dwarf mosaic virus (MDMV) strains A, D, E and F, maize leaf fleck virus (MLFV), maize line virus (NELV), maize mosaic virus (MMV), maize mottle and chlorotic stunt virus, maize pellucid ringspot virus (MPRV), maize raya gruesa virus (MRGV), maize rayado fino virus (MRFV), maize red leaf and red stripe virus (MRSV), maize
20 ring mottle virus (MRMV), maize rio cuarto virus (MRCV), maize rough dwarf virus (MRDV), maize sterile stunt virus (strains of barley yellow striate virus), maize streak virus (MSV), maize chlorotic stripe, maize hoja Maize stripe virus blanca, maize stunting virus, maize tassel abortion virus (MTAV), maize vein enation virus (MVEV), maize wallaby ear virus (MAVEV), maize white leaf virus,
25 maize white line mosaic virus (NTVVLMV), millet red leaf virus (NMV), Northern cereal mosaic virus (NCMV), oat pseudorosette virus, oat sterile dwarf virus (OSDV), rice black-streaked dwarf virus (RBSDV), rice stripe virus (RSV), sorghum mosaic virus (SrMV), formerly sugarcane mosaic virus (SCMV) strains H, I and M, sugarcane Fiji disease virus (FDV), sugarcane mosaic virus (SCMV)
30 strains A, B, D, E, SC, BC, Sabi and NM vein enation virus, and wheat spot mosaic virus (WSMV).

Bacterial pathogens include but are not limited to *Pseudomonas avenae* subsp. *avenae*, *Xanthomonas campestris* pv. *holcicola*, *Enterobacter dissolvens*, *Erwinia dissolvens*, *Erwinia carotovora* subsp. *carotovora*, *Erwinia chrysanthemi* pv. *zeae*, *Pseudomonas andropogonis*, *Pseudomonas syringae* pv. *coronafaciens*,
 5 *Clavibacter michiganensis* subsp., *Corynebacterium michiganense* pv. *nebraskense*, *Pseudomonas syringae* pv. *syringae*, Hemiparasitic bacteria (see under fungi), *Bacillus subtilis*, *Erwinia stewartii*, and *Spiroplasma kunkelii*.

Fungal pathogens include but are not limited to *Collelotrichum graminicola*, *Glomerella graminicola* Politis, *Glomerella lucumanensis*, *Aspergillus flavus*,
 10 *Rhizoctonia solani* Kuhn, *Thanatephorus cucumeris*, *Acremonium strictum* W. Gams, *Cephalosporium acremonium* Auct. non Corda *Lasiodiplodia theobromae* = *BoIr odiplochia y theobromae* Borde blanco *Marasmiellus* sp., *Physoderma maydis*, *Cephalosporium Corticium sasakii*, *Curvularia clavata*, *C. maculans*, *Cochhobolus eragrostidis*, *Curvularia inaequahs*, *C. intermedia*
 15 (teleomorph *Cochhobolus intermedius*), *Curvularia lunata* (teleomorph: *Cochliobolus lunatus*), *Curvularia pallescens* (teleomorph - *Cochliobolus pallescens*), *Curvularia senegalensis*, *C. luberculata* (teleomorph: *Cochliobolus tuberculatus*), *Didymella exitalis* *Diplodiaftumenti* (teleomorph - *Botryosphaeria festucae*), *Diplodia maydis* = *Stenocarpella maydis*, *Stenocarpella*
 20 *macrospora* = *Diplodia macrospora*, *Sclerophthora rayssiae* var. *zeae*, *Sclerophthora macrospora* = *Sclerospora macrospora*, *Sclerospora graminicola*, *Peronosclerospora maydis* = *Sclerospora maydis*, *Peronosclerospora philippinensis*, *Sclerospora philippinensis*, *Peronosclerospora sorghi* = *Sclerospora sorghi*, *Peronosclerospora spontanea* = *Sclerospora spontanea*, *Peronosclerospora*
 25 *sacchari* = *Sclerospora sacchari*, *Nigrospora oryzae* (teleomorph: *Khuskia oryzae*) *A. Iternaria alternata* = *A. tenuis*, *Aspergillus glaucus*, *A. niger*, *Aspergillus spp.*, *Botrytis cinerea*, *Cunninghamella* sp., *Curvularia pallescens*, *Doratomyces slemonitis* = *Cephalotrichum slemonitis*, *Fusarium culmorum*, *Gonatobotrys simplex*, *Pithomyces maydicus*, *Rhizopus microsporus* Tiegh., *R. stolonifer* = *R.*
 30 *nigricans*, *Scopulariopsis brumptii*, *Claviceps gigantea* (anamorph: *Sphacelia* sp.) *Aureobasidium zeae* = *Kabatiella zeae*, *Fusarium subglutinans* = *F. moniliforme*

- var. *subglutinans*, *Fusarium moniliforme*, *Fusarium avenaceum* (teleomorph - *Gibberella avenacea*), *Botryosphaeria zeae* = *Physalospora zeae* (anamorph: *Allacrophoma zeae*), *Cercospora sorghi* = *C. sorghi* var. *maydis*, *Helminthosporium pedicellatum* (teleomorph: *Selosphaeriapedicellata*), *Cladosporium cladosporioides*
- 5 = *Hormodendrum cladosporioides*, *C. herbarum* (teleomorph - *Mycosphaerella tassiana*), *Cephalosporium maydis*, *A. Iternaria alternata*, *A. scochyta maydis*, *A. tritici*, *A. zeicola*, *Bipolaris victoriae*, *Helminthosporium victoriae* (teleomorph *Cochhoholus victoriae*), *C sativus* (anamorph: *Bipolaris sorokiniana* = *H. sorokinianum* = *H. sativum*), *Epicoccum nigrum*, *Exserohilum prolatum* =
- 10 *Drechslera prolata* (teleomorph: *Setosphaeriaprolata*), *Graphium penicillioides*, *Leptosphaeria maydis*, *Leptothyrium zeae*, *Ophiosphaerella herpotricha* (anamorph - *Scolecosporiella* sp.), *Pataphaeosphaeria michotii*, *Phoma* sp., *Septoria zeae*, *S. zeicola*, *S. zeina* *Setosphaeria turcica*, *Exserohilum turcicum* = *Helminthosporium furcicum*, *Cochhoholus carbonum*, *Bipolaris zeicola* = *Helminthosporium*
- 15 *carhonum*, *Penicilhum* spp., *P. chrysogenum*, *P. expansum*, *P. oxalicum*, *Phaeocystostroma ambiguum*, *Phaeocylosporella zeae*, *Phaeosphaeria maydis* = *Sphaerulina maydis*, *Botryosphaeria festucae* = *Physalospora zeicola* (anamorph: *Diplodiaftumenfi*), *Herniparasitic bacteria and fungi* *Pyrenochaeta Phoma terrestris* = *Pyrenochaeta terrestris*, *Pythium* spp., *P. arrhenomanes*, *P.*
- 20 *graminicola*, *Pythium aphanidermatum* = *P. hutleri* L., *Rhizoctonia zeae* (teleomorph: *Waitea circinata*), *Rhizoctonia solani*, minor *A Iternaria alternata*, *Cercospora sorghi*, *Dictochaetaftrtilis*, *Fusarium acuminatum* (teleomorph *Gihherella acuminata*), *E. equiseti* (teleomorph: *G. intricans*), *E. oxysporum*, *E. pallidoroseum*, *E. poae*, *E. roseum*, *G. cyanogena* (anamorph: *E. sulphureum*),
- 25 *Microdochium holleyi*, *Mucor* sp., *Periconia circinata*, *Phytophthora cactorum*, *P. drechsleri*, *P. nicotianae* var. *parasitica*, *Rhizopus arrhizus*, *Setosphaeria rostrata*, *Exserohilum rostratum* = *Helminthosporium rostratum*, *Puccinia sorghi*, *Physopella pallescens*, *P. zeae*, *Sclerotium rofsii* Sacc. (teleomorph- *Athelia rotfsii*), *Bipolaris sorokiniana*, *B. zeicola* = *Helminthosporium carbonum*, *Diplodia maydis*,
- 30 *Exserohilum pedicillatum*, *Exserohilum furcicum* = *Helminthosporium turcicum*, *Fusarium avenaceum*, *E. culmorum*, *E. moniliforme*, *Gibberella zeae* (anamorph - *E.*

- graminearum*), *Macrophominaphaseolina*, *Penicillium spp.*, *Phomopsis sp.*, *Pythium spp.*, *Rhizoctonia solani*, *R. zae*, *Sclerotium rolfsii*, *Spicaria sp.*, *Selenophoma sp.*, *Gaeumannomyces graminis*, *Myrothecium gramineum*, *Monascus purpureus*, *M. ruber* Smut, *Ustilago zae* = *U. maydis* Smut, *Ustilaginoidea virens*
- 5 Smut, *Sphacelotheca reiliana* = *Sporisorium holci*, *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis* = *Helminthosporium maydis*), *Stenocarpella macrospora* = *Diplodia macrospora*, *Cercospora sorghi*, *Fusarium episphaeria*, *E. merismoides*, *F. oxysporum* Schlechtend, *E. poae*, *E. roseum*, *E. solani* (teleomorph: *Nectria haematococca*), *F. tricinctum*, *Mariannaea elegans*, *Mucor sp.*,
- 10 *Rhopoglyphus zae*, *Spicaria sp.*, *Aspergillus spp.*, *Penicillium spp.*, *Trichoderma viride* = *T. lignorum* teleomorph: *Hypocrea sp.*, *Stenocarpella maydis* = *Diplodia zae*, *Ascochyta ischaemi*, *Phyllosticta maydis* (telomorph: *Mycosphaerella zae-maydis*), and *Gloeocercospora sorghi*.

- Parasitic nematodes include but are not limited to *Awl Dolichodorus spp.*, *D.*
- 15 *heterocephalus* Bulb and stem (Europe), *Ditylenchus dipsaci* Burrowing Radopholus similis Cyst Heterodera avenae, *H. zae*, *Punctodera chalcensis* Dagger *Xiphinema spp.*, *X. americanum*, *X. mediterraneum* False root-knot *Nacobbus dorsalis* Lance, *Columbia Hoplolaimus columbus* Lance *Hoplolaimus spp.*, *H. galeatus* Lesion *Pratylenchus spp.*, *P. brachyurus*, *P. crenatus*, *P. hexincisus*, *P. neglectus*, *P.*
- 20 *penetrans*, *P. scribneri*, *P. thornei*, *P. zae* Needle Longidorus spp., *L. breviannulatus* Ring *Criconebella spp.*, *C. ornata* Root-knot *Meloidogyne spp.*, *M. chitwoodi*, *M. incognita*, *M. javanica* Spiral *Helicotylenchus spp.*, *Belonolaimus spp.*, *B. longicaudatus* Stubby-root *Paratrichodorus spp.*, *P. christiei*, *P. minor*, *Ouinisulcius aculus*, and *Trichodorus spp.*

- 25 "Promoter" refers to a nucleotide sequence, usually upstream (5') to its coding sequence, which controls the expression of the coding sequence by providing the recognition for RNA polymerase and other factors required for proper transcription. "Promoter" includes a minimal promoter that is a short DNA sequence comprised of a TATA box and other sequences that serve to specify the site of
- 30 transcription initiation, to which regulatory elements are added for control of expression. "Promoter" also refers to a nucleotide sequence that includes a minimal

promoter plus regulatory elements that is capable of controlling the expression of a coding sequence or functional RNA. This type of promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an "enhancer" is a DNA sequence which can stimulate promoter activity and may be an innate element of the promoter or a heterologous element inserted to enhance the level or tissue specificity of a promoter. It is capable of operating in both orientations (normal or flipped), and is capable of functioning even when moved either upstream or downstream from the promoter. Both enhancers and other upstream promoter elements bind sequence-specific DNA-binding proteins that mediate their effects. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even be comprised of synthetic DNA segments. A promoter may also contain DNA sequences that are involved in the binding of protein factors which control the effectiveness of transcription initiation in response to physiological or developmental conditions.

The "initiation site" is the position surrounding the first nucleotide that is part of the transcribed sequence, which is also defined as position +1. With respect to this site all other sequences of the gene and its controlling regions are numbered. Downstream sequences (i.e., further protein encoding sequences in the 3' direction) are denominated positive, while upstream sequences (mostly of the controlling regions in the 5' direction) are denominated negative.

Promoter elements, particularly a TATA element, that are inactive or that have greatly reduced promoter activity in the absence of upstream activation are referred to as "minimal or core promoters." In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription. A "minimal or core promoter" thus consists only of all basal elements needed for transcription initiation, e.g., a TATA box and/or an initiator.

"Constitutive expression" refers to expression using a constitutive or regulated promoter. "Conditional" and "regulated expression" refer to expression controlled by a regulated promoter.

"Constitutive promoter" refers to a promoter that is able to express the open

reading frame (ORF) that it controls in all or nearly all of the plant tissues during all or nearly all developmental stages of the plant. Each of the transcription-activating elements do not exhibit an absolute tissue-specificity, but mediate transcriptional activation in most plant parts at a level of $\geq 1\%$ of the level reached in the part of the plant in which transcription is most active.

"Regulated promoter" refers to promoters that direct gene expression not constitutively, but in a temporally- and/or spatially-regulated manner, and includes both tissue-specific and inducible promoters. It includes natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. Different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. New promoters of various types useful in plant cells are constantly being discovered, numerous examples may be found in the compilation by Okamuro et al. (1989). Typical regulated promoters useful in plants include but are not limited to safener-inducible promoters, promoters derived from the tetracycline-inducible system, promoters derived from salicylate-inducible systems, promoters derived from alcohol-inducible systems, promoters derived from glucocorticoid-inducible system, promoters derived from pathogen-inducible systems, and promoters derived from ecdysone-inducible systems.

"Tissue-specific promoter" refers to regulated promoters that are not expressed in all plant cells but only in one or more cell types in specific organs (such as leaves or seeds), specific tissues (such as embryo or cotyledon), or specific cell types (such as leaf parenchyma or seed storage cells). These also include promoters that are temporally regulated, such as in early or late embryogenesis, during fruit ripening in developing seeds or fruit, in fully differentiated leaf, or at the onset of senescence.

"Inducible promoter" refers to those regulated promoters that can be turned on in one or more cell types by an external stimulus, such as a chemical, light, hormone, stress, or a pathogen.

"Operably-linked" refers to the association of nucleic acid sequences on single nucleic acid fragment so that the function of one is affected by the other. For

example, a regulatory DNA sequence is said to be "operably linked to" or "associated with" a DNA sequence that codes for an RNA or a polypeptide if the two sequences are situated such that the regulatory DNA sequence affects expression of the coding DNA sequence (i.e., that the coding sequence or functional RNA is under the transcriptional control of the promoter). Coding sequences can be operably-linked to regulatory sequences in sense or antisense orientation.

"Expression" refers to the transcription and/or translation of an endogenous gene, ORF or portion thereof, or a transgene in plants. For example, in the case of antisense constructs, expression may refer to the transcription of the antisense DNA only. In addition, expression refers to the transcription and stable accumulation of sense (mRNA) or functional RNA. Expression may also refer to the production of protein.

"Specific expression" is the expression of gene products which is limited to one or a few plant tissues (spatial limitation) and/or to one or a few plant developmental stages (temporal limitation). It is acknowledged that hardly a true specificity exists: promoters seem to be preferably switch on in some tissues, while in other tissues there can be no or only little activity. This phenomenon is known as leaky expression. However, with specific expression in this invention is meant preferable expression in one or a few plant tissues.

The "expression pattern" of a promoter (with or without enhancer) is the pattern of expression levels which shows where in the plant and in what developmental stage transcription is initiated by said promoter. Expression patterns of a set of promoters are said to be complementary when the expression pattern of one promoter shows little overlap with the expression pattern of the other promoter. The level of expression of a promoter can be determined by measuring the 'steady state' concentration of a standard transcribed reporter mRNA. This measurement is indirect since the concentration of the reporter mRNA is dependent not only on its synthesis rate, but also on the rate with which the mRNA is degraded. Therefore, the steady state level is the product of synthesis rates and degradation rates.

The rate of degradation can however be considered to proceed at a fixed rate when the transcribed sequences are identical, and thus this value can serve as a

measure of synthesis rates. When promoters are compared in this way techniques available to those skilled in the art are hybridization S1-RNase analysis, northern blots and competitive RT-PCR. This list of techniques in no way represents all available techniques, but rather describes commonly used procedures used to
5 analyze transcription activity and expression levels of mRNA.

The analysis of transcription start points in practically all promoters has revealed that there is usually no single base at which transcription starts, but rather a more or less clustered set of initiation sites, each of which accounts for some start points of the mRNA. Since this distribution varies from promoter to promoter the
10 sequences of the reporter mRNA in each of the populations would differ from each other. Since each mRNA species is more or less prone to degradation, no single degradation rate can be expected for different reporter mRNAs. It has been shown for various eukaryotic promoter sequences that the sequence surrounding the initiation site ('initiator') plays an important role in determining the level of RNA
15 expression directed by that specific promoter. This includes also part of the transcribed sequences. The direct fusion of promoter to reporter sequences would therefore lead to suboptimal levels of transcription.

A commonly used procedure to analyze expression patterns and levels is through determination of the 'steady state' level of protein accumulation in a cell.
20 Commonly used candidates for the reporter gene, known to those skilled in the art are β -glucuronidase (GUS), chloramphenicol acetyl transferase (CAT) and proteins with fluorescent properties, such as green fluorescent protein (GFP) from *Aequora victoria*. In principle, however, many more proteins are suitable for this purpose, provided the protein does not interfere with essential plant functions. For
25 quantification and determination of localization a number of tools are suited. Detection systems can readily be created or are available which are based on, e.g., immunochemical, enzymatic, fluorescent detection and quantification. Protein levels can be determined in plant tissue extracts or in intact tissue using *in situ* analysis of protein expression.

30 Generally, individual transformed lines with one chimeric promoter reporter construct will vary in their levels of expression of the reporter gene. Also frequently

observed is the phenomenon that such transformants do not express any detectable product (RNA or protein). The variability in expression is commonly ascribed to 'position effects', although the molecular mechanisms underlying this inactivity are usually not clear.

5 The term "average expression" is used here as the average level of expression found in all lines that do express detectable amounts of reporter gene, so leaving out of the analysis plants that do not express any detectable reporter mRNA or protein.

 "Root expression level" indicates the expression level found in protein
10 extracts of complete plant roots. Likewise, leaf, and stem expression levels, are determined using whole extracts from leaves and stems. It is acknowledged however, that within each of the plant parts just described, cells with variable functions may exist, in which promoter activity may vary.

 "Non-specific expression" refers to constitutive expression or low level,
15 basal ('leaky') expression in nondesired cells or tissues from a 'regulated promoter'.

 "Altered levels" refers to the level of expression in transgenic organisms that differs from that of normal or untransformed organisms.

 "Overexpression" refers to the level of expression in transgenic cells or organisms that exceeds levels of expression in normal or untransformed
20 (nontransgenic) cells or organisms.

 "Antisense inhibition" refers to the production of antisense RNA transcripts capable of suppressing the expression of protein from an endogenous gene or a transgene.

 "Co-suppression" and "transwitch" each refer to the production of sense
25 RNA transcripts capable of suppressing the expression of identical or substantially similar transgene or endogenous genes (U.S. Patent No. 5,231,020).

 "Gene silencing" refers to homology-dependent suppression of viral genes, transgenes, or endogenous nuclear genes. Gene silencing may be transcriptional, when the suppression is due to decreased transcription of the affected genes, or post-
30 transcriptional, when the suppression is due to increased turnover (degradation) of

RNA species homologous to the affected genes (English et al., 1996). Gene silencing includes virus-induced gene silencing (Ruiz et al. 1998).

"Silencing suppressor" gene refers to a gene whose expression leads to counteracting gene silencing and enhanced expression of silenced genes. Silencing suppressor genes may be of plant, non-plant, or viral origin. Examples include, but are not limited to HC-Pro, P1-HC-Pro, and 2b proteins. Other examples include one or more genes in TGMV-B genome.

The terms "heterologous DNA sequence," "exogenous DNA segment" or "heterologous nucleic acid," as used herein, each refer to a sequence that originates from a source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the terms refer to a DNA segment that is foreign or heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides. A "homologous" DNA sequence is a DNA sequence that is naturally associated with a host cell into which it is introduced.

"Homologous to" in the context of nucleotide sequence identity refers to the similarity between the nucleotide sequence of two nucleic acid molecules or between the amino acid sequences of two protein molecules. Estimates of such homology are provided by either DNA-DNA or DNA-RNA hybridization under conditions of stringency as is well understood by those skilled in the art (as described in Haines and Higgins (eds.), Nucleic Acid Hybridization, IRL Press, Oxford, U.K.), or by the comparison of sequence similarity between two nucleic acids or proteins.

The term "substantially similar" refers to nucleotide and amino acid sequences that represent functional and/or structural equivalents of *Arabidopsis* sequences disclosed herein. For example, altered nucleotide sequences which simply reflect the degeneracy of the genetic code but nonetheless encode amino acid

sequences that are identical to a particular amino acid sequence are substantially similar to the particular sequences. In addition, amino acid sequences that are substantially similar to a particular sequence are those wherein overall amino acid identity is at least 65% or greater to the instant sequences. Modifications that result in equivalent nucleotide or amino acid sequences are well within the routine skill in the art. Moreover, the skilled artisan recognizes that equivalent nucleotide sequences encompassed by this invention can also be defined by their ability to hybridize, under low, moderate and/or stringent conditions (e.g., 0.1X SSC, 0.1% SDS, 65°C), with the nucleotide sequences that are within the literal scope of the instant claims.

"Target gene" refers to a gene on the replicon that expresses the desired target coding sequence, functional RNA, or protein. The target gene is not essential for replicon replication. Additionally, target genes may comprise native non-viral genes inserted into a non-native organism, or chimeric genes, and will be under the control of suitable regulatory sequences. Thus, the regulatory sequences in the target gene may come from any source, including the virus. Target genes may include coding sequences that are either heterologous or homologous to the genes of a particular plant to be transformed. However, target genes do not include native viral genes. Typical target genes include, but are not limited to genes encoding a structural protein, a seed storage protein, a protein that conveys herbicide resistance, and a protein that conveys insect resistance. Proteins encoded by target genes are known as "foreign proteins". The expression of a target gene in a plant will typically produce an altered plant trait.

The term "altered plant trait" means any phenotypic or genotypic change in a transgenic plant relative to the wild-type or non-transgenic plant host.

"Transcription Stop Fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as polyadenylation signal sequences, capable of terminating transcription. Examples include the 3' non-regulatory regions of genes encoding nopaline synthase and the small subunit of ribulose biphosphate carboxylase.

"Replication gene" refers to a gene encoding a viral replication protein. In addition to the ORF of the replication protein, the replication gene may also contain other overlapping or non-overlapping ORF(s), as are found in viral sequences in nature. While not essential for replication, these additional ORFs may enhance replication and/or viral DNA accumulation. Examples of such additional ORFs are AC3 and AL3 in ACMV and TGMV geminiviruses, respectively.

"Chimeric *trans*-acting replication gene" refers either to a replication gene in which the coding sequence of a replication protein is under the control of a regulated plant promoter other than that in the native viral replication gene, or a modified native viral replication gene, for example, in which a site specific sequence(s) is inserted in the 5' transcribed but untranslated region. Such chimeric genes also include insertion of the known sites of replication protein binding between the promoter and the transcription start site that attenuate transcription of viral replication protein gene.

"Chromosomally-integrated" refers to the integration of a foreign gene or DNA construct into the host DNA by covalent bonds. Where genes are not "chromosomally integrated" they may be "transiently expressed." Transient expression of a gene refers to the expression of a gene that is not integrated into the host chromosome but functions independently, either as part of an autonomously replicating plasmid or expression cassette, for example, or as part of another biological system such as a virus.

"Production tissue" refers to mature, harvestable tissue consisting of non-dividing, terminally-differentiated cells. It excludes young, growing tissue consisting of germline, meristematic, and not-fully-differentiated cells.

"Germline cells" refer to cells that are destined to be gametes and whose genetic material is heritable.

"*Trans*-activation" refers to switching on of gene expression or replicon replication by the expression of another (regulatory) gene in *trans*.

The term "transformation" refers to the transfer of a nucleic acid fragment into the genome of a host cell, resulting in genetically stable inheritance. Host cells containing the transformed nucleic acid fragments are referred to as "transgenic"

cells, and organisms comprising transgenic cells are referred to as "transgenic organisms". Examples of methods of transformation of plants and plant cells include *Agrobacterium*-mediated transformation (De Blaere et al., 1987) and particle bombardment technology (Klein et al. 1987; U.S. Patent No. 4,945,050). Whole
5 plants may be regenerated from transgenic cells by methods well known to the skilled artisan (see, for example, Fromm et al., 1990).

"Transformed," "transgenic," and "recombinant" refer to a host organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the
10 genome generally known in the art and are disclosed in Sambrook et al., 1989. See also Innis et al., 1995 and Gelfand, 1995; and Innis and Gelfand, 1999. Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially mismatched primers, and the like. For example,
15 "transformed," "transformant," and "transgenic" plants or calli have been through the transformation process and contain a foreign gene integrated into their chromosome. The term "untransformed" refers to normal plants that have not been through the transformation process.

"Transiently transformed" refers to cells in which transgenes and foreign
20 DNA have been introduced (for example, by such methods as *Agrobacterium*-mediated transformation or biolistic bombardment), but not selected for stable maintenance.

"Stably transformed" refers to cells that have been selected and regenerated on a selection media following transformation.

25 "Transient expression" refers to expression in cells in which a virus or a transgene is introduced by viral infection or by such methods as *Agrobacterium*-mediated transformation, electroporation, or biolistic bombardment, but not selected for its stable maintenance.

"Genetically stable" and "heritable" refer to chromosomally-integrated
30 genetic elements that are stably maintained in the plant and stably inherited by progeny through successive generations.

"Primary transformant" and "T0 generation" refer to transgenic plants that are of the same genetic generation as the tissue which was initially transformed (i.e., not having gone through meiosis and fertilization since transformation).

5 "Secondary transformants" and the "T1, T2, T3, etc. generations" refer to transgenic plants derived from primary transformants through one or more meiotic and fertilization cycles. They may be derived by self-fertilization of primary or secondary transformants or crosses of primary or secondary transformants with other transformed or untransformed plants.

10 "Wild-type" refers to a virus or organism found in nature without any known mutation.

"Genome" refers to the complete genetic material of an organism.

15 The term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, composed of monomers (nucleotides) containing a sugar, phosphate and a base which is either a purine or pyrimidine. Unless specifically limited, the term encompasses nucleic acids containing known analogs of natural nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer et al., 1991; Ohtsuka et al., 1985; Rossolini et al. 1994). A "nucleic acid fragment" is a fraction of a given nucleic acid molecule. In higher plants, 25 deoxyribonucleic acid (DNA) is the genetic material while ribonucleic acid (RNA) is involved in the transfer of information contained within DNA into proteins. The term "nucleotide sequence" refers to a polymer of DNA or RNA which can be single- or double-stranded, optionally containing synthetic, non-natural or altered 30 nucleotide bases capable of incorporation into DNA or RNA polymers. The terms

"nucleic acid" or "nucleic acid sequence" may also be used interchangeably with gene, cDNA, DNA and RNA encoded by a gene.

The invention encompasses isolated or substantially purified nucleic acid or protein compositions. In the context of the present invention, an "isolated" or "purified" DNA molecule or an "isolated" or "purified" polypeptide is a DNA molecule or polypeptide that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or polypeptide may exist in a purified form or may exist in a non-native environment such as, for example, a transgenic host cell. For example, an "isolated" or "purified" nucleic acid molecule or protein, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. Preferably, an "isolated" nucleic acid is free of sequences (preferably protein encoding sequences) that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A protein that is substantially free of cellular material includes preparations of protein or polypeptide having less than about 30%, 20%, 10%, 5%, (by dry weight) of contaminating protein. When the protein of the invention, or biologically active portion thereof, is recombinantly produced, preferably culture medium represents less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-protein of interest chemicals.

The nucleotide sequences of the invention include both the naturally occurring sequences as well as mutant (variant) forms. Such variants will continue to possess the desired activity, i.e., either promoter activity or the activity of the product encoded by the open reading frame of the non-variant nucleotide sequence.

Thus, by "variants" is intended substantially similar sequences. For nucleotide sequences comprising an open reading frame, variants include those

sequences that, because of the degeneracy of the genetic code, encode the identical amino acid sequence of the native protein. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization

5 techniques. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those generated, for example, by using site-directed mutagenesis and for open reading frames, encode the native protein, as well as those that encode a polypeptide having amino acid substitutions relative to the native protein. Generally, nucleotide sequence variants of the invention will have at least
10 40, 50, 60, to 70%, e.g., preferably 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, to 79%, generally at least 80%, e.g., 81%-84%, at least 85%, e.g., 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, to 98% and 99% nucleotide sequence identity to the native (wild type or endogenous) nucleotide sequence.

“Conservatively modified variations” of a particular nucleic acid sequence
15 refers to those nucleic acid sequences that encode identical or essentially identical amino acid sequences, or where the nucleic acid sequence does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given polypeptide. For instance the codons CGT, CGC, CGA, CGG, AGA, and
20 AGG all encode the amino acid arginine. Thus, at every position where an arginine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded protein. Such nucleic acid variations are “silent variations” which are one species of “conservatively modified variations.” Every nucleic acid sequence described herein which encodes a polypeptide also
25 describes every possible silent variation, except where otherwise noted. One of skill will recognize that each codon in a nucleic acid (except ATG, which is ordinarily the only codon for methionine) can be modified to yield a functionally identical molecule by standard techniques. Accordingly, each “silent variation” of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

30 The nucleic acid molecules of the invention can be “optimized” for enhanced expression in plants of interest. See, for example, EPA 035472; WO 91/16432;

Perlak et al., 1991; and Murray et al., 1989. In this manner, the open reading frames in genes or gene fragments can be synthesized utilizing plant-preferred codons. See, for example, Campbell and Gowri, 1990 for a discussion of host-preferred codon usage. Thus, the nucleotide sequences can be optimized for expression in any plant.

5 It is recognized that all or any part of the gene sequence may be optimized or synthetic. That is, synthetic or partially optimized sequences may also be used. Variant nucleotide sequences and proteins also encompass sequences and protein derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different coding sequences can be manipulated
10 to create a new polypeptide possessing the desired properties. In this manner, libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer,
15 1994; Stemmer, 1994; Cramer et al., 1997; Moore et al., 1997; Zhang et al., 1997; Cramer et al., 1998; and U.S. Patent Nos. 5,605,793 and 5,837,458.

By "variant" polypeptide is intended a polypeptide derived from the native protein by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of
20 one or more amino acids at one or more sites in the native protein; or substitution of one or more amino acids at one or more sites in the native protein. Such variants may result from, for example, genetic polymorphism or from human manipulation. Methods for such manipulations are generally known in the art.

Thus, the polypeptides may be altered in various ways including amino acid
25 substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the polypeptides can be prepared by mutations in the DNA. Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel, 1985; Kunkel et al., 1987; U. S. Patent No. 4,873,192; Walker and Gaastra,
30 1983 and the references cited therein. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be

found in the model of Dayhoff et al. (1978). Conservative substitutions, such as exchanging one amino acid with another having similar properties, are preferred.

Individual substitutions deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids (typically less than 5%, more typically less than 1%) in an encoded sequence are "conservatively modified variations," where the alterations result in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. The following five groups each contain amino acids that are conservative substitutions for one another:

10 Aliphatic: Glycine (G), Alanine (A), Valine (V), Leucine (L), Isoleucine (I); Aromatic: Phenylalanine (F), Tyrosine (Y), Tryptophan (W); Sulfur-containing: Methionine (M), Cysteine (C); Basic: Arginine (R), Lysine (K), Histidine (H); Acidic: Aspartic acid (D), Glutamic acid (E), Asparagine (N), Glutamine (Q). See also, Creighton, 1984. In addition, individual substitutions, deletions or additions which

15 alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence are also "conservatively modified variations."

"Expression cassette" as used herein means a DNA sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operably linked to the nucleotide sequence of interest which

20 is operably linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the nucleotide sequence of

25 interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. The expression of the nucleotide sequence in the expression cassette may be under the control of a

30 constitutive promoter or of an inducible promoter which initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a

multicellular organism, the promoter can also be specific to a particular tissue or organ or stage of development.

"Vector" is defined to include, inter alia, any plasmid, cosmid, phage or *Agrobacterium* binary vector in double or single stranded linear or circular form

5 which may or may not be self transmissible or mobilizable, and which can transform prokaryotic or eukaryotic host either by integration into the cellular genome or exist extrachromosomally (e.g. autonomous replicating plasmid with an origin of replication).

Specifically included are shuttle vectors by which is meant a DNA vehicle
10 capable, naturally or by design, of replication in two different host organisms, which may be selected from actinomycetes and related species, bacteria and eukaryotic (e.g. higher plant, mammalian, yeast or fungal cells).

Preferably the nucleic acid in the vector is under the control of, and operably linked to, an appropriate promoter or other regulatory elements for transcription in a
15 host cell such as a microbial, e.g. bacterial, or plant cell. The vector may be a bi-functional expression vector which functions in multiple hosts. In the case of genomic DNA, this may contain its own promoter or other regulatory elements and in the case of cDNA this may be under the control of an appropriate promoter or other regulatory elements for expression in the host cell.

"Cloning vectors" typically contain one or a small number of restriction
20 endonuclease recognition sites at which foreign DNA sequences can be inserted in a determinable fashion without loss of essential biological function of the vector, as well as a marker gene that is suitable for use in the identification and selection of cells transformed with the cloning vector. Marker genes typically include genes that
25 provide tetracycline resistance, hygromycin resistance or ampicillin resistance.

A "transgenic plant" is a plant having one or more plant cells that contain an expression vector.

"Plant tissue" includes differentiated and undifferentiated tissues or plants,
including but not limited to roots, stems, shoots, leaves, pollen, seeds, tumor tissue
30 and various forms of cells and culture such as single cells, protoplast, embryos, and callus tissue. The plant tissue may be in plants or in organ, tissue or cell culture.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence identity", and (e) "substantial identity".

5 (a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full length cDNA or gene sequence, or the complete cDNA or gene sequence.

10 (b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40,
15 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well known in the art. Thus, the determination of percent identity between any two sequences can be
20 accomplished using a mathematical algorithm. Preferred, non-limiting examples of such mathematical algorithms are the algorithm of Myers and Miller, 1988; the local homology algorithm of Smith et al. 1981; the homology alignment algorithm of Needleman and Wunsch 1970; the search-for-similarity-method of Pearson and Lipman 1988; the algorithm of Karlin and Altschul, 1990, modified as in Karlin and
25 Altschul, 1993.

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and
30 GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG), 575

Science Drive, Madison, Wisconsin, USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins et al. 1988; Higgins et al. 1989; Corpet et al. 1988; Huang et al. 1992; and Pearson et al. 1994. The ALIGN program is based on the algorithm of Myers and Miller, *supra*. The BLAST programs of Altschul et al., 1990, are based on the algorithm of Karlin and Altschul *supra*.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul (1993). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than

about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul et al. 1997. Alternatively, PSI-
5 BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul et al., *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g. BLASTN for nucleotide sequences, BLASTX for proteins) can be used. The BLASTN program (for nucleotide sequences) uses as defaults a
10 wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989). See <http://www.ncbi.nlm.nih.gov>. Alignment may also be performed manually by inspection.

15 For purposes of the present invention, comparison of nucleotide sequences for determination of percent sequence identity to the promoter sequences disclosed herein is preferably made using the BlastN program (version 1.4.7 or later) with its default parameters or any equivalent program. By "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates
20 an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the preferred program.

(c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences makes reference to the residues in the two
25 sequences that are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g.,
30 charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent

sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity." Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a

5 conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program
10 PC/GENE (Intelligenetics, Mountain View, California).

(d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the
15 reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of
20 comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, or 79%, preferably at least 80%, 81%, 82%, 83%, 84%, 85%,
25 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, and most preferably at least 95%, 96%, 97%, 98%, or 99% sequence identity, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins
30 encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity

of amino acid sequences for these purposes normally means sequence identity of at least 70%, more preferably at least 80%, 90%, and most preferably at least 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions (see below).

- 5 Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1°C to about 20°C, depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions
- 10 are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide
- 15 encoded by the second nucleic acid.

- (e)(ii) The term "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, or 79%, preferably 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, or even more
- 20 preferably, 95%, 96%, 97%, 98% or 99%, sequence identity to the reference sequence over a specified comparison window. Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch (1970). An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second
- 25 peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution.

- For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer,
- 30 subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then

calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

As noted above, another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions. The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA. "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

"Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as Southern and Northern hybridization are sequence dependent, and are different under different environmental parameters. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, 1984; $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with >90% identity are sought, the T_m can be decreased 10°C . Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point T_m for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent

conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point T_m ; moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point T_m ; low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point T_m . Using the equation, hybridization and wash compositions, and desired T_m , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen, 1993. Generally, highly stringent hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point T_m for the specific sequence at a defined ionic strength and pH.

15 An example of highly stringent wash conditions is 0.15 M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2X SSC wash at 65°C for 15 minutes (see, Sambrook, *infra*, for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, e.g., more than 20 100 nucleotides, is 1X SSC at 45°C for 15 minutes. An example low stringency wash for a duplex of, e.g., more than 100 nucleotides, is 4-6X SSC at 40°C for 15 minutes. For short probes (e.g., about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.5 M, more preferably about 0.01 to 1.0 M, Na ion concentration (or other salts) at pH 7.0 to 8.3, and the 25 temperature is typically at least about 30°C and at least about 60°C for long probes (e.g., >50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2X (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids that do not 30 hybridize to each other under stringent conditions are still substantially identical if

the proteins that they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or Northern blot is 50% formamide, e.g., hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C.

The following are examples of sets of hybridization/wash conditions that may be used to clone orthologous nucleotide sequences that are substantially identical to reference nucleotide sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

“DNA shuffling” is a method to introduce mutations or rearrangements, preferably randomly, in a DNA molecule or to generate exchanges of DNA sequences between two or more DNA molecules, preferably randomly. The DNA

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molecule resulting from DNA shuffling is a shuffled DNA molecule that is a non-naturally occurring DNA molecule derived from at least one template DNA molecule. The shuffled DNA preferably encodes a variant polypeptide modified with respect to the polypeptide encoded by the template DNA, and may have an
5 altered biological activity with respect to the polypeptide encoded by the template DNA.

“Recombinant DNA molecule” is a combination of DNA sequences that are joined together using recombinant DNA technology and procedures used to join together DNA sequences as described, for example, in Sambrook et al., 1989.

10 The word “plant” refers to any plant, particularly to seed plant, and “plant cell” is a structural and physiological unit of the plant, which comprises a cell wall but may also refer to a protoplast. The plant cell may be in form of an isolated single cell or a cultured cell, or as a part of higher organized unit such as, for example, a plant tissue, or a plant organ.

15 “Significant increase” is an increase that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater.

“Significantly less” means that the decrease is larger than the margin of error inherent in the measurement technique, preferably a decrease by about 2-fold or
20 greater.

II. DNA Sequences for Transformation

Virtually any DNA composition may be used for delivery to recipient plant cells, e.g., monocotyledonous cells, to ultimately produce fertile transgenic plants in accordance with the present invention. For example, DNA segments in the form of
25 vectors and plasmids, or linear DNA fragments, in some instances containing only the DNA element to be expressed in the plant, and the like, may be employed. The construction of vectors which may be employed in conjunction with the present invention will be known to those of skill of the art in light of the present disclosure (see, e.g., Sambrook et al., 1989; Gelvin et al., 1990).

30 Vectors, plasmids, cosmids, YACs (yeast artificial chromosomes), BACs (bacterial artificial chromosomes) and DNA segments for use in transforming such

cells will, of course, generally comprise the cDNA, gene or genes which one desires to introduce into the cells. These DNA constructs can further include structures such as promoters, enhancers, polylinkers, or even regulatory genes as desired. The DNA segment or gene chosen for cellular introduction will often encode a protein
5 which will be expressed in the resultant recombinant cells, such as will result in a screenable or selectable trait and/or which will impart an improved phenotype to the regenerated plant. However, this may not always be the case, and the present invention also encompasses transgenic plants incorporating non-expressed transgenes.

10 In certain embodiments, it is contemplated that one may wish to employ replication-competent viral vectors in monocot transformation. Such vectors include, for example, wheat dwarf virus (WDV) "shuttle" vectors, such as pW1-11 and PW1-GUS (Ugaki et al., 1991). These vectors are capable of autonomous replication in maize cells as well as *E. coli*, and as such may provide increased
15 sensitivity for detecting DNA delivered to transgenic cells. A replicating vector may also be useful for delivery of genes flanked by DNA sequences from transposable elements such as Ac, Ds, or Mu. It has been proposed (Laufs et al., 1990) that transposition of these elements within the maize genome requires DNA replication. It is also contemplated that transposable elements would be useful for introducing
20 DNA fragments lacking elements necessary for selection and maintenance of the plasmid vector in bacteria, e.g., antibiotic resistance genes and origins of DNA replication. It is also proposed that use of a transposable element such as Ac, Ds, or Mu would actively promote integration of the desired DNA and hence increase the frequency of stably transformed cells. The use of a transposable element such as
25 Ac, Ds, or Mu may actively promote integration of the DNA of interest and hence increase the frequency of stably transformed cells. Transposable elements may be useful to allow separation of genes of interest from elements necessary for selection and maintenance of a plasmid vector in bacteria or selection of a transformant. By use of a transposable element, desirable and undesirable DNA sequences may be
30 transposed apart from each other in the genome, such that through genetic

segregation in progeny, one may identify plants with either the desirable or the undesirable DNA sequences.

DNA useful for introduction into plant cells includes that which has been derived or isolated from any source, that may be subsequently characterized as to structure, size and/or function, chemically altered, and later introduced into plants. An example of DNA "derived" from a source, would be a DNA sequence that is identified as a useful fragment within a given organism, and which is then chemically synthesized in essentially pure form. An example of such DNA "isolated" from a source would be a useful DNA sequence that is excised or removed from said source by chemical means, e.g., by the use of restriction endonucleases, so that it can be further manipulated, e.g., amplified, for use in the invention, by the methodology of genetic engineering. Such DNA is commonly referred to as "recombinant DNA."

Therefore useful DNA includes completely synthetic DNA, semi-synthetic DNA, DNA isolated from biological sources, and DNA derived from introduced RNA. Generally, the introduced DNA is not originally resident in the plant genotype which is the recipient of the DNA, but it is within the scope of the invention to isolate a gene from a given plant genotype, and to subsequently introduce multiple copies of the gene into the same genotype, e.g., to enhance production of a given gene product such as a storage protein or a protein that confers tolerance or resistance to water deficit.

The introduced DNA includes but is not limited to, DNA from plant genes, and non-plant genes such as those from bacteria, yeasts, animals or viruses. The introduced DNA can include modified genes, portions of genes, or chimeric genes, including genes from the same or different maize genotype. The term "chimeric gene" or "chimeric DNA" is defined as a gene or DNA sequence or segment comprising at least two DNA sequences or segments from species which do not combine DNA under natural conditions, or which DNA sequences or segments are positioned or linked in a manner which does not normally occur in the native genome of untransformed plant.

The introduced DNA used for transformation herein may be circular or linear, double-stranded or single-stranded. Generally, the DNA is in the form of chimeric DNA, such as plasmid DNA, that can also contain coding regions flanked by regulatory sequences which promote the expression of the recombinant DNA present in the resultant plant. For example, the DNA may itself comprise or consist of a promoter that is active in a plant which is derived from a source other than that plant, or may utilize a promoter already present in a plant genotype that is the transformation target.

Generally, the introduced DNA will be relatively small, i.e., less than about 30 kb to minimize any susceptibility to physical, chemical, or enzymatic degradation which is known to increase as the size of the DNA increases. As noted above, the number of proteins, RNA transcripts or mixtures thereof which is introduced into the plant genome is preferably preselected and defined, e.g., from one to about 5-10 such products of the introduced DNA may be formed.

Two principal methods for the control of expression are known, viz.: overexpression and underexpression. Overexpression can be achieved by insertion of one or more than one extra copy of the selected gene. It is, however, not unknown for plants or their progeny, originally transformed with one or more than one extra copy of a nucleotide sequence, to exhibit the effects of underexpression as well as overexpression. For underexpression there are two principle methods which are commonly referred to in the art as "antisense downregulation" and "sense downregulation" (sense downregulation is also referred to as "cosuppression"). Generically these processes are referred to as "gene silencing". Both of these methods lead to an inhibition of expression of the target gene.

Obtaining sufficient levels of transgene expression in the appropriate plant tissues is an important aspect in the production of genetically engineered crops. Expression of heterologous DNA sequences in a plant host is dependent upon the presence of an operably linked promoter that is functional within the plant host. Choice of the promoter sequence will determine when and where within the organism the heterologous DNA sequence is expressed.

Furthermore, it is contemplated that promoters combining elements from more than one promoter may be useful. For example, U.S. Patent No. 5,491,288 discloses combining a Cauliflower Mosaic Virus promoter with a histone promoter. Thus, the elements from the promoters disclosed herein may be combined with
5 elements from other promoters.

Promoters which are useful for plant transgene expression include those that are inducible, viral, synthetic, constitutive (Odell et al., 1985), temporally regulated, spatially regulated, tissue-specific, and spatio-temporally regulated.

Where expression in specific tissues or organs is desired, tissue-specific
10 promoters may be used. In contrast, where gene expression in response to a stimulus is desired, inducible promoters are the regulatory elements of choice. Where continuous expression is desired throughout the cells of a plant, constitutive promoters are utilized. Additional regulatory sequences upstream and/or downstream from the core promoter sequence may be included in expression
15 constructs of transformation vectors to bring about varying levels of expression of heterologous nucleotide sequences in a transgenic plant.

A. Transcription Regulatory Sequences

1. Promoters

The choice of promoter will vary depending on the temporal and
20 spatial requirements for expression, and also depending on the target species. In some cases, expression in multiple tissues is desirable. While in others, tissue-specific, e.g., leaf-specific, seed-specific, petal-specific, anther-specific, or pith-specific, expression is desirable. Although many promoters from dicotyledons have been shown to be operational in monocotyledons and *vice versa*, ideally
25 dicotyledonous promoters are selected for expression in dicotyledons, and monocotyledonous promoters for expression in monocotyledons. However, there is no restriction to the provenance of selected promoters; it is sufficient that they are operational in driving the expression of the nucleotide sequences in the desired cell.

These promoters include, but are not limited to, constitutive, inducible,
30 temporally regulated, developmentally regulated, spatially-regulated, chemically regulated, stress-responsive, tissue-specific, viral and synthetic promoters. Promoter

sequences are known to be strong or weak. A strong promoter provides for a high level of gene expression, whereas a weak promoter provides for a very low level of gene expression. An inducible promoter is a promoter that provides for the turning on and off of gene expression in response to an exogenously added agent, or to an environmental or developmental stimulus. A bacterial promoter such as the P_{tac} promoter can be induced to varying levels of gene expression depending on the level of isothiopyl galactoside added to the transformed bacterial cells. An isolated promoter sequence that is a strong promoter for heterologous nucleic acid is advantageous because it provides for a sufficient level of gene expression to allow for easy detection and selection of transformed cells and provides for a high level of gene expression when desired.

Within a plant promoter region there are several domains that are necessary for full function of the promoter. The first of these domains lies immediately upstream of the structural gene and forms the "core promoter region" containing consensus sequences, normally 70 base pairs immediately upstream of the gene. The core promoter region contains the characteristic CAAT and TATA boxes plus surrounding sequences, and represents a transcription initiation sequence that defines the transcription start point for the structural gene.

The presence of the core promoter region defines a sequence as being a promoter: if the region is absent, the promoter is non-functional. Furthermore, the core promoter region is insufficient to provide full promoter activity. A series of regulatory sequences upstream of the core constitute the remainder of the promoter. The regulatory sequences determine expression level, the spatial and temporal pattern of expression and, for an important subset of promoters, expression under inductive conditions (regulation by external factors such as light, temperature, chemicals, hormones).

A range of naturally-occurring promoters are known to be operative in plants and have been used to drive the expression of heterologous (both foreign and endogenous) genes in plants: for example, the constitutive 35S cauliflower mosaic virus (CaMV) promoter, the ripening-enhanced tomato polygalacturonase promoter (Bird et al., 1988), the E8 promoter (Diekmann & Fischer, 1988) and the fruit specific

2A1 promoter (Pear et al., 1989) and many others, e.g., U2 and U5 snRNA promoters from maize, the promoter from alcohol dehydrogenase, the Z4 promoter from a gene encoding the Z4 22 kD zein protein, the Z10 promoter from a gene encoding a 10 kD zein protein, a Z27 promoter from a gene encoding a 27 kD zein protein, the A20 promoter from the gene encoding a 19 kD -zein protein, inducible promoters, such as the light inducible promoter derived from the pea rbcS gene and the actin promoter from rice, e.g., the actin 2 promoter (WO 00/70067); seed specific promoters, such as the phaseolin promoter from beans, may also be used. The nucleotide sequences of this invention can also be expressed under the regulation of promoters that are chemically regulated. This enables the nucleic acid sequence or encoded polypeptide to be synthesized only when the crop plants are treated with the inducing chemicals. Chemical induction of gene expression is detailed in EP 0 332 104 (to Ciba-Geigy) and U.S. Patent 5,614,395. A preferred promoter for chemical induction is the tobacco PR-1a promoter.

Examples of some constitutive promoters which have been described include the rice actin 1 (Wang et al., 1992; U.S. Patent No. 5,641,876), CaMV 35S (Odell et al., 1985), CaMV 19S (Lawton et al., 1987), *nos*, *Adh*, sucrose synthase; and the ubiquitin promoters.

Examples of tissue specific promoters which have been described include the lectin (Vodkin, 1983; Lindstrom et al., 1990) corn alcohol dehydrogenase 1 (Vogel et al., 1989; Dennis et al., 1984), corn light harvesting complex (Simpson, 1986; Bansal et al., 1992), corn heat shock protein (Odell et al., 1985), pea small subunit RuBP carboxylase (Poulsen et al., 1986), Ti plasmid mannopine synthase (Langridge et al., 1989), Ti plasmid nopaline synthase (Langridge et al., 1989), petunia chalcone isomerase (vanTunen et al., 1988), bean glycine rich protein 1 (Keller et al., 1989), truncated CaMV 35s (Odell et al., 1985), potato patatin (Wenzler et al., 1989), root cell (Yamamoto et al., 1990), maize zein (Reina et al., 1990; Kriz et al., 1987; Wandelt et al., 1989; Langridge et al., 1983; Reina et al., 1990), globulin-1 (Belanger et al., 1991), α -tubulin, *cab* (Sullivan et al., 1989), PEPCase (Hudspeth & Grula, 1989), R gene complex-associated promoters

(Chandler et al., 1989), histone, and chalcone synthase promoters (Franken et al., 1991). Tissue specific enhancers are described in Fromm et al. (1989).

Inducible promoters that have been described include the ABA- and turgor-inducible promoters, the promoter of the auxin-binding protein gene (Schwob et al., 1993), the UDP glucose flavonoid glycosyl-transferase gene promoter (Ralston et al., 1988), the MPI proteinase inhibitor promoter (Cordero et al., 1994), and the glyceraldehyde-3-phosphate dehydrogenase gene promoter (Kohler et al., 1995; Quigley et al., 1989; Martinez et al., 1989).

Several other tissue-specific regulated genes and/or promoters have been reported in plants. These include genes encoding the seed storage proteins (such as napin, cruciferin, beta-conglycinin, and phaseolin) zein or oil body proteins (such as oleosin), or genes involved in fatty acid biosynthesis (including acyl carrier protein, stearyl-ACP desaturase. And fatty acid desaturases (fad 2-1)), and other genes expressed during embryo development (such as Bce4, see, for example, EP 255378 and Kridl et al., 1991). Particularly useful for seed-specific expression is the pea vicilin promoter (Czako et al., 1992). (See also U.S. Pat. No. 5,625,136, herein incorporated by reference.) Other useful promoters for expression in mature leaves are those that are switched on at the onset of senescence, such as the SAG promoter from Arabidopsis (Gan et al., 1995).

A class of fruit-specific promoters expressed at or during antithesis through fruit development, at least until the beginning of ripening, is discussed in U.S. 4,943,674. cDNA clones that are preferentially expressed in cotton fiber have been isolated (John et al., 1992). cDNA clones from tomato displaying differential expression during fruit development have been isolated and characterized (Mansson et al., 1985, Slater et al., 1985). The promoter for polygalacturonase gene is active in fruit ripening. The polygalacturonase gene is described in U.S. Patent No. 4,535,060, U.S. Patent No. 4,769,061, U.S. Patent No. 4,801,590, and U.S. Patent No. 5,107,065, which disclosures are incorporated herein by reference.

Other examples of tissue-specific promoters include those that direct expression in leaf cells following damage to the leaf (for example, from chewing insects), in tubers (for example, patatin gene promoter), and in fiber cells (an

example of a developmentally-regulated fiber cell protein is E6 (John et al., 1992). The E6 gene is most active in fiber, although low levels of transcripts are found in leaf, ovule and flower.

The tissue-specificity of some "tissue-specific" promoters may not be absolute and may be tested by one skilled in the art using the diphtheria toxin sequence. One can also achieve tissue-specific expression with "leaky" expression by a combination of different tissue-specific promoters (Beals et al., 1997). Other tissue-specific promoters can be isolated by one skilled in the art (see U.S. 5,589,379). Several inducible promoters ("gene switches") have been reported. Many are described in the review by Gatz (1996) and Gatz (1997). These include tetracycline repressor system, *Lac* repressor system, copper-inducible systems, salicylate-inducible systems (such as the PR1a system), glucocorticoid- (Aoyama et al., 1997) and ecdysone-inducible systems. Also included are the benzene sulphonamide- (U.S. Patent No. 5,364,780) and alcohol-(WO 97/06269 and WO 97/06268) inducible systems and glutathione S-transferase promoters. Other studies have focused on genes inducibly regulated in response to environmental stress or stimuli such as increased salinity. Drought, pathogen and wounding. (Graham et al., 1985; Graham et al., 1985, Smith et al., 1986). Accumulation of metalcarboxypeptidase-inhibitor protein has been reported in leaves of wounded potato plants (Graham et al., 1981). Other plant genes have been reported to be induced methyl jasmonate, elicitors, heat-shock, anaerobic stress, or herbicide safeners.

Regulated expression of the chimeric transacting viral replication protein can be further regulated by other genetic strategies. For example, *Cre*-mediated gene activation as described by Odell et al. 1990. Thus, a DNA fragment containing 3' regulatory sequence bound by lox sites between the promoter and the replication protein coding sequence that blocks the expression of a chimeric replication gene from the promoter can be removed by *Cre*-mediated excision and result in the expression of the *trans*-acting replication gene. In this case, the chimeric *Cre* gene, the chimeric *trans*-acting replication gene, or both can be under the control of tissue- and developmental- specific or inducible promoters. An alternate genetic strategy is

the use of tRNA suppressor gene. For example, the regulated expression of a tRNA suppressor gene can conditionally control expression of a *trans*-acting replication protein coding sequence containing an appropriate termination codon as described by Ulmasov et al. 1997. Again, either the chimeric tRNA suppressor gene, the
5 chimeric transacting replication gene, or both can be under the control of tissue- and developmental-specific or inducible promoters.

Frequently it is desirable to have continuous or inducible expression of a DNA sequence throughout the cells of an organism in a tissue-independent manner. For example, increased resistance of a plant to infection by soil- and airborne-
10 pathogens might be accomplished by genetic manipulation of the plant's genome to comprise a continuous promoter operably linked to a heterologous pathogen-resistance gene such that pathogen-resistance proteins are continuously expressed throughout the plant's tissues.

Alternatively, it might be desirable to inhibit expression of a native DNA
15 sequence within a plant's tissues to achieve a desired phenotype. In this case, such inhibition might be accomplished with transformation of the plant to comprise a constitutive, tissue-independent promoter operably linked to an antisense nucleotide sequence, such that constitutive expression of the antisense sequence produces an RNA transcript that interferes with translation of the mRNA of the native DNA
20 sequence.

To define a minimal promoter region, a DNA segment representing the promoter region is removed from the 5' region of the gene of interest and operably linked to the coding sequence of a marker (reporter) gene by recombinant DNA techniques well known to the art. The reporter gene is operably linked downstream
25 of the promoter, so that transcripts initiating at the promoter proceed through the reporter gene. Reporter genes generally encode proteins which are easily measured, including, but not limited to, chloramphenicol acetyl transferase (CAT), beta-glucuronidase (GUS), green fluorescent protein (GFP), beta-galactosidase (beta-GAL), and luciferase.

30 The construct containing the reporter gene under the control of the promoter is then introduced into an appropriate cell type by transfection techniques well

known to the art. To assay for the reporter protein, cell lysates are prepared and appropriate assays, which are well known in the art, for the reporter protein are performed. For example, if CAT were the reporter gene of choice, the lysates from cells transfected with constructs containing CAT under the control of a promoter
5 under study are mixed with isotopically labeled chloramphenicol and acetyl-coenzyme A (acetyl-CoA). The CAT enzyme transfers the acetyl group from acetyl-CoA to the 2- or 3-position of chloramphenicol. The reaction is monitored by thin-layer chromatography, which separates acetylated chloramphenicol from unreacted material. The reaction products are then visualized by autoradiography.

10 The level of enzyme activity corresponds to the amount of enzyme that was made, which in turn reveals the level of expression from the promoter of interest. This level of expression can be compared to other promoters to determine the relative strength of the promoter under study. In order to be sure that the level of expression is determined by the promoter, rather than by the stability of the mRNA,
15 the level of the reporter mRNA can be measured directly, such as by Northern blot analysis.

Once activity is detected, mutational and/or deletional analyses may be employed to determine the minimal region and/or sequences required to initiate transcription. Thus, sequences can be deleted at the 5' end of the promoter region
20 and/or at the 3' end of the promoter region, and nucleotide substitutions introduced. These constructs are then introduced to cells and their activity determined.

In one embodiment, the promoter may be a gamma zein promoter, an oleosin ole16 promoter, a globulinI promoter, an actin I promoter, an actin cl promoter, a sucrose synthetase promoter, an INOPS promoter, an EXM5 promoter, a globulin2
25 promoter, a b-32, ADPG- pyrophosphorylase promoter, an LtpI promoter, an Ltp2 promoter, an oleosin ole17 promoter, an oleosin ole18 promoter, an actin 2 promoter, a pollen-specific protein promoter, a pollen-specific pectate lyase promoter, an anther-specific protein promoter (Huffman), an anther-specific gene RTS2 promoter, a pollen- specific gene promoter, a tapetum-specific gene promoter,
30 tapetum- specific gene RAB24 promoter, a anthranilate synthase alpha subunit promoter, an alpha zein promoter, an anthranilate synthase beta subunit promoter, a

dihydrodipicolinate synthase promoter, a Thil promoter, an alcohol dehydrogenase promoter, a cab binding protein promoter, an H3C4 promoter, a RUBISCO SS starch branching enzyme promoter, an ACCase promoter, an actin3 promoter, an actin7 promoter, a regulatory protein GF14-12 promoter, a ribosomal protein L9 promoter, a cellulose biosynthetic enzyme promoter, an S-adenosyl-L-homocysteine hydrolase promoter, a superoxide dismutase promoter, a C-kinase receptor promoter, a phosphoglycerate mutase promoter, a root-specific RCc3 mRNA promoter, a glucose-6 phosphate isomerase promoter, a pyrophosphate-fructose 6-phosphatetphosphotransferase promoter, an ubiquitin promoter, a beta-ketoacyl-ACP synthase promoter, a 33 kDa photosystem 11 promoter, an oxygen evolving protein promoter, a 69 kDa vacuolar ATPase subunit promoter, a metallothionein-like protein promoter, a glyceraldehyde-3 -phosphate dehydrogenase promoter, an ABA- and ripening- inducible-like protein promoter, a phenylalanine ammonia lyase promoter, an adenosine triphosphatase S-adenosyl-L-homocysteine hydrolase promoter, an a- tubulin promoter, a cab promoter, a PEPCase promoter, an R gene promoter, a lectin promoter, a light harvesting complex promoter, a heat shock protein promoter, a chalcone synthase promoter, a zein promoter, a globulin-1 promoter, an ABA promoter, an auxin-binding protein promoter, a UDP glucose flavonoid glycosyl-transferase gene promoter, an NTI promoter, an actin promoter, an opaque 2 promoter, a b70 promoter, an oleosin promoter, a CaMV 35S promoter, a CaMV 19S promoter, a histone promoter, a turgor-inducible promoter, a pea small subunit RuBP carboxylase promoter, a Ti plasmid mannopine synthase promoter, Ti plasmid nopaline synthase promoter, a petunia chalcone isomerase promoter, a bean glycine rich protein I promoter, a CaMV 35S transcript promoter, a potato patatin promoter, or a S-E9 small subunit RuBP carboxylase promoter.

2. Other Regulatory Elements

In addition to promoters, a variety of 5' and 3' transcriptional regulatory sequences are also available for use in the present invention. Transcriptional terminators are responsible for the termination of transcription and correct mRNA polyadenylation. The 3' nontranslated regulatory DNA sequence preferably includes from about 50 to about 1,000, more preferably about 100 to about 1,000, nucleotide

base pairs and contains plant transcriptional and translational termination sequences. Appropriate transcriptional terminators and those which are known to function in plants include the CaMV 35S terminator, the *tml* terminator, the nopaline synthase terminator, the pea *rbcS* E9 terminator, the terminator for the T7 transcript from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3' end of the protease inhibitor I or II genes from potato or tomato, although other 3' elements known to those of skill in the art can also be employed. Alternatively, one also could use a gamma coixin, oleosin 3 or other terminator from the genus *Coix*.

Preferred 3' elements include those from the nopaline synthase gene of *Agrobacterium tumefaciens* (Bevan et al., 1983), the terminator for the T7 transcript from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3' end of the protease inhibitor I or II genes from potato or tomato.

As the DNA sequence between the transcription initiation site and the start of the coding sequence, i.e., the untranslated leader sequence, can influence gene expression, one may also wish to employ a particular leader sequence. Preferred leader sequences are contemplated to include those which include sequences predicted to direct optimum expression of the attached gene, i.e., to include a preferred consensus leader sequence which may increase or maintain mRNA stability and prevent inappropriate initiation of translation. The choice of such sequences will be known to those of skill in the art in light of the present disclosure. Sequences that are derived from genes that are highly expressed in plants will be most preferred.

Other sequences that have been found to enhance gene expression in transgenic plants include intron sequences (e.g., from *Adh1*, *bronzel*, *actin1*, *actin 2* (WO 00/760067), or the sucrose synthase intron) and viral leader sequences (e.g., from TMV, MCMV and AMV). For example, a number of non-translated leader sequences derived from viruses are known to enhance expression. Specifically, leader sequences from Tobacco Mosaic Virus (TMV), Maize Chlorotic Mottle Virus (MCMV), and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (e.g., Gallie et al., 1987; Skuzeski et al., 1990). Other leaders known in the art include but are not limited to: Picornavirus leaders, for example,

EMCV leader (Encephalomyocarditis 5 noncoding region) (Elroy-Stein et al., 1989); Potyvirus leaders, for example, TEV leader (Tobacco Etch Virus); MDMV leader (Maize Dwarf Mosaic Virus); Human immunoglobulin heavy-chain binding protein (BiP) leader, (Macejak et al., 1991); Untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), (Jobling et al., 1987; Tobacco mosaic virus leader (TMV), (Gallie et al., 1989; and Maize Chlorotic Mottle Virus leader (MCMV) (Lommel et al., 1991. See also, Della-Cioppa et al., 1987.

Regulatory elements such as Adh intron 1 (Callis et al., 1987), sucrose synthase intron (Vasil et al., 1989) or TMV omega element (Gallie, et al., 1989), may further be included where desired.

Examples of enhancers include elements from the CaMV 35S promoter, octopine synthase genes (Ellis et al., 1987), the rice actin I gene, the maize alcohol dehydrogenase gene (Callis et al., 1987), the maize shrunken I gene (Vasil et al., 1989), TMV Omega element (Gallie et al., 1989) and promoters from non-plant eukaryotes (e.g. yeast; Ma et al., 1988).

Vectors for use in accordance with the present invention may be constructed to include the ocs enhancer element. This element was first identified as a 16 bp palindromic enhancer from the octopine synthase (ocs) gene of utililane (Ellis et al., 1987), and is present in at least 10 other promoters (Bouchez et al., 1989). The use of an enhancer element, such as the ocs element and particularly multiple copies of the element, will act to increase the level of transcription from adjacent promoters when applied in the context of monocot transformation.

Ultimately, the most desirable DNA segments for introduction into for example a monocot genome may be homologous genes or gene families which encode a desired trait (e.g., increased yield per acre) and which are introduced under the control of novel promoters or enhancers, etc., or perhaps even homologous or tissue specific (e.g., root-, collar/sheath-, whorl-, stalk-, earshank-, kernel- or leaf-specific) promoters or control elements. Indeed, it is envisioned that a particular use of the present invention will be the targeting of a gene in a constitutive manner or a root-specific manner. For example, insect resistant genes may be expressed specifically in the whorl and collar/sheath tissues which are targets for the first and

second broods, respectively, of ECB. Likewise, genes encoding proteins with particular activity against rootworm may be targeted directly to root tissues.

Vectors for use in tissue-specific targeting of genes in transgenic plants will typically include tissue-specific promoters and may also include other tissue-specific control elements such as enhancer sequences. Promoters which direct specific or enhanced expression in certain plant tissues will be known to those of skill in the art in light of the present disclosure. These include, for example, the *rbcS* promoter, specific for green tissue; the *ocs*, *nos* and *mas* promoters which have higher activity in roots or wounded leaf tissue; a truncated (-90 to +8) 35S promoter which directs enhanced expression in roots, an alpha-tubulin gene that directs expression in roots and promoters derived from zein storage protein genes which direct expression in endosperm. It is particularly contemplated that one may advantageously use the 16 bp *ocs* enhancer element from the octopine synthase (*ocs*) gene (Ellis et al., 1987; Bouchez et al., 1989), especially when present in multiple copies, to achieve enhanced expression in roots.

Tissue specific expression may be functionally accomplished by introducing a constitutively expressed gene (all tissues) in combination with an antisense gene that is expressed only in those tissues where the gene product is not desired. For example, a gene coding for the crystal toxin protein from *B. thuringiensis* (Bt) may be introduced such that it is expressed in all tissues using the 35S promoter from Cauliflower Mosaic Virus. Expression of an antisense transcript of the Bt gene in a maize kernel, using for example a zein promoter, would prevent accumulation of the Bt protein in seed. Hence the protein encoded by the introduced gene would be present in all tissues except the kernel.

Expression of some genes in transgenic plants will be desired only under specified conditions. For example, it is proposed that expression of certain genes that confer resistance to environmental stress factors such as drought will be desired only under actual stress conditions. It is contemplated that expression of such genes throughout a plants development may have detrimental effects. It is known that a large number of genes exist that respond to the environment. For example, expression of some genes such as *rbcS*, encoding the small subunit of ribulose

bisphosphate carboxylase, is regulated by light as mediated through phytochrome. Other genes are induced by secondary stimuli. For example, synthesis of abscisic acid (ABA) is induced by certain environmental factors, including but not limited to water stress. A number of genes have been shown to be induced by ABA (Skriver and Mundy, 1990). It is also anticipated that expression of genes conferring resistance to insect predation would be desired only under conditions of actual insect infestation. Therefore, for some desired traits inducible expression of genes in transgenic plants will be desired.

Expression of a gene in a transgenic plant will be desired only in a certain time period during the development of the plant. Developmental timing is frequently correlated with tissue specific gene expression. For example, expression of zein storage proteins is initiated in the endosperm about 15 days after pollination.

Additionally, vectors may be constructed and employed in the intracellular targeting of a specific gene product within the cells of a transgenic plant or in directing a protein to the extracellular environment. This will generally be achieved by joining a DNA sequence encoding a transit or signal peptide sequence to the coding sequence of a particular gene. The resultant transit, or signal, peptide will transport the protein to a particular intracellular, or extracellular destination, respectively, and will then be post-translationally removed. Transit or signal peptides act by facilitating the transport of proteins through intracellular membranes, e.g., vacuole, vesicle, plastid and mitochondrial membranes, whereas signal peptides direct proteins through the extracellular membrane.

A particular example of such a use concerns the direction of a herbicide resistance gene, such as the EPSPS gene, to a particular organelle such as the chloroplast rather than to the cytoplasm. This is exemplified by the use of the rbcS transit peptide which confers plastid-specific targeting of proteins. In addition, it is proposed that it may be desirable to target certain genes responsible for male sterility to the mitochondria, or to target certain genes for resistance to phytopathogenic organisms to the extracellular spaces, or to target proteins to the vacuole.

By facilitating the transport of the protein into compartments inside and outside the cell, these sequences may increase the accumulation of gene product

protecting them from proteolytic degradation. These sequences also allow for additional mRNA sequences from highly expressed genes to be attached to the coding sequence of the genes. Since mRNA being translated by ribosomes is more stable than naked mRNA, the presence of translatable mRNA in front of the gene
5 may increase the overall stability of the mRNA transcript from the gene and thereby increase synthesis of the gene product. Since transit and signal sequences are usually post- translationally removed from the initial translation product, the use of these sequences allows for the addition of extra translated sequences that may not appear on the final polypeptide. Targeting of certain proteins may be desirable in
10 order to enhance the stability of the protein (U.S. Patent No. 5,545,818).

It may be useful to target DNA itself within a cell. For example, it may be useful to target introduced DNA to the nucleus as this may increase the frequency of transformation. Within the nucleus itself it would be useful to target a gene in order to achieve site specific integration. For example, it would be useful to have an gene
15 introduced through transformation replace an existing gene in the cell.

Other elements include those that can be regulated by endogenous or exogenous agents, e.g., by zinc finger proteins, including naturally occurring zinc finger proteins or chimeric zinc finger proteins (see, e.g., U.S. Patent No. 5,789,538, WO 99/48909; WO 99/45132; WO 98/53060; WO 98/53057; WO 98/53058; WO
20 00/23464; WO 95/19431; and WO 98/54311) or myb-like transcription factors. For example, a chimeric zinc finger protein may include amino acid sequences which bind to a specific DNA sequence (the zinc finger) and amino acid sequences that activate (e.g., GAL 4 sequences) or repress the transcription of the sequences linked to the specific DNA sequence.

25 3. Preferred Nucleic Acid Molecules of the Invention

The invention relates to an isolated plant, e.g., *Arabidopsis*, *Chenopodium* and rice, nucleic acid molecule comprising a gene having an open reading frame, the expression of which is altered in response to pathogen infection, as well as the endogenous plant promoters for those genes. However, the expression of these
30 genes may also be altered in response to non-pathogens, e.g., in response to environmental stimuli. The nucleic acid molecules can be used in pathogen control

strategies, e.g., by overexpressing nucleic acid molecules which can confer tolerance to a cell, or by altering the expression of host genes which are required for pathogen infection, e.g., by “knocking out” the expression of at least one genomic copy of the gene. Plants having genetic disruptions in host genes may be less susceptible to infection, e.g., due to a decrease or absence of a host protein needed for infection, or, alternatively, hypersusceptible to infection. Plants that are hypersusceptible to infection may be useful to prepare transgenic plants as the expression of the gene(s) which was disrupted may be related to gene silencing.

Preferred sources from which the nucleic acid molecules of the invention can be obtained or isolated include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea ultilane*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, duckweed (*Lemna*), barley, vegetables, ornamentals, and conifers.

Duckweed (*Lemna*, see WO 00/07210) includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S.*

punctata); genus *Woffia* (*Wa. Angusta*, *Wa. Arrhiza*, *Wa. Australina*, *Wa. Borealis*, *Wa. Brasiliensis*, *Wa. Columbiana*, *Wa. Elongata*, *Wa. Globosa*, *Wa. Microscopica*, *Wa. Neglecta*) and genus *Wofiella* (*Wl. utila*, *Wl. utilane n*, *Wl. gladiata*, *Wl. utila*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*). Any other
5 genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt, Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae— A
10 Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)).

Vegetables from which to obtain or isolate the nucleic acid molecules of the invention include, but are not limited to, tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such
15 as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals from which to obtain or isolate the nucleic acid molecules of the invention include, but are not limited to, azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation
20 (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga*
25 *utilane*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants from which the nucleic acid molecules of the invention can be isolated or obtained include, but are not limited to, beans and peas.
30 Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, and the like. Legumes include,

- but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo.
- 5 Papaya, garlic, pea, peach, pepper, petunia, strawberry, sorghum, sweet potato, turnip, safflower, corn, pea, endive, gourd, grape, snap bean, chicory, cotton, tobacco, aubergine, beet, buckwheat, broad bean, nectarine, avocado, mango, banana, groundnut, potato,peanut, lettuce, pineapple, spinach, squash, sugarbeet, sugarcane, sweet corn, chrysanthemum.
- 10 Other preferred sources of the nucleic acid molecules of the invention include *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, tritcale, vine, yams,
- 15 apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, ultilan sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, ultilane, and zucchini.
- 20 Yet other sources of nucleic acid molecules are ornamental plants including, but not limited to, impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and
- 25 Zinnia, and plants such as those shown in Table 1.

Table 1

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Cucurbitaceae	<i>Cucumis sativus</i>	Cucumber		http://www.cucurbit.org/
	<i>Cucumis melo</i>	Melon		http://genome.cornell.edu/cg
	<i>Citrullus lanatus</i>	Watermelon		
	<i>Cucurbita pepo</i>	Squash – summer		
	<i>Cucurbita maxima</i>	Squash – winter		
	<i>Cucurbita moschata</i>	Pumpkin /butternut		
Total				http://www.nal.usda.gov/pgdic/Map_proj/

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Solanaceae	<i>Lycopersicon esculentum</i>	Tomato	<ul style="list-style-type: none"> • 15x BAC on variety Heinz 1706 order from Clemson Genome center (www.genome.clemson.edu) • 11.6x BAC of L. cheesmanii (originates from J. Giovannoni) available from Clemson genome center (www.genome.clemson.edu) • EST collection from TIGR (www.tigr.org/tdb/lgi/index.html) • EST collection from Clemson Genome Center (www.genome.clemson.edu) • TAG 99:254-271, 1999 (esculentum x pennelli) • TAG 89:1007-1013, 1994 (peruvianum) • Plant Cell Reports 12:293-297, 1993 (RAPDs) • Genetics 132:1141-1160, 1992 (potato x tomato) • Genetics 120:1095-1105, 1988 (RFLP potato and tomato) • Genetics 115:387-393, 1986 (esculentum x pennelli isozyme and cDNAs) 	genome.cornell.edu/solgene http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=solgenes http://genome.cornell.edu/tgc/ http://tgrc.ucdavis.edu/
	<i>Capsicum annuum</i>	Pepper		http://neptune.netimages.com/~chile/science.html

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
	<i>Capsicum frutescens</i>	Chile pepper		
	<i>Solanum melongena</i>	Eggplant		
	(<i>Nicotiana tabacum</i>)	(Tobacco)		
	(<i>Solanum tuberosum</i>)	(Potato)		
	(<i>Petunia x hybrida hort. Ex E. Vilm.</i>)	(Petunia)	4x BAC of <i>Petunia hybrida</i> 7984 available from Clemson genome center (www.genome.clemson.edu)	
Total				http://www.national.usda.gov/pgdic/Map_proj/
Brassicaceae	<i>Brassica oleracea</i> L. var. <i>italica</i>	Broccoli		http://res.agr.cornell.edu/ecorc/cwmt/crucifer/traits/index.htm http://geneous.cit.cornell.edu/cabbage/abolutcab.html
	<i>Brassica oleracea</i> L. var. <i>capitata</i>	Cabbage		
	<i>Brassica rapa</i>	Chinese Cabbage		
	<i>Brassica oleracea</i> L. var. <i>botrytis</i>	Cauliflower		
	<i>Raphanus sativus</i> var. <i>niger</i>	Daikon		
	(<i>Brassica napus</i>)	(Oilseed rape)		http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=brassicadb

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
		Arabidopsis	12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=agr
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Umbelliferae	<i>Daucus carota</i>	Carrot		
Compositae	<i>Lactuca sativa</i>	Lettuce		
	<i>Helianthus annuus</i>	(Sunflower)		
Total				
Chenopodiaceae	<i>Spinacia oleracea</i>	Spinach		
	(<i>Beta vulgaris</i>)	(Sugar Beet)		
Total				
Leguminosae	<i>Phaseolus vulgaris</i>	Bean	4.3x BAC available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=beangen
	<i>Pisum sativum</i>	Pea		
	(<i>Glycine max</i>)	(Soybean)	7.5x and 7.9x BACs available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase
Total			http://www.nal.usda.gov/pgdic/Map_proj/	

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Gramineae	<i>Zea mays</i>	Sweet Corn	Novartis BACs for Mo17 and B73 have been donated to Clemson Genome Center (www.genome.clemson.edu)	
	(<i>Zea mays</i>)	(Field Corn)		http://www.agron.missouri.edu/mnl/
Total			http://www.nal.usda.gov/pgdic/Map_proj/	
Liliaceae	<i>Allium cepa</i>	Onion		
		Leek		
		(Garlic)		
		(Asparagus)		
Total			http://www.nal.usda.gov/pgdic/Map_proj/	

Preferred forage and turf grass nucleic acid sources for the nucleic acid molecules of the invention include, but are not limited to, alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop. Yet other preferred sources include, but are not limited to, crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean, barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, oat, rye, rape, wheat, millet, tobacco, and the like), and even more preferably corn, rice and soybean.

According to one embodiment, the present invention is directed to a nucleic acid molecule comprising a nucleotide sequence isolated or obtained from any plant which encodes a polypeptide having at least 70% amino acid sequence identity to a polypeptide encoded by a gene comprising any one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737, or a gene comprising SEQ ID NOs:1001-1094, 2137-2661 or 4738-6813. Based on the *Arabidopsis*, *Chenopodium* and rice nucleic acid sequences of the present invention, orthologs may be identified or isolated from the genome of any desired organism, preferably from another plant, according to

well known techniques based on their sequence similarity to the *Arabidopsis*,
Chenopodium and rice nucleic acid sequences, e.g., hybridization, PCR or computer
generated sequence comparisons. For example, all or a portion of a particular
Arabidopsis, *Chenopodium* and rice nucleic acid sequence is used as a probe that
5 selectively hybridizes to other gene sequences present in a population of cloned
genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries)
from a chosen source organism. Further, suitable genomic and cDNA libraries may
be prepared from any cell or tissue of an organism. Such techniques include
hybridization screening of plated DNA libraries (either plaques or colonies; see, e.g.,
10 Sambrook et al., 1989) and amplification by PCR using oligonucleotide primers
preferably corresponding to sequence domains conserved among related polypeptide
or subsequences of the nucleotide sequences provided herein (see, e.g., Innis et al.,
1990). These methods are particularly well suited to the isolation of gene sequences
from organisms closely related to the organism from which the probe sequence is
15 derived. The application of these methods using the *Arabidopsis* sequences as
probes is well suited for the isolation of gene sequences from any source organism,
preferably other plant species. In a PCR approach, oligonucleotide primers can be
designed for use in PCR reactions to amplify corresponding DNA sequences from
cDNA or genomic DNA extracted from any plant of interest. Methods for designing
20 PCR primers and PCR cloning are generally known in the art.

In hybridization techniques, all or part of a known nucleotide sequence is
used as a probe that selectively hybridizes to other corresponding nucleotide
sequences present in a population of cloned genomic DNA fragments or cDNA
fragments (i.e., genomic or cDNA libraries) from a chosen organism. The
25 hybridization probes may be genomic DNA fragments, cDNA fragments, RNA
fragments, or other oligonucleotides, and may be labeled with a detectable group
such as ^{32}P , or any other detectable marker. Thus, for example, probes for
hybridization can be made by labeling synthetic oligonucleotides based on the
sequence of the invention. Methods for preparation of probes for hybridization and
30 for construction of cDNA and genomic libraries are generally known in the art and
are disclosed in Sambrook et al. (1989). In general, sequences that hybridize to the

sequences disclosed herein will have at least 40% to 50%, about 60% to 70% and even about 80% 85%, 90%, 95% to 98% or more identity with the disclosed sequences. That is, the sequence similarity of sequences may range, sharing at least about 40% to 50%, about 60% to 70%, and even about 80%, 85%, 90%, 95% to
5 98% sequence similarity.

The nucleic acid molecules of the invention can also be identified by, for example, a search of known databases for genes encoding polypeptides having a specified amino acid sequence identity or DNA having a specified nucleotide sequence identity. Methods of alignment of sequences for comparison are well
10 known in the art and are described hereinabove.

4. Methods for Mutagenizing DNA

It is specifically contemplated by the inventors that one could mutagenize DNA having a promoter or open reading frame to, for example, potentially improve the utility of the DNA for expression of transgenes in plants. The mutagenesis can
15 be carried out at random and the mutagenized sequences screened for activity in a trial-by-error procedure. Alternatively, particular sequences which provide the promoter with desirable expression characteristics, or a promoter with expression enhancement activity, could be identified and these or similar sequences introduced into the sequences via mutation. It is further contemplated that one could
20 mutagenize these sequences in order to enhance their expression of transgenes in a particular species.

The means for mutagenizing a DNA segment of the current invention are well-known to those of skill in the art. As indicated, modifications may be made by random or site-specific mutagenesis procedures. The DNA may be modified by
25 altering its structure through the addition or deletion of one or more nucleotides from the sequence which encodes the corresponding un-modified sequences.

Mutagenesis may be performed in accordance with any of the techniques known in the art, such as, and not limited to, synthesizing an oligonucleotide having one or more mutations within the sequence of a particular regulatory region. In
30 particular, site-specific mutagenesis is a technique useful in the preparation of promoter mutants, through specific mutagenesis of the underlying DNA. The

technique further provides a ready ability to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA. Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Typically, a primer of about 17 to about 75 nucleotides or more in length is preferred, with about 10 to about 25 or more residues on both sides of the junction of the sequence being altered.

In general, the technique of site-specific mutagenesis is well known in the art, as exemplified by various publications. As will be appreciated, the technique typically employs a phage vector which exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially available and their use is generally well known to those skilled in the art.

Double stranded plasmids also are routinely employed in site directed mutagenesis which eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double stranded vector which includes within its sequence a DNA sequence which encodes the promoter. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation.

This heteroduplex vector is then used to transform or transfect appropriate cells, such as *E. coli* cells, and cells are selected which include recombinant vectors bearing the mutated sequence arrangement. Vector DNA can then be isolated from

these cells and used for plant transformation. A genetic selection scheme was devised by Kunkel et al. (1987) to enrich for clones incorporating mutagenic oligonucleotides. Alternatively, the use of PCR with commercially available thermostable enzymes such as Taq polymerase may be used to incorporate a mutagenic oligonucleotide primer into an amplified DNA fragment that can then be cloned into an appropriate cloning or expression vector. The PCR-mediated mutagenesis procedures of Tomic et al. (1990) and Upender et al. (1995) provide two examples of such protocols. A PCR employing a thermostable ligase in addition to a thermostable polymerase also may be used to incorporate a phosphorylated mutagenic oligonucleotide into an amplified DNA fragment that may then be cloned into an appropriate cloning or expression vector. The mutagenesis procedure described by Michael (1994) provides an example of one such protocol.

The preparation of sequence variants of DNA segments using site-directed mutagenesis is provided as a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of DNA sequences may be obtained. For example, recombinant vectors encoding the desired promoter sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants.

In addition, an unmodified or modified nucleotide sequence of the present invention can be varied by shuffling the sequence of the invention. To test for a function of variant DNA sequences according to the invention, the sequence of interest is operably linked to a selectable or screenable marker gene and expression of the marker gene is tested in transient expression assays with protoplasts or in stably transformed plants. It is known to the skilled artisan that DNA sequences capable of driving expression of an associated nucleotide sequence are build in a modular way. Accordingly, expression levels from shorter DNA fragments may be different than the one from the longest fragment and may be different from each other. For example, deletion of a down-regulating upstream element will lead to an increase in the expression levels of the associated nucleotide sequence while deletion of an up-regulating element will decrease the expression levels of the associated nucleotide sequence. It is also known to the skilled artisan that deletion of

development-specific or a tissue-specific element will lead to a temporally or spatially altered expression profile of the associated nucleotide sequence.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" also is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template-dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (see, for example, Watson and Rarnstad, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U.S. Patent No. 4,237,224. A number of template dependent processes are available to amplify the target sequences of interest present in a sample, such methods being well known in the art and specifically disclosed herein below.

Where a clone comprising a promoter has been isolated in accordance with the instant invention, one may wish to delimit the essential promoter regions within the clone. One efficient, targeted means for preparing mutagenizing promoters relies upon the identification of putative regulatory elements within the promoter sequence. This can be initiated by comparison with promoter sequences known to be expressed in similar tissue-specific or developmentally unique manner. Sequences which are shared among promoters with similar expression patterns are likely candidates for the binding of transcription factors and are thus likely elements which confer expression patterns. Confirmation of these putative regulatory elements can be achieved by deletion analysis of each putative regulatory region followed by functional analysis of each deletion construct by assay of a reporter gene which is functionally attached to each construct. As such, once a starting promoter sequence

is provided, any of a number of different deletion mutants of the starting promoter could be readily prepared.

As indicated above, deletion mutants, deletion mutants of the promoter of the invention also could be randomly prepared and then assayed. With this strategy, a series of constructs are prepared, each containing a different portion of the clone (a subclone), and these constructs are then screened for activity. A suitable means for screening for activity is to attach a deleted promoter or intron construct which contains a deleted segment to a selectable or screenable marker, and to isolate only those cells expressing the marker gene. In this way, a number of different, deleted promoter constructs are identified which still retain the desired, or even enhanced, activity. The smallest segment which is required for activity is thereby identified through comparison of the selected constructs. This segment may then be used for the construction of vectors for the expression of exogenous genes.

B. Marker Genes

In order to improve the ability to identify transformants, one may desire to employ a selectable or screenable marker gene as, or in addition to, the expressible gene of interest. "Marker genes" are genes that impart a distinct phenotype to cells expressing the marker gene and thus allow such transformed cells to be distinguished from cells that do not have the marker. Such genes may encode either a selectable or screenable marker, depending on whether the marker confers a trait which one can 'select' for by chemical means, i.e., through the use of a selective agent (e.g., a herbicide, antibiotic, or the like), or whether it is simply a trait that one can identify through observation or testing, i.e., by 'screening' (e.g., the R-locus trait, the green fluorescent protein (GFP)). Of course, many examples of suitable marker genes are known to the art and can be employed in the practice of the invention.

Included within the terms selectable or screenable marker genes are also genes which encode a "secretable marker" whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected by their catalytic activity.

Secretable proteins fall into a number of classes, including small, diffusible proteins detectable, e.g., by ELISA; small active enzymes detectable in extracellular solution (e.g., alpha-amylase, beta-lactamase, phosphinothricin acetyltransferase); and proteins that are inserted or trapped in the cell wall (e.g., proteins that include a leader sequence such as that found in the expression unit of extensin or tobacco PR-S).

With regard to selectable secretable markers, the use of a gene that encodes a protein that becomes sequestered in the cell wall, and which protein includes a unique epitope is considered to be particularly advantageous. Such a secreted antigen marker would ideally employ an epitope sequence that would provide low background in plant tissue, a promoter-leader sequence that would impart efficient expression and targeting across the plasma membrane, and would produce protein that is bound in the cell wall and yet accessible to antibodies. A normally secreted wall protein modified to include a unique epitope would satisfy all such requirements.

One example of a protein suitable for modification in this manner is extensin, or hydroxyproline rich glycoprotein (HPRG). For example, the maize HPRG (Steifel et al., 1990) molecule is well characterized in terms of molecular biology, expression and protein structure. However, any one of a variety of utilane and/or glycine-rich wall proteins (Keller et al., 1989) could be modified by the addition of an antigenic site to create a screenable marker.

One exemplary embodiment of a secretable screenable marker concerns the use of a maize sequence encoding the wall protein HPRG, modified to include a 15 residue epitope from the pro-region of murine interleukin, however, virtually any detectable epitope may be employed in such embodiments, as selected from the extremely wide variety of antigen-antibody combinations known to those of skill in the art. The unique extracellular epitope can then be straightforwardly detected using antibody labeling in conjunction with chromogenic or fluorescent adjuncts.

Elements of the present disclosure may be exemplified in detail through the use of the bar and/or GUS genes, and also through the use of various other markers. Of course, in light of this disclosure, numerous other possible selectable and/or

screenable marker genes will be apparent to those of skill in the art in addition to the one set forth hereinbelow. Therefore, it will be understood that the following discussion is exemplary rather than exhaustive. In light of the techniques disclosed herein and the general recombinant techniques which are known in the art, the present invention renders possible the introduction of any gene, including marker genes, into a recipient cell to generate a transformed plant.

1. Selectable Markers

Possible selectable markers for use in connection with the present invention include, but are not limited to, a *neo* gene which codes for kanamycin resistance and can be selected for using kanamycin, G418, paromomycin, and the like; a *bar* gene which codes for bialaphos or phosphinothricin resistance; a gene which encodes an altered EPSP synthase protein (Hinchee et al., 1988) thus conferring glyphosate resistance; a nitrilase gene such as *bxn* from *Klebsiella ozaenae* which confers resistance to bromoxynil (Stalker et al., 1988); a mutant acetolactate synthase gene (ALS) which confers resistance to imidazolinone, sulfonyleurea or other ALS-inhibiting chemicals (European Patent Application 154,204, 1985); a methotrexate-resistant DHFR gene (Thillet et al., 1988); a dalapon dehalogenase gene that confers resistance to the herbicide dalapon; a mutated anthranilate synthase gene that confers resistance to 5-methyl tryptophan. Preferred selectable marker genes encode phosphinothricin acetyltransferase; glyphosate resistant EPSPS, aminoglycoside phosphotransferase; hygromycin phosphotransferase, or neomycin phosphotransferase. Where a mutant EPSP synthase gene is employed, additional benefit may be realized through the incorporation of a suitable chloroplast transit peptide, CTP (European Patent Application 0,218,571, 1987).

An illustrative embodiment of a selectable marker gene capable of being used in systems to select transformants is the genes that encode the enzyme phosphinothricin acetyltransferase, such as the *bar* gene from *Streptomyces hygroscopicus* or the *pat* gene from *Streptomyces viridochromogenes*. The enzyme phosphinothricin acetyl transferase (PAT) inactivates the active ingredient in the herbicide bialaphos, phosphinothricin (PPT). PPT inhibits glutamine synthetase, (Murakami et al., 1986; Twell et al., 1989) causing rapid accumulation of ammonia

and cell death. The success in using this selective system in conjunction with monocots was particularly surprising because of the major difficulties which have been reported in transformation of cereals.

Where one desires to employ a bialaphos resistance gene in the practice of the invention, a particularly useful gene for this purpose is the *bar* or *pat* genes obtainable from species of *Streptomyces* (e.g., ATCC No. 21,705). The cloning of the *bar* gene has been described (Murakami et al., 1986; Thompson et al., 1987) as has the use of the *bar* gene in the context of plants other than monocots (De Block et al., 1987; De Block et al., 1989).

Selection markers resulting in positive selection, such as a phosphomannose isomerase gene, as described in patent application WO 93/05163, may also be used. Alternative genes to be used for positive selection are described in WO 94/20627 and encode xyloisomerases and phosphomanno-isomerases such as mannose-6-phosphate isomerase and mannose-1-phosphate isomerase; phosphomanno mutase; mannose epimerases such as those which convert carbohydrates to mannose or mannose to carbohydrates such as glucose or galactose; phosphatases such as mannose or xylose phosphatase, mannose-6-phosphatase and mannose-1-phosphatase, and permeases which are involved in the transport of mannose, or a derivative, or a precursor thereof into the cell. Transformed cells are identified without damaging or killing the non-transformed cells in the population and without co-introduction of antibiotic or herbicide resistance genes. As described in WO 93/05163, in addition to the fact that the need for antibiotic or herbicide resistance genes is eliminated, it has been shown that the positive selection method is often far more efficient than traditional negative selection.

2. Screenable Markers

Screenable markers that may be employed include, but are not limited to, a beta-glucuronidase (GUS) or *uidA* gene which encodes an enzyme for which various chromogenic substrates are known; an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues (Dellaporta et al., 1988); a beta-lactamase gene (Sutcliffe, 1978), which encodes an

enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a *xylE* gene (Zukowsky et al., 1983) which encodes a catechol dioxygenase that can convert chromogenic catechols; an α -amylase gene (Ikuta et al., 1990); a tyrosinase gene (Katz et al., 1983) which encodes an enzyme
5 capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to form the easily detectable compound melanin; a β -galactosidase gene, which encodes an enzyme for which there are chromogenic substrates; a luciferase (*lux*) gene (Ow et al., 1986), which allows for bioluminescence detection; or even an aequorin gene (Prasher et al., 1985), which may be employed in calcium-sensitive
10 bioluminescence detection, or a green fluorescent protein gene (Niedz et al., 1995).

Genes from the maize R gene complex are contemplated to be particularly useful as screenable markers. The R gene complex in maize encodes a protein that acts to regulate the production of anthocyanin pigments in most seed and plant tissue. A gene from the R gene complex was applied to maize transformation,
15 because the expression of this gene in transformed cells does not harm the cells. Thus, an R gene introduced into such cells will cause the expression of a red pigment and, if stably incorporated, can be visually scored as a red sector. If a maize line is carries dominant ultila for genes encoding the enzymatic intermediates in the anthocyanin biosynthetic pathway (C2, A1, A2, Bz1 and Bz2)
20 (Roth et al., 1990), but carries a recessive allele at the R locus, transformation of any cell from that line with R will result in red pigment formation. Exemplary lines include Wisconsin 22 which contains the rg-Stadler allele and TR112, a K55 derivative which is r-g, b, P1. Alternatively any genotype of maize can be utilized if the C1 and R alleles are introduced together.

25 It is further proposed that R gene regulatory regions may be employed in chimeric constructs in order to provide mechanisms for controlling the expression of chimeric genes. More diversity of phenotypic expression is known at the R locus than at any other locus (Coe et al., 1988). It is contemplated that regulatory regions obtained from regions 5' to the structural R gene would be valuable in directing the
30 expression of genes, e.g., insect resistance, drought resistance, herbicide tolerance or other protein coding regions. For the purposes of the present invention, it is

believed that any of the various R gene family members may be successfully employed (e.g., P, S, Lc, etc.). However, the most preferred will generally be Sn (particularly Sn:bol3). Sn is a dominant member of the R gene complex and is functionally similar to the R and B loci in that Sn controls the tissue specific
5 deposition of anthocyanin pigments in certain seedling and plant cells, therefore, its phenotype is similar to R.

A further screenable marker contemplated for use in the present invention is firefly luciferase, encoded by the *lux* gene. The presence of the *lux* gene in transformed cells may be detected using, for example, X-ray film, scintillation
10 counting, fluorescent spectrophotometry, low-light video cameras, photon counting cameras or multiwell luminometry. It is also envisioned that this system may be developed for populational screening for bioluminescence, such as on tissue culture plates, or even for whole plant screening. Where use of a screenable marker gene such as *lux* or GFP is desired, benefit may be realized by creating a gene fusion
15 between the screenable marker gene and a selectable marker gene, for example, a GFP-NPTII gene fusion. This could allow, for example, selection of transformed cells followed by screening of transgenic plants or seeds.

C. Exogenous Genes for Modification of Plant Phenotypes

Genes of interest are reflective of the commercial markets and interests of
20 those involved in the development of the crop. Crops and markets of interest changes, and as developing nations open up world markets, new crops and technologies will also emerge. In addition, as the understanding of agronomic traits and characteristics such as yield and heterosis increase, the choice of genes for transformation will change accordingly. General categories of genes of interest
25 include, for example, those genes involved in information, such as zinc fingers, those involved in communication, such as kinases, and those involved in housekeeping, such as heat shock proteins. More specific categories of transgenes, for example, include genes encoding important traits for agronomics, insect resistance, disease resistance, herbicide resistance, sterility, grain characteristics, and
30 commercial products. Genes of interest include, generally, those involved in starch, oil, carbohydrate, or nutrient metabolism, as well as those affecting kernel size,

sucrose loading, zinc finger proteins, see, e.g., U.S. Patent No. 5,789,538, WO 99/48909; WO 99/45132; WO 98/53060; WO 98/53057; WO 98/53058; WO 00/23464; WO 95/19431; and WO 98/54311, and the like.

One skilled in the art recognizes that the expression level and regulation of a transgene in a plant can vary significantly from line to line. Thus, one has to test several lines to find one with the desired expression level and regulation. Once a line is identified with the desired regulation specificity of a chimeric Cre transgene, it can be crossed with lines carrying different inactive replicons or inactive transgene for activation.

Other sequences which may be linked to the gene of interest which encodes a polypeptide are those which can target to a specific organelle, e.g., to the mitochondria, nucleus, or plastid, within the plant cell. Targeting can be achieved by providing the polypeptide with an appropriate targeting peptide sequence, such as a secretory signal peptide (for secretion or cell wall or membrane targeting, a plastid transit peptide, a chloroplast transit peptide, e.g., the chlorophyll a/b binding protein, a mitochondrial target peptide, a vacuole targeting peptide, or a nuclear targeting peptide, and the like. For example, the small subunit of ribulose biphosphate carboxylase transit peptide, the EPSPS transit peptide or the dihydrodipicolinic acid synthase transit peptide may be used. For examples of plastid organelle targeting sequences (see WO 00/12732). Plastids are a class of plant organelles derived from proplastids and include chloroplasts, leucoplasts, aravloplast, and chromoplasts. The plastids are major sites of biosynthesis in plants. In addition to photosynthesis in the chloroplast, plastids are also sites of lipid biosynthesis, nitrate reduction to ammonium, and starch storage. And while plastids contain their own circular genome, most of the proteins localized to the plastids are encoded by the nuclear genome and are imported into the organelle from the cytoplasm.

Transgenes used with the present invention will often be genes that direct the expression of a particular protein or polypeptide product, but they may also be non-expressible DNA segments, e.g., transposons such as Ds that do not direct their own transposition. As used herein, an "expressible gene" is any gene that is capable of being transcribed into RNA (e.g., mRNA, antisense RNA, etc.) or translated into a

protein, expressed as a trait of interest, or the like, etc., and is not limited to selectable, screenable or non-selectable marker genes. The invention also contemplates that, where both an expressible gene that is not necessarily a marker gene is employed in combination with a marker gene, one may employ the separate
5 genes on either the same or different DNA segments for transformation. In the latter case, the different vectors are delivered concurrently to recipient cells to maximize cotransformation.

The choice of the particular DNA segments to be delivered to the recipient cells will often depend on the purpose of the transformation. One of the major
10 purposes of transformation of crop plants is to add some commercially desirable, agronomically important traits to the plant. Such traits include, but are not limited to, herbicide resistance or tolerance; insect resistance or tolerance; disease resistance or tolerance (viral, bacterial, fungal, nematode); stress tolerance and/or resistance, as exemplified by resistance or tolerance to drought, heat, chilling, freezing, excessive
15 moisture, salt stress; oxidative stress; increased yields; food content and makeup; physical appearance; male sterility; drydown; standability; prolificacy; starch properties; oil quantity and quality; and the like. One may desire to incorporate one or more genes conferring any such desirable trait or traits, such as, for example, a gene or genes encoding pathogen resistance.

In certain embodiments, the present invention contemplates the transformation of a recipient cell with more than one advantageous transgene. Two or more transgenes can be supplied in a single transformation event using either distinct transgene-encoding vectors, or using a single vector incorporating two or more gene coding sequences. For example, plasmids bearing the *bar* and *aroA*
25 expression units in either convergent, divergent, or colinear orientation, are considered to be particularly useful. Further preferred combinations are those of an insect resistance gene, such as a *Bt* gene, along with a protease inhibitor gene such as pinII, or the use of *bar* in combination with either of the above genes. Of course, any two or more transgenes of any description, such as those conferring herbicide,
30 insect, disease (viral, bacterial, fungal, nematode) or drought resistance, male

sterility, drydown, standability, prolificacy, starch properties, oil quantity and quality, or those increasing yield or nutritional quality may be employed as desired.

1. Herbicide Resistance

The genes encoding phosphinothricin acetyltransferase (*bar* and *pat*),
5 glyphosate tolerant EPSP synthase genes, the glyphosate degradative enzyme gene
gox encoding glyphosate oxidoreductase, *deh* (encoding a dehalogenase enzyme that
inactivates dalapon), herbicide resistant (e.g., sulfonylurea and imidazolinone)
acetolactate synthase, and *bxn* genes (encoding a nitrilase enzyme that degrades
bromoxynil) are good examples of herbicide resistant genes for use in
10 transformation. The *bar* and *pat* genes code for an enzyme, phosphinothricin
acetyltransferase (PAT), which inactivates the herbicide phosphinothricin and
prevents this compound from inhibiting glutamine synthetase enzymes. The enzyme
5-enolpyruvylshikimate 3-phosphate synthase (EPSP Synthase), is normally
inhibited by the herbicide N-(phosphonomethyl)glycine (glyphosate). However,
15 genes are known that encode glyphosate-resistant EPSP Synthase enzymes.

These genes are particularly contemplated for use in monocot
transformation. The *deh* gene encodes the enzyme dalapon dehalogenase and
confers resistance to the herbicide dalapon. The *bxn* gene codes for a specific
nitrilase enzyme that converts bromoxynil to a non-herbicidal degradation product.

20 2. Insect Resistance

An important aspect of the present invention concerns the introduction of
insect resistance-conferring genes into plants. Potential insect resistance genes
which can be introduced include *Bacillus thuringiensis* crystal toxin genes or *Bt*
genes (Watrud et al., 1985). *Bt* genes may provide resistance to lepidopteran or
25 coleopteran pests such as European Corn Borer (ECB) and corn rootworm (CRW).
Preferred *Bt* toxin genes for use in such embodiments include the CryIA(b) and
CryIA(c) genes. Endotoxin genes from other species of *B. thuringiensis* which
affect insect growth or development may also be employed in this regard.

The poor expression of *Bt* toxin genes in plants is a well-documented
30 phenomenon, and the use of different promoters, fusion proteins, and leader
sequences has not led to significant increases in *Bt* protein expression (Vaeck et al.,

1989; Barton et al., 1987). It is therefore contemplated that the most advantageous *Bt* genes for use in the transformation protocols disclosed herein will be those in which the coding sequence has been modified to effect increased expression in plants, and more particularly, those in which maize preferred codons have been used. Examples of such modified *Bt* toxin genes include the variant *Bt* CryIA(b) gene termed Iab6 (Perlak et al., 1991) and the synthetic CryIA(c) genes termed 1800a and 1800b.

Protease inhibitors may also provide insect resistance (Johnson et al., 1989), and will thus have utility in plant transformation. The use of a protease inhibitor II gene, *pinII*, from tomato or potato is envisioned to be particularly useful. Even more advantageous is the use of a *pinIII* gene in combination with a *Bt* toxin gene, the combined effect of which has been discovered by the present inventors to produce synergistic insecticidal activity. Other genes which encode inhibitors of the insects' digestive system, or those that encode enzymes or co-factors that facilitate the production of inhibitors, may also be useful. This group may be exemplified by oryzacystatin and amylase inhibitors, such as those from wheat and barley.

Also, genes encoding lectins may confer additional or alternative insecticide properties. Lectins (originally termed phytohemagglutinins) are multivalent carbohydrate-binding proteins which have the ability to agglutinate red blood cells from a range of species. Lectins have been identified recently as insecticidal agents with activity against weevils, ECB and rootworm (Murdock et al., 1990; Czapla and Lang, 1990). Lectin genes contemplated to be useful include, for example, barley and wheat germ agglutinin (WGA) and rice lectins (Gatehouse et al., 1984), with WGA being preferred.

Genes controlling the production of large or small polypeptides active against insects when introduced into the insect pests, such as, e.g., lytic peptides, peptide hormones and toxins and venoms, form another aspect of the invention. For example, it is contemplated that the expression of juvenile hormone esterase, directed towards specific insect pests, may also result in insecticidal activity, or perhaps cause cessation of metamorphosis (Hammock et al., 1990).

Transgenic plants expressing genes which encode enzymes that affect the integrity of the insect cuticle form yet another aspect of the invention. Such genes include those encoding, e.g., chitinase, proteases, lipases and also genes for the production of nikkomycin, a compound that inhibits chitin synthesis, the

5 introduction of any of which is contemplated to produce insect resistant maize plants. Genes that code for activities that affect insect molting, such those affecting the production of ecdysteroid UDP-glucosyl transferase, also fall within the scope of the useful transgenes of the present invention.

Genes that code for enzymes that facilitate the production of compounds that

10 reduce the nutritional quality of the host plant to insect pests are also encompassed by the present invention. It may be possible, for instance, to confer insecticidal activity on a plant by altering its sterol composition. Sterols are obtained by insects from their diet and are used for hormone synthesis and membrane stability. Therefore alterations in plant sterol composition by expression of novel genes, e.g.,

15 those that directly promote the production of undesirable sterols or those that convert desirable sterols into undesirable forms, could have a negative effect on insect growth and/or development and hence endow the plant with insecticidal activity. Lipxygenases are naturally occurring plant enzymes that have been shown to exhibit anti-nutritional effects on insects and to reduce the nutritional quality of

20 their diet. Therefore, further embodiments of the invention concern transgenic plants with enhanced lipxygenase activity which may be resistant to insect feeding.

The present invention also provides methods and compositions by which to achieve qualitative or quantitative changes in plant secondary metabolites. One example concerns transforming plants to produce DIMBOA which, it is

25 contemplated, will confer resistance to European corn borer, rootworm and several other maize insect pests. Candidate genes that are particularly considered for use in this regard include those genes at the *bx* locus known to be involved in the synthetic DIMBOA pathway (Dunn et al., 1981). The introduction of genes that can regulate the production of maysin, and genes involved in the production of dhurrin in

30 sorghum, is also contemplated to be of use in facilitating resistance to earworm and rootworm, respectively.

Tripsacum dactyloides is a species of grass that is resistant to certain insects, including corn root worm. It is anticipated that genes encoding proteins that are toxic to insects or are involved in the biosynthesis of compounds toxic to insects will be isolated from *Tripsacum* and that these novel genes will be useful in

5 conferring resistance to insects. It is known that the basis of insect resistance in *Tripsacum* is genetic, because said resistance has been transferred to *Zea mays* via sexual crosses (Branson and Guss, 1972).

Further genes encoding proteins characterized as having potential insecticidal activity may also be used as transgenes in accordance herewith. Such

10 genes include, for example, the cowpea trypsin inhibitor (CpTI; Hilder et al., 1987) which may be used as a rootworm deterrent; genes encoding avermectin (Campbell, 1989; Ikeda et al., 1987) which may prove particularly useful as a corn rootworm deterrent; ribosome inactivating protein genes; and even genes that regulate plant structures. Transgenic maize including anti-insect antibody genes and genes that

15 code for enzymes that can covert a non-toxic insecticide (pro-insecticide) applied to the outside of the plant into an insecticide inside the plant are also contemplated.

3. Environment or Stress Resistance

Improvement of a plant's ability to tolerate various environmental stresses such as, but not limited to, drought, excess moisture, chilling, freezing, high

20 temperature, salt, and oxidative stress, can also be effected through expression of heterologous, or overexpression of homologous genes. Benefits may be realized in terms of increased resistance to freezing temperatures through the introduction of an "antifreeze" protein such as that of the Winter Flounder (Cutler et al., 1989) or synthetic gene derivatives thereof. Improved chilling tolerance may also be

25 conferred through increased expression of glycerol-3-phosphate acetyltransferase in chloroplasts (Murata et al., 1992; Wolter et al., 1992). Resistance to oxidative stress (often exacerbated by conditions such as chilling temperatures in combination with high light intensities) can be conferred by expression of superoxide dismutase (Gupta et al., 1993), and may be improved by glutathione reductase (Bowler et al.,

30 1992). Such strategies may allow for tolerance to freezing in newly emerged fields

as well as extending later maturity higher yielding varieties to earlier relative maturity zones.

Expression of novel genes that favorably effect plant water content, total water potential, osmotic potential, and turgor can enhance the ability of the plant to tolerate drought. As used herein, the terms "drought resistance" and "drought tolerance" are used to refer to a plants increased resistance or tolerance to stress induced by a reduction in water availability, as compared to normal circumstances, and the ability of the plant to function and survive in lower-water environments, and perform in a relatively superior manner. In this aspect of the invention it is proposed, for example, that the expression of a gene encoding the biosynthesis of osmotically-active solutes can impart protection against drought. Within this class of genes are DNAs encoding mannitol dehydrogenase (Lee and Saier, 1982) and trehalose-6-phosphate synthase (Kaasen et al., 1992). Through the subsequent action of native phosphatases in the cell or by the introduction and coexpression of a specific phosphatase, these introduced genes will result in the accumulation of either mannitol or trehalose, respectively, both of which have been well documented as protective compounds able to mitigate the effects of stress. Mannitol accumulation in transgenic tobacco has been verified and preliminary results indicate that plants expressing high levels of this metabolite are able to tolerate an applied osmotic stress (Tarczynski et al., cited supra (1992), 1993).

Similarly, the efficacy of other metabolites in protecting either enzyme function (e.g. alanopine or propionic acid) or membrane integrity (e.g., alanopine) has been documented (Loomis et al., 1989), and therefore expression of gene encoding the biosynthesis of these compounds can confer drought resistance in a manner similar to or complimentary to mannitol. Other examples of naturally occurring metabolites that are osmotically active and/or provide some direct protective effect during drought and/or desiccation include sugars and sugar derivatives such as fructose, erythritol (Coxson et al., 1992), sorbitol, dulcitol (Karsten et al., 1992), glucosylglycerol (Reed et al., 1984; Erdmann et al., 1992), sucrose, stachyose (Koster and Leopold, 1988; Blackman et al., 1992), ononitol and pinitol (Vernon and Bohnert, 1992), and raffinose (Bernal-Lugo and Leopold, 1992).

Other osmotically active solutes which are not sugars include, but are not limited to, proline and glycine-betaine (Wyn-Jones and Storey, 1981). Continued canopy growth and increased reproductive fitness during times of stress can be augmented by introduction and expression of genes such as those controlling the osmotically active compounds discussed above and other such compounds, as represented in one exemplary embodiment by the enzyme myoinositol 0-methyltransferase.

It is contemplated that the expression of specific proteins may also increase drought tolerance. Three classes of Late Embryogenic Proteins have been assigned based on structural similarities (see Dure et al., 1989). All three classes of these proteins have been demonstrated in maturing (i.e., desiccating) seeds. Within these 3 types of proteins, the Type-II (dehydrin-type) have generally been implicated in drought and/or desiccation tolerance in vegetative plant parts (i.e. Mundy and Chua, 1988; Piatkowski et al., 1990; Yamaguchi-Shinozaki et al., 1992). Recently, expression of a Type-III LEA (HVA-1) in tobacco was found to influence plant height, maturity and drought tolerance (Fitzpatrick, 1993). Expression of structural genes from all three groups may therefore confer drought tolerance. Other types of proteins induced during water stress include thiol proteases, aldolases and transmembrane transporters (Guerrero et al., 1990), which may confer various protective and/or repair-type functions during drought stress. The expression of a gene that effects lipid biosynthesis and hence membrane composition can also be useful in conferring drought resistance on the plant.

Many genes that improve drought resistance have complementary modes of action. Thus, combinations of these genes might have additive and/or synergistic effects in improving drought resistance in plants. Many of these genes also improve freezing tolerance (or resistance); the physical stresses incurred during freezing and drought are similar in nature and may be mitigated in similar fashion. Benefit may be conferred via constitutive expression of these genes, but the preferred means of expressing these novel genes may be through the use of a turgor-induced promoter (such as the promoters for the turgor-induced genes described in Guerrero et al. 1990 and Shagan et al., 1993). Spatial and temporal expression patterns of these genes may enable maize to better withstand stress.

Expression of genes that are involved with specific morphological traits that allow for increased water extractions from drying soil would be of benefit. For example, introduction and expression of genes that alter root characteristics may enhance water uptake. Expression of genes that enhance reproductive fitness during times of stress would be of significant value. For example, expression of DNAs that improve the synchrony of pollen shed and receptiveness of the female flower parts, i.e., silks, would be of benefit. In addition, expression of genes that minimize kernel abortion during times of stress would increase the amount of grain to be harvested and hence be of value. Regulation of cytokinin levels in monocots, such as maize, by introduction and expression of an isopentenyl transferase gene with appropriate regulatory sequences can improve monocot stress resistance and yield (Gan et al., Science, 270:1986 (1995)).

Given the overall role of water in determining yield, it is contemplated that enabling plants to utilize water more efficiently, through the introduction and expression of novel genes, will improve overall performance even when soil water availability is not limiting. By introducing genes that improve the ability of plants to maximize water usage across a full range of stresses relating to water availability, yield stability or consistency of yield performance may be realized.

4. Disease Resistance

It is proposed that increased resistance to diseases may be realized through introduction of genes into plants period. It is possible to produce resistance to diseases caused by viruses, bacteria, fungi, root pathogens, insects and nematodes. It is also contemplated that control of mycotoxin producing organisms may be realized through expression of introduced genes.

Resistance to viruses may be produced through expression of novel genes. For example, it has been demonstrated that expression of a viral coat protein in a transgenic plant can impart resistance to infection of the plant by that virus and perhaps other closely related viruses (Cuozzo et al., 1988, Hemenway et al., 1988, Abel et al., 1986). It is contemplated that expression of antisense genes targeted at essential viral functions may impart resistance to said virus. For example, an antisense gene targeted at the gene responsible for replication of viral nucleic acid

may inhibit said replication and lead to resistance to the virus. It is believed that interference with other viral functions through the use of antisense genes may also increase resistance to viruses. Further it is proposed that it may be possible to achieve resistance to viruses through other approaches, including, but not limited to the use of satellite viruses.

It is proposed that increased resistance to diseases caused by bacteria and fungi may be realized through introduction of novel genes. It is contemplated that genes encoding so-called "peptide antibiotics," pathogenesis related (PR) proteins, toxin resistance, and proteins affecting host-pathogen interactions such as morphological characteristics will be useful. Peptide antibiotics are polypeptide sequences which are inhibitory to growth of bacteria and other microorganisms. For example, the classes of peptides referred to as cecropins and magainins inhibit growth of many species of bacteria and fungi. It is proposed that expression of PR proteins in plants may be useful in conferring resistance to bacterial disease. These genes are induced following pathogen attack on a host plant and have been divided into at least five classes of proteins (Bol et al., 1990). Included amongst the PR proteins are beta-1,3-glucanases, chitinases, and osmotin and other proteins that are believed to function in plant resistance to disease organisms. Other genes have been identified that have antifungal properties, e.g., UDA (stinging nettle lectin) and hevein (Broakgert et al., 1989; Barkai-Golan et al., 1978). It is known that certain plant diseases are caused by the production of phytotoxins. Resistance to these diseases could be achieved through expression of a novel gene that encodes an enzyme capable of degrading or otherwise inactivating the phytotoxin. Expression novel genes that alter the interactions between the host plant and pathogen may be useful in reducing the ability the disease organism to invade the tissues of the host plant, e.g., an increase in the waxiness of the leaf cuticle or other morphological characteristics.

Plant parasitic nematodes are a cause of disease in many plants. It is proposed that it would be possible to make the plant resistant to these organisms through the expression of novel genes. It is anticipated that control of nematode infestations would be accomplished by altering the ability of the nematode to

recognize or attach to a host plant and/or enabling the plant to produce nematicidal compounds, including but not limited to proteins.

5. Mycotoxin Reduction/Elimination

Production of mycotoxins, including aflatoxin and fumonisin, by fungi associated with plants is a significant factor in rendering the grain not useful. These fungal organisms do not cause disease symptoms and/or interfere with the growth of the plant, but they produce chemicals (mycotoxins) that are toxic to animals. Inhibition of the growth of these fungi would reduce the synthesis of these toxic substances and, therefore, reduce grain losses due to mycotoxin contamination. Novel genes may be introduced into plants that would inhibit synthesis of the mycotoxin without interfering with fungal growth. Expression of a novel gene which encodes an enzyme capable of rendering the mycotoxin nontoxic would be useful in order to achieve reduced mycotoxin contamination of grain. The result of any of the above mechanisms would be a reduced presence of mycotoxins on grain.

15 6. Grain Composition or Quality

Genes may be introduced into plants, particularly commercially important cereals such as maize, wheat or rice, to improve the grain for which the cereal is primarily grown. A wide range of novel transgenic plants produced in this manner may be envisioned depending on the particular end use of the grain. For example, the largest use of maize grain is for feed or food. Introduction of genes that alter the composition of the grain may greatly enhance the feed or food value. The primary components of maize grain are starch, protein, and oil. Each of these primary components of maize grain may be improved by altering its level or composition. Several examples may be mentioned for illustrative purposes but in no way provide an exhaustive list of possibilities.

The protein of many cereal grains is suboptimal for feed and food purposes especially when fed to pigs, poultry, and humans. The protein is deficient in several amino acids that are essential in the diet of these species, requiring the addition of supplements to the grain. Limiting essential amino acids may include lysine, methionine, tryptophan, threonine, valine, arginine, and histidine. Some amino acids become limiting only after the grain is supplemented with other inputs for feed

formulations. For example, when the grain is supplemented with soybean meal to meet lysine requirements, methionine becomes limiting. The levels of these essential amino acids in seeds and grain may be elevated by mechanisms which include, but are not limited to, the introduction of genes to increase the biosynthesis of the amino acids, decrease the degradation of the amino acids, increase the storage of the amino acids in proteins, or increase transport of the amino acids to the seeds or grain.

One mechanism for increasing the biosynthesis of the amino acids is to introduce genes that deregulate the amino acid biosynthetic pathways such that the plant can no longer adequately control the levels that are produced. This may be done by deregulating or bypassing steps in the amino acid biosynthetic pathway which are normally regulated by levels of the amino acid end product of the pathway. Examples include the introduction of genes that encode deregulated versions of the enzymes aspartokinase or dihydrodipicolinic acid (DHDP)-synthase for increasing lysine and threonine production, and anthranilate synthase for increasing tryptophan production. Reduction of the catabolism of the amino acids may be accomplished by introduction of DNA sequences that reduce or eliminate the expression of genes encoding enzymes that catalyse steps in the catabolic pathways such as the enzyme lysine-ketoglutarate reductase.

The protein composition of the grain may be altered to improve the balance of amino acids in a variety of ways including elevating expression of native proteins, decreasing expression of those with poor composition, changing the composition of native proteins, or introducing genes encoding entirely new proteins possessing superior composition. DNA may be introduced that decreases the expression of members of the zein family of storage proteins. This DNA may encode ribozymes or antisense sequences directed to impairing expression of zein proteins or expression of regulators of zein expression such as the opaque-2 gene product. The protein composition of the grain may be modified through the phenomenon of cosuppression, i.e., inhibition of expression of an endogenous gene through the expression of an identical structural gene or gene fragment introduced through transformation (Goring et al., 1991). Additionally, the introduced DNA may encode

enzymes which degrade seines. The decreases in zein expression that are achieved may be accompanied by increases in proteins with more desirable amino acid composition or increases in other major seed constituents such as starch.

Alternatively, a chimeric gene may be introduced that comprises a coding sequence

- 5 for a native protein of adequate amino acid composition such as for one of the globulin proteins or 10 kD zein of maize and a promoter or other regulatory sequence designed to elevate expression of said protein. The coding sequence of said gene may include additional or replacement codons for essential amino acids. Further, a coding sequence obtained from another species, or, a partially or
- 10 completely synthetic sequence encoding a completely unique peptide sequence designed to enhance the amino acid composition of the seed may be employed.

The introduction of genes that alter the oil content of the grain may be of value. Increases in oil content may result in increases in metabolizable energy

- content and density of the seeds for uses in feed and food. The introduced genes
- 15 may encode enzymes that remove or reduce rate-limitations or regulated steps in fatty acid or lipid biosynthesis. Such genes may include, but are not limited to, those that encode acetyl-CoA carboxylase, ACP-acyltransferase, beta-ketoacyl-ACP synthase, plus other well known fatty acid biosynthetic activities. Other possibilities are genes that encode proteins that do not possess enzymatic activity such as acyl
- 20 carrier protein. Additional examples include 2-acetyltransferase, oleosin pyruvate dehydrogenase complex, acetyl CoA synthetase, ATP citrate lyase, ADP-glucose pyrophosphorylase and genes of the carnitine-CoA- acetyl-CoA shuttles. It is anticipated that expression of genes related to oil biosynthesis will be targeted to the plastid, using a plastid transit peptide sequence and preferably expressed in the seed
- 25 embryo. Genes may be introduced that alter the balance of fatty acids present in the oil providing a more healthful or nutritive feedstuff. The introduced DNA may also encode sequences that block expression of enzymes involved in fatty acid biosynthesis, altering the proportions of fatty acids present in the grain such as described below.

Genes may be introduced that enhance the nutritive value of the starch component of the grain, for example by increasing the degree of branching, resulting in improved utilization of the starch in cows by delaying its metabolism.

Besides affecting the major constituents of the grain, genes may be introduced that affect a variety of other nutritive, processing, or other quality aspects of the grain as used for feed or food. For example, pigmentation of the grain may be increased or decreased. Enhancement and stability of yellow pigmentation is desirable in some animal feeds and may be achieved by introduction of genes that result in enhanced production of xanthophylls and carotenes by eliminating rate-limiting steps in their production. Such genes may encode altered forms of the enzymes phytoene synthase, phytoene desaturase, or lycopene synthase. Alternatively, unpigmented white corn is desirable for production of many food products and may be produced by the introduction of DNA which blocks or eliminates steps in pigment production pathways.

Feed or food comprising some cereal grains possesses insufficient quantities of vitamins and must be supplemented to provide adequate nutritive value. Introduction of genes that enhance vitamin biosynthesis in seeds may be envisioned including, for example, vitamins A, E, B₁₂, choline, and the like. For example, maize grain also does not possess sufficient mineral content for optimal nutritive value. Genes that affect the accumulation or availability of compounds containing phosphorus, sulfur, calcium, manganese, zinc, and iron among others would be valuable. An example may be the introduction of a gene that reduced phytic acid production or encoded the enzyme phytase which enhances phytic acid breakdown. These genes would increase levels of available phosphate in the diet, reducing the need for supplementation with mineral phosphate.

Numerous other examples of improvement of cereals for feed and food purposes might be described. The improvements may not even necessarily involve the grain, but may, for example, improve the value of the grain for silage. Introduction of DNA to accomplish this might include sequences that alter lignin production such as those that result in the "brown midrib" phenotype associated with superior feed value for cattle.

In addition to direct improvements in feed or food value, genes may also be introduced which improve the processing of grain and improve the value of the products resulting from the processing. The primary method of processing certain grains such as maize is via wetmilling. Maize may be improved through the expression of novel genes that increase the efficiency and reduce the cost of processing such as by decreasing steeping time.

Improving the value of wetmilling products may include altering the quantity or quality of starch, oil, corn gluten meal, or the components of corn gluten feed. Elevation of starch may be achieved through the identification and elimination of rate limiting steps in starch biosynthesis or by decreasing levels of the other components of the grain resulting in proportional increases in starch. An example of the former may be the introduction of genes encoding ADP-glucose pyrophosphorylase enzymes with altered regulatory activity or which are expressed at higher level. Examples of the latter may include selective inhibitors of, for example, protein or oil biosynthesis expressed during later stages of kernel development.

The properties of starch may be beneficially altered by changing the ratio of amylose to amylopectin, the size of the starch molecules, or their branching pattern. Through these changes a broad range of properties may be modified which include, but are not limited to, changes in gelatinization temperature, heat of gelatinization, clarity of films and pastes, Theological properties, and the like. To accomplish these changes in properties, genes that encode granule-bound or soluble starch synthase activity or branching enzyme activity may be introduced alone or combination. DNA such as antisense constructs may also be used to decrease levels of endogenous activity of these enzymes. The introduced genes or constructs may possess regulatory sequences that time their expression to specific intervals in starch biosynthesis and starch granule development. Furthermore, it may be advisable to introduce and express genes that result in the *in vivo* derivatization, or other modification, of the glucose moieties of the starch molecule. The covalent attachment of any molecule may be envisioned, limited only by the existence of enzymes that catalyze the derivatizations and the accessibility of appropriate

substrates in the starch granule. Examples of important derivations may include the addition of functional groups such as amines, carboxyls, or phosphate groups which provide sites for subsequent *in vitro* derivatizations or affect starch properties through the introduction of ionic charges. Examples of other modifications may include direct changes of the glucose units such as loss of hydroxyl groups or their oxidation to aldehyde or carboxyl groups.

Oil is another product of wetmilling of corn and other grains, the value of which may be improved by introduction and expression of genes. The quantity of oil that can be extracted by wetmilling may be elevated by approaches as described for feed and food above. Oil properties may also be altered to improve its performance in the production and use of cooking oil, shortenings, lubricants or other oil-derived products or improvement of its health attributes when used in the food-related applications. Novel fatty acids may also be synthesized which upon extraction can serve as starting materials for chemical syntheses. The changes in oil properties may be achieved by altering the type, level, or lipid arrangement of the fatty acids present in the oil. This in turn may be accomplished by the addition of genes that encode enzymes that catalyze the synthesis of novel fatty acids and the lipids possessing them or by increasing levels of native fatty acids while possibly reducing levels of precursors. Alternatively DNA sequences may be introduced which slow or block steps in fatty acid biosynthesis resulting in the increase in precursor fatty acid intermediates. Genes that might be added include desaturases, epoxidases, hydratases, dehydratases, and other enzymes that catalyze reactions involving fatty acid intermediates. Representative examples of catalytic steps that might be blocked include the desaturations from stearic to oleic acid and oleic to linolenic acid resulting in the respective accumulations of stearic and oleic acids.

Improvements in the other major cereal wetmilling products, gluten meal and gluten feed, may also be achieved by the introduction of genes to obtain novel plants. Representative possibilities include but are not limited to those described above for improvement of food and feed value.

In addition it may further be considered that the plant be used for the production or manufacturing of useful biological compounds that were either not

produced at all, or not produced at the same level, in the plant previously. The novel plants producing these compounds are made possible by the introduction and expression of genes by transformation methods. The possibilities include, but are not limited to, any biological compound which is presently produced by any organism such as proteins, nucleic acids, primary and intermediary metabolites, carbohydrate polymers, etc. The compounds may be produced by the plant, extracted upon harvest and/or processing, and used for any presently recognized useful purpose such as pharmaceuticals, fragrances, industrial enzymes to name a few.

Further possibilities to exemplify the range of grain traits or properties potentially encoded by introduced genes in transgenic plants include grain with less breakage susceptibility for export purposes or larger grit size when processed by dry milling through introduction of genes that enhance gamma-zein synthesis, popcorn with improved popping quality and expansion volume through genes that increase pericarp thickness, corn with whiter grain for food uses through introduction of genes that effectively block expression of enzymes involved in pigment production pathways, and improved quality of alcoholic beverages or sweet corn through introduction of genes which affect flavor such as the shrunken gene (encoding sucrose synthase) for sweet corn.

7. Plant Agronomic Characteristics

Two of the factors determining where plants can be grown are the average daily temperature during the growing season and the length of time between frosts. Within the areas where it is possible to grow a particular plant, there are varying limitations on the maximal time it is allowed to grow to maturity and be harvested.

The plant to be grown in a particular area is selected for its ability to mature and dry down to harvestable moisture content within the required period of time with maximum possible yield. Therefore, plant of varying maturities are developed for different growing locations. Apart from the need to dry down sufficiently to permit harvest is the desirability of having maximal drying take place in the field to minimize the amount of energy required for additional drying post-harvest. Also the more readily the grain can dry down, the more time there is available for growth and

kernel fill. Genes that influence maturity and/or dry down can be identified and introduced into plant lines using transformation techniques to create new varieties adapted to different growing locations or the same growing location but having improved yield to moisture ratio at harvest. Expression of genes that are involved in regulation of plant development may be especially useful, e.g., the liguleless and rough sheath genes that have been identified in plants.

Genes may be introduced into plants that would improve standability and other plant growth characteristics. For example, expression of novel genes which confer stronger stalks, improved root systems, or prevent or reduce ear droppage would be of great value to the corn farmer. Introduction and expression of genes that increase the total amount of photoassimilate available by, for example, increasing light distribution and/or interception would be advantageous. In addition the expression of genes that increase the efficiency of photosynthesis and/or the leaf canopy would further increase gains in productivity. Such approaches would allow for increased plant populations in the field.

Delay of late season vegetative senescence would increase the flow of assimilate into the grain and thus increase yield. Overexpression of genes within plants that are associated with "stay green" or the expression of any gene that delays senescence would achieve be advantageous. For example, a non-yellowing mutant has been identified in *Festuca pratensis* (Davies et al., 1990). Expression of this gene as well as others may prevent premature breakdown of chlorophyll and thus maintain canopy function.

8. Nutrient Utilization

The ability to utilize available nutrients and minerals may be a limiting factor in growth of many plants. It is proposed that it would be possible to alter nutrient uptake, tolerate pH extremes, mobilization through the plant, storage pools, and availability for metabolic activities by the introduction of novel genes. These modifications would allow a plant to more efficiently utilize available nutrients. It is contemplated that an increase in the activity of, for example, an enzyme that is normally present in the plant and involved in nutrient utilization would increase the availability of a nutrient. An example of such an enzyme would be phytase. It is

also contemplated that expression of a novel gene may make a nutrient source available that was previously not accessible, e.g., an enzyme that releases a component of nutrient value from a more complex molecule, perhaps a macromolecule.

5 9. Male Sterility

Male sterility is useful in the production of hybrid seed. It is proposed that male sterility may be produced through expression of novel genes. For example, it has been shown that expression of genes that encode proteins that interfere with development of the male inflorescence and/or gametophyte result in male sterility. Chimeric ribonuclease genes that express in the anthers of transgenic tobacco and oilseed rape have been demonstrated to lead to male sterility (Mariani et al, 1990).

For example, a number of mutations were discovered in maize that confer cytoplasmic male sterility. One mutation in particular, referred to as T cytoplasm, also correlates with sensitivity to Southern corn leaf blight. A DNA sequence, designated TURF-13 (Levings, 1990), was identified that correlates with T cytoplasm. It would be possible through the introduction of TURF-13 via transformation to separate male sterility from disease sensitivity. As it is necessary to be able to restore male fertility for breeding purposes and for grain production, it is proposed that genes encoding restoration of male fertility may also be introduced.

20 10. Negative Selectable Markers

Introduction of genes encoding traits that can be selected against may be useful for eliminating undesirable linked genes. When two or more genes are introduced together by cotransformation, the genes will be linked together on the host chromosome. For example, a gene encoding a *Bt* gene that confers insect resistance on the plant may be introduced into a plant together with a *bar* gene that is useful as a selectable marker and confers resistance to the herbicide Ignite® on the plant. However, it may not be desirable to have an insect resistant plant that is also resistant to the herbicide Ignite®. It is proposed that one could also introduce an antisense *bar* gene that is expressed in those tissues where one does not want expression of the *bar* gene, e.g., in whole plant parts. Hence, although the *bar* gene is expressed and is useful as a selectable marker, it is not useful to confer herbicide

resistance on the whole plant. The *bar* antisense gene is a negative selectable marker.

Negative selection is necessary in order to screen a population of transformants for rare homologous recombinants generated through gene targeting.

- 5 For example, a homologous recombinant may be identified through the inactivation of a gene that was previously expressed in that cell. The antisense gene to neomycin phosphotransferase II (*nptII*) has been investigated as a negative selectable marker in tobacco (*Nicotiana tabacum*) and *Arabidopsis thaliana* (Xiang and Guerra, 1993). In this example both sense and antisense *nptII* genes are introduced into a plant
- 10 through transformation and the resultant plants are sensitive to the antibiotic kanamycin. An introduced gene that integrates into the host cell chromosome at the site of the antisense *nptII* gene, and inactivates the antisense gene, will make the plant resistant to kanamycin and other aminoglycoside antibiotics. Therefore, rare site specific recombinants may be identified by screening for antibiotic resistance.
- 15 Similarly, any gene, native to the plant or introduced through transformation, that when inactivated confers resistance to a compound, may be useful as a negative selectable marker.

- It is contemplated that negative selectable markers may also be useful in other ways. One application is to construct transgenic lines in which one could
- 20 select for transposition to unlinked sites. In the process of tagging it is most common for the transposable element to move to a genetically linked site on the same chromosome. A selectable marker for recovery of rare plants in which transposition has occurred to an unlinked locus would be useful. For example, the enzyme cytosine deaminase may be useful for this purpose (Stouggard, 1993). In
- 25 the presence of this enzyme the compound 5-fluorocytosine is converted to 5-fluoruracil which is toxic to plant and animal cells. If a transposable element is linked to the gene for the enzyme cytosine deaminase, one may select for transposition to unlinked sites by selecting for transposition events in which the resultant plant is now resistant to 5-fluorocytosine. The parental plants and plants
- 30 containing transpositions to linked sites will remain sensitive to 5-fluorocytosine. Resistance to 5-fluorocytosine is due to loss of the cytosine deaminase gene through

genetic segregation of the transposable element and the cytosine deaminase gene. Other genes that encode proteins that render the plant sensitive to a certain compound will also be useful in this context. For example, T-DNA gene 2 from *Agrobacterium tumefaciens* encodes a protein that catalyzes the conversion of alpha-naphthalene acetamide (NAM) to alpha-naphthalene acetic acid (NAA) renders plant cells sensitive to high concentrations of NAM (Depicker et al., 1988).

It is also contemplated that negative selectable markers may be useful in the construction of transposon tagging lines. For example, by marking an autonomous transposable element such as Ac, Master Mu, or En/Spn with a negative selectable marker, one could select for transformants in which the autonomous element is not stably integrated into the genome. This would be desirable, for example, when transient expression of the autonomous element is desired to activate in *trans* the transposition of a defective transposable element, such as Ds, but stable integration of the autonomous element is not desired. The presence of the autonomous element may not be desired in order to stabilize the defective element, i.e., prevent it from further transposing. However, it is proposed that if stable integration of an autonomous transposable element is desired in a plant the presence of a negative selectable marker may make it possible to eliminate the autonomous element during the breeding process.

11. Non-Protein-Expressing Sequences

a. RNA-Expressing

DNA may be introduced into plants for the purpose of expressing RNA transcripts that function to affect plant phenotype yet are not translated into protein. Two examples are antisense RNA and RNA with ribozyme activity. Both may serve possible functions in reducing or eliminating expression of native or introduced plant genes.

Genes may be constructed or isolated, which when transcribed, produce antisense RNA that is complementary to all or part(s) of a targeted messenger RNA(s). The antisense RNA reduces production of the polypeptide product of the messenger RNA. The polypeptide product may be any protein encoded by the plant genome. The aforementioned genes will be referred to as antisense genes. An

antisense gene may thus be introduced into a plant by transformation methods to produce a novel transgenic plant with reduced expression of a selected protein of interest. For example, the protein may be an enzyme that catalyzes a reaction in the plant. Reduction of the enzyme activity may reduce or eliminate products of the reaction which include any enzymatically synthesized compound in the plant such as fatty acids, amino acids, carbohydrates, nucleic acids and the like. Alternatively, the protein may be a storage protein, such as a zein, or a structural protein, the decreased expression of which may lead to changes in seed amino acid composition or plant morphological changes respectively. The possibilities cited above are provided only by way of example and do not represent the full range of applications.

Genes may also be constructed or isolated, which when transcribed produce RNA enzymes, or ribozymes, which can act as endoribonucleases and catalyze the cleavage of RNA molecules with selected sequences. The cleavage of selected messenger RNA's can result in the reduced production of their encoded polypeptide products. These genes may be used to prepare novel transgenic plants which possess them. The transgenic plants may possess reduced levels of polypeptides including but not limited to the polypeptides cited above that may be affected by antisense RNA.

It is also possible that genes may be introduced to produce novel transgenic plants which have reduced expression of a native gene product by a mechanism of cosuppression. It has been demonstrated in tobacco, tomato, and petunia (Goring et al, 1991; Smith et al., 1990; Napoli et al., 1990; van der Krol et al., 1990) that expression of the sense transcript of a native gene will reduce or eliminate expression of the native gene in a manner similar to that observed for antisense genes. The introduced gene may encode all or part of the targeted native protein but its translation may not be required for reduction of levels of that native protein.

b. Non-RNA-Expressing

For example, DNA elements including those of transposable elements such as Ds, Ac, or Mu, may be inserted into a gene and cause mutations. These DNA elements may be inserted in order to inactivate (or activate) a gene and thereby "tag" a particular trait. In this instance the transposable element does not cause instability

of the tagged mutation, because the utility of the element does not depend on its ability to move in the genome. Once a desired trait is tagged, the introduced DNA sequence may be used to clone the corresponding gene, e.g., using the introduced DNA sequence as a PCR primer together with PCR gene cloning techniques (Shapiro, 1983; Dellaporta et al., 1988). Once identified, the entire gene(s) for the particular trait, including control or regulatory regions where desired may be isolated, cloned and manipulated as desired. The utility of DNA elements introduced into an organism for purposed of gene tagging is independent of the DNA sequence and does not depend on any biological activity of the DNA sequence, i.e., transcription into RNA or translation into protein. The sole function of the DNA element is to disrupt the DNA sequence of a gene.

It is contemplated that unexpressed DNA sequences, including novel synthetic sequences could be introduced into cells as proprietary "labels" of those cells and plants and seeds thereof. It would not be necessary for a label DNA element to disrupt the function of a gene endogenous to the host organism, as the sole function of this DNA would be to identify the origin of the organism. For example, one could introduce a unique DNA sequence into a plant and this DNA element would identify all cells, plants, and progeny of these cells as having arisen from that labeled source. It is proposed that inclusion of label DNAs would enable one to distinguish proprietary germplasm or germplasm derived from such, from unlabelled germplasm.

Another possible element which may be introduced is a matrix attachment region element (MAR), such as the chicken lysozyme A element (Stief et al., 1989), which can be positioned around an expressible gene of interest to effect an increase in overall expression of the gene and diminish position dependant effects upon incorporation into the plant genome (Stief et al., 1989; Phi-Van et al., 1990).

III. Transformed (Transgenic) Plants of the Invention and Methods of Preparation

Plant species may be transformed with the DNA construct of the present invention by the DNA-mediated transformation of plant cell protoplasts and

subsequent regeneration of the plant from the transformed protoplasts in accordance with procedures well known in the art.

Any plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a vector of the present invention. The term "organogenesis," as used herein, means a process by which shoots and roots are developed sequentially from meristematic centers; the term "embryogenesis," as used herein, means a process by which shoots and roots develop together in a concerted fashion (not sequentially), whether from somatic cells or gametes. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristems, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and utilane meristem).

Plants of the present invention may take a variety of forms. The plants may be chimeras of transformed cells and non-transformed cells; the plants may be clonal transformants (e.g., all cells transformed to contain the expression cassette); the plants may comprise grafts of transformed and untransformed tissues (e.g., a transformed root stock grafted to an untransformed scion in citrus species). The transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, first generation (or T1) transformed plants may be selfed to give homozygous second generation (or T2) transformed plants, and the T2 plants further propagated through classical breeding techniques. A dominant selectable marker (such as npt II) can be associated with the expression cassette to assist in breeding.

Thus, the present invention provides a transformed (transgenic) plant cell, *in planta* or *ex planta*, including a transformed plastid or other organelle, e.g., nucleus, mitochondria or chloroplast. The present invention may be used for transformation of any plant species, including, but not limited to, cells from corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye

- (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea utilane*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, duckweed (*Lemna*), barley, vegetables, ornamentals, and conifers.
- 15 Duckweed (*Lemna*, see WO 00/07210) includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. Angusta*, *Wa. Arrhiza*, *Wa. Australina*, *Wa. Borealis*, *Wa. Brasiliensis*, *Wa. Columbiana*, *Wa. Elongata*, *Wa. Globosa*, *Wa. Microscopica*, *Wa. Neglecta*) and genus *Wofiella* (*Wl. utila*, *Wl. utilanen*, *Wl. gladiata*, *Wl. utila*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*). Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present
- 25 invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt, Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae – A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)).
- 30 Vegetables within the scope of the invention include tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima

beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.),

5 tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey

10 pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga utilane*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar,

15 locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus,

20 e.g., trefoil, lens, e.g., lentil, and false indigo. Preferred forage and turf grass for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop.

Papaya, garlic, pea, peach, pepper, petunia, strawberry, sorghum, sweet potato, turnip, safflower, corn, pea, endive, gourd, grape, snap bean, chicory, cotton,

25 tobacco, aubergine, beet, buckwheat, broad bean, nectarine, avocado, mango, banana, groundnut, potato, peanut, lettuce, pineapple, spinach, squash, sugarbeet, sugarcane, sweet corn, chrysanthemum.

Other plants within the scope of the invention include *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus,

30 fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio,

Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, utilian sprouts, onion, carrot, leek, beet, broad
5 bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, utilane, and zucchini.

Ornamental plants within the scope of the invention include impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint
Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo,
10 Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia. Other plants within the scope of the invention are shown in Table 1 (above).

Preferably, transgenic plants of the present invention are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola,
15 soybean, barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.), and even more preferably corn, rice and soybean.

Transformation of plants can be undertaken with a single DNA molecule or multiple DNA molecules (i.e., co-transformation), and both these techniques are suitable for use with the expression cassettes of the present invention. Numerous
20 transformation vectors are available for plant transformation, and the expression cassettes of this invention can be used in conjunction with any such vectors. The selection of vector will depend upon the preferred transformation technique and the target species for transformation.

A variety of techniques are available and known to those skilled in the art for
25 introduction of constructs into a plant cell host. These techniques generally include transformation with DNA employing *A. tumefaciens* or *A. rhizogenes* as the transforming agent, liposomes, PEG precipitation, electroporation, DNA injection, direct DNA uptake, microprojectile bombardment, particle acceleration, and the like (See, for example, EP 295959 and EP 138341) (see below). However, cells other
30 than plant cells may be transformed with the expression cassettes of the invention. The general descriptions of plant expression vectors and reporter genes, and

Agrobacterium and *Agrobacterium*-mediated gene transfer, can be found in Gruber et al. (1993).

Expression vectors containing genomic or synthetic fragments can be introduced into protoplasts or into intact tissues or isolated cells. Preferably
5 expression vectors are introduced into intact tissue. General methods of culturing plant tissues are provided for example by Maki et al., (1993); and by Phillips et al. (1988). Preferably, expression vectors are introduced into maize or other plant tissues using a direct gene transfer method such as microprojectile-mediated delivery, DNA injection, electroporation and the like. More preferably expression
10 vectors are introduced into plant tissues using the microprojectile media delivery with the biolistic device. See, for example, Tomes et al. (1995). The vectors of the invention can not only be used for expression of structural genes but may also be used in exon-trap cloning, or promoter trap procedures to detect differential gene expression in varieties of tissues, (Lindsey et al., 1993; Auch & Reth et al.).

15 It is particularly preferred to use the binary type vectors of Ti and Ri plasmids of *Agrobacterium spp.* Ti-derived vectors transform a wide variety of higher plants, including monocotyledonous and dicotyledonous plants, such as soybean, cotton, rape, tobacco, and rice (Pacciotti et al., 1985; Byrne et al., 1987; Sukhapinda et al., 1987; Park et al., 1985; Hiei et al., 1994). The use of T-DNA to
20 transform plant cells has received extensive study and is amply described (EP 120516; Hoekema, 1985; Knauf, et al., 1983; and An et al., 1985). For introduction into plants, the chimeric genes of the invention can be inserted into binary vectors as described in the examples.

Other transformation methods are available to those skilled in the art, such as
25 direct uptake of foreign DNA constructs (see EP 295959), techniques of electroporation (Fromm et al., 1986) or high velocity ballistic bombardment with metal particles coated with the nucleic acid constructs (Kline et al., 1987, and U.S. Patent No. 4,945,050). Once transformed, the cells can be regenerated by those skilled in the art. Of particular relevance are the recently described methods to
30 transform foreign genes into commercially important crops, such as rapeseed (De Block et al., 1989), sunflower (Everett et al., 1987), soybean (McCabe et al., 1988;

Hinchee et al., 1988; Chee et al., 1989; Christou et al., 1989; EP 301749), rice (Hiei et al., 1994), and corn (Gordon Kamm et al., 1990; Fromm et al., 1990).

Those skilled in the art will appreciate that the choice of method might depend on the type of plant, i.e., monocotyledonous or dicotyledonous, targeted for transformation. Suitable methods of transforming plant cells include, but are not limited to, microinjection (Crossway et al., 1986), electroporation (Riggs et al., 1986), *Agrobacterium*-mediated transformation (Hinchee et al., 1988), direct gene transfer (Paszowski et al., 1984), and ballistic particle acceleration using devices available from Agracetus, Inc., Madison, Wis. And BioRad, Hercules, Calif. (see, for example, Sanford et al., U.S. Pat. No. 4,945,050; and McCabe et al., 1988). Also see, Weissinger et al., 1988; Sanford et al., 1987 (onion); Christou et al., 1988 (soybean); McCabe et al., 1988 (soybean); Datta et al., 1990 (rice); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Fromm et al., 1990 (maize); and Gordon-Kamm et al., 1990 (maize); Svab et al., 1990 (tobacco chloroplast); Koziel et al., 1993 (maize); Shimamoto et al., 1989 (rice); Christou et al., 1991 (rice); European Patent Application EP 0 332 581 (orchardgrass and other Pooideae); Vasil et al., 1993 (wheat); Weeks et al., 1993 (wheat). In one embodiment, the protoplast transformation method for maize is employed (European Patent Application EP 0 292 435, U. S. Pat. No. 5,350,689).

In another embodiment, a nucleotide sequence of the present invention is directly transformed into the plastid genome. Plastid transformation technology is extensively described in U.S. Patent Nos. 5,451,513, 5,545,817, and 5,545,818, in PCT application no. WO 95/16783, and in McBride et al., 1994. The basic technique for chloroplast transformation involves introducing regions of cloned plastid DNA flanking a selectable marker together with the gene of interest into a suitable target tissue, e.g., using biolistics or protoplast transformation (e.g., calcium chloride or PEG mediated transformation). The 1 to 1.5 kb flanking regions, termed targeting sequences, facilitate orthologous recombination with the plastid genome and thus allow the replacement or modification of specific regions of the plastome. Initially, point mutations in the chloroplast 16S rRNA and rps12 genes conferring resistance to spectinomycin and/or streptomycin are utilized as selectable markers

for transformation (Svab et al., 1990; Staub et al., 1992). This resulted in stable homoplasmic transformants at a frequency of approximately one per 100 bombardments of target leaves. The presence of cloning sites between these markers allowed creation of a plastid targeting vector for introduction of foreign genes (Staub et al., 1993). Substantial increases in transformation frequency are obtained by replacement of the recessive rRNA or r-protein antibiotic resistance genes with a dominant selectable marker, the bacterial *aadA* gene encoding the spectinomycin-detoxifying enzyme aminoglycoside-3'-adenyltransferase (Svab et al., 1993). Other selectable markers useful for plastid transformation are known in the art and encompassed within the scope of the invention. Typically, approximately 15-20 cell division cycles following transformation are required to reach a homoplastidic state. Plastid expression, in which genes are inserted by orthologous recombination into all of the several thousand copies of the circular plastid genome present in each plant cell, takes advantage of the enormous copy number advantage over nuclear-expressed genes to permit expression levels that can readily exceed 10% of the total soluble plant protein. In a preferred embodiment, a nucleotide sequence of the present invention is inserted into a plastid targeting vector and transformed into the plastid genome of a desired plant host. Plants homoplasmic for plastid genomes containing a nucleotide sequence of the present invention are obtained, and are preferentially capable of high expression of the nucleotide sequence.

Agrobacterium tumefaciens cells containing a vector comprising an expression cassette of the present invention, wherein the vector comprises a Ti plasmid, are useful in methods of making transformed plants. Plant cells are infected with an *Agrobacterium tumefaciens* as described above to produce a transformed plant cell, and then a plant is regenerated from the transformed plant cell. Numerous *Agrobacterium* vector systems useful in carrying out the present invention are known.

For example, vectors are available for transformation using *Agrobacterium tumefaciens*. These typically carry at least one T-DNA border sequence and include vectors such as pBIN19 (Bevan, 1984). In one preferred embodiment, the

expression cassettes of the present invention may be inserted into either of the binary vectors pCIB200 and pCIB2001 for use with *Agrobacterium*. These vector cassettes for *Agrobacterium*-mediated transformation wear constructed in the following manner. PTJS75kan was created by NarI digestion of pTJS75

5 (Schmidhauser & Helinski, 1985) allowing excision of the tetracycline-resistance gene, followed by insertion of an AccI fragment from pUC4K carrying an NPTII (Messing & Vierra, 1982; Bevan et al., 1983; McBride et al., 1990). XhoI linkers were ligated to the EcoRV fragment of pCIB7 which contains the left and right T-DNA borders, a plant selectable nos/nptII chimeric gene and the pUC polylinker
10 (Rothstein et al., 1987), and the XhoI- digested fragment was cloned into Sall-digested pTJS75kan to create pCIB200 (see also EP 0 332 104, example 19). PCIB200 contains the following unique polylinker restriction sites: EcoRI, SstI, KpnI, BglII, XbaI, and Sall. The plasmid pCIB2001 is a derivative of pCIB200 which was created by the insertion into the polylinker of additional restriction sites.
15 Unique restriction sites in the polylinker of pCIB2001 are EcoRI, SstI, KpnI, BglII, XbaI, Sall, MluI, BclI, AvrII, ApaI, HpaI, and StuI. PCIB2001, in addition to containing these unique restriction sites also has plant and bacterial kanamycin selection, left and right T-DNA borders for *Agrobacterium*-mediated transformation, the RK2-derived trfA function for mobilization between *E. coli* and other hosts, and
20 the OriT and OriV functions also from RK2. The pCIB2001 polylinker is suitable for the cloning of plant expression cassettes containing their own regulatory signals.

An additional vector useful for *Agrobacterium*-mediated transformation is the binary vector pCIB 10, which contains a gene encoding kanamycin resistance for selection in plants, T-DNA right and left border sequences and incorporates
25 sequences from the wide host- range plasmid pRK252 allowing it to replicate in both *E. coli* and *Agrobacterium*. Its construction is described by Rothstein et al., 1987. Various derivatives of pCIB10 have been constructed which incorporate the gene for hygromycin B phosphotransferase described by Gritz et al., 1983. These derivatives enable selection of transgenic plant cells on hygromycin only (pCIB743),
30 or hygromycin and kanamycin (pCIB715, pCIB717).

Methods using either a form of direct gene transfer or *Agrobacterium*-mediated transfer usually, but not necessarily, are undertaken with a selectable marker which may provide resistance to an antibiotic (e.g., kanamycin, hygromycin or methotrexate) or a herbicide (e.g., phosphinothricin). The choice of selectable
5 marker for plant transformation is not, however, critical to the invention.

For certain plant species, different antibiotic or herbicide selection markers may be preferred. Selection markers used routinely in transformation include the nptII gene which confers resistance to kanamycin and related antibiotics (Messing & Vierra, 1982; Bevan et al., 1983), the bar gene which confers resistance to the
10 herbicide phosphinothricin (White et al., 1990, Spencer et al., 1990), the hph gene which confers resistance to the antibiotic hygromycin (Blochinger & Diggelmann), and the dhfr gene, which confers resistance to methotrexate (Bourouis et al., 1983).

One such vector useful for direct gene transfer techniques in combination with selection by the herbicide Basta (or phosphinothricin) is pCIB3064. This
15 vector is based on the plasmid pCIB246, which comprises the CaMV 35S promoter in operational fusion to the *E. coli* GUS gene and the CaMV 35S transcriptional terminator and is described in the PCT published application WO 93/07278, herein incorporated by reference. One gene useful for conferring resistance to phosphinothricin is the bar gene from *Streptomyces viridochromogenes* (Thompson
20 et al., 1987). This vector is suitable for the cloning of plant expression cassettes containing their own regulatory signals.

An additional transformation vector is pSOG35 which utilizes the *E. coli* gene dihydrofolate reductase (DHFR) as a selectable marker conferring resistance to methotrexate. PCR was used to amplify the 35S promoter (about 800 bp), intron 6
25 from the maize Adh1 gene (about 550 bp) and 18 bp of the GUS untranslated leader sequence from pSOG10. A 250 bp fragment encoding the *E. coli* dihydrofolate reductase type II gene was also amplified by PCR and these two PCR fragments were assembled with a SacI-PstI fragment from pBI221 (Clontech) which comprised the pUC19 vector backbone and the nopaline synthase terminator. Assembly of
30 these fragments generated pSOG19 which contains the 35S promoter in fusion with the intron 6 sequence, the GUS leader, the DHFR gene and the nopaline synthase

terminator. Replacement of the GUS leader in pSOG19 with the leader sequence from Maize Chlorotic Mottle Virus check (MCMV) generated the vector pSOG35. pSOG19 and pSOG35 carry the pUC-derived gene for ampicillin resistance and have HindIII, SphI, PstI and EcoRI sites available for the cloning of foreign sequences.

IV. Production and Characterization of Stably Transformed Plants

Transgenic plant cells are then placed in an appropriate selective medium for selection of transgenic cells which are then grown to callus. Shoots are grown from callus and plantlets generated from the shoot by growing in rooting medium. The various constructs normally will be joined to a marker for selection in plant cells. Conveniently, the marker may be resistance to a biocide (particularly an antibiotic, such as kanamycin, G418, bleomycin, hygromycin, chloramphenicol, herbicide, or the like). The particular marker used will allow for selection of transformed cells as compared to cells lacking the DNA which has been introduced. Components of DNA constructs including transcription cassettes of this invention may be prepared from sequences which are native (endogenous) or foreign (exogenous) to the host. By "foreign" it is meant that the sequence is not found in the wild-type host into which the construct is introduced. Heterologous constructs will contain at least one region which is not native to the gene from which the transcription-initiation-region is derived.

To confirm the presence of the transgenes in transgenic cells and plants, a variety of assays may be performed. Such assays include, for example, "molecular biological" assays well known to those of skill in the art, such as Southern and Northern blotting, *in situ* hybridization and nucleic acid-based amplification methods such as PCR or RT-PCR; "biochemical" assays, such as detecting the presence of a protein product, e.g., by immunological means (ELISAs and Western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the phenotype of the whole regenerated plant, e.g., for disease or pest resistance.

DNA may be isolated from cell lines or any plant parts to determine the presence of the preselected nucleic acid segment through the use of techniques well

known to those skilled in the art. Note that intact sequences will not always be present, presumably due to rearrangement or deletion of sequences in the cell.

The presence of nucleic acid elements introduced through the methods of this invention may be determined by polymerase chain reaction (PCR). Using this technique discreet fragments of nucleic acid are amplified and detected by gel electrophoresis. This type of analysis permits one to determine whether a preselected nucleic acid segment is present in a stable transformant, but does not prove integration of the introduced preselected nucleic acid segment into the host cell genome. In addition, it is not possible using PCR techniques to determine whether transformants have exogenous genes introduced into different sites in the genome, i.e., whether transformants are of independent origin. It is contemplated that using PCR techniques it would be possible to clone fragments of the host genomic DNA adjacent to an introduced preselected DNA segment.

Positive proof of DNA integration into the host genome and the independent identities of transformants may be determined using the technique of Southern hybridization. Using this technique specific DNA sequences that were introduced into the host genome and flanking host DNA sequences can be identified. Hence the Southern hybridization pattern of a given transformant serves as an identifying characteristic of that transformant. In addition it is possible through Southern hybridization to demonstrate the presence of introduced preselected DNA segments in high molecular weight DNA, i.e., confirm that the introduced preselected DNA segment has been integrated into the host cell genome. The technique of Southern hybridization provides information that is obtained using PCR, e.g., the presence of a preselected DNA segment, but also demonstrates integration into the genome and characterizes each individual transformant.

It is contemplated that using the techniques of dot or slot blot hybridization which are modifications of Southern hybridization techniques one could obtain the same information that is derived from PCR, e.g., the presence of a preselected DNA segment.

Both PCR and Southern hybridization techniques can be used to demonstrate transmission of a preselected DNA segment to progeny. In most instances the

characteristic Southern hybridization pattern for a given transformant will segregate in progeny as one or more Mendelian genes (Spencer et al., 1992); Laursen et al., 1994) indicating stable inheritance of the gene. The nonchimeric nature of the callus and the parental transformants (R_0) was suggested by germline transmission and the identical Southern blot hybridization patterns and intensities of the transforming DNA in callus, R_0 plants and R_1 progeny that segregated for the transformed gene.

Whereas DNA analysis techniques may be conducted using DNA isolated from any part of a plant, RNA may only be expressed in particular cells or tissue types and hence it will be necessary to prepare RNA for analysis from these tissues. PCR techniques may also be used for detection and quantitation of RNA produced from introduced preselected DNA segments. In this application of PCR it is first necessary to reverse transcribe RNA into DNA, using enzymes such as reverse transcriptase, and then through the use of conventional PCR techniques amplify the DNA. In most instances PCR techniques, while useful, will not demonstrate integrity of the RNA product. Further information about the nature of the RNA product may be obtained by Northern blotting. This technique will demonstrate the presence of an RNA species and give information about the integrity of that RNA. The presence or absence of an RNA species can also be determined using dot or slot blot Northern hybridizations. These techniques are modifications of Northern blotting and will only demonstrate the presence or absence of an RNA species.

While Southern blotting and PCR may be used to detect the preselected DNA segment in question, they do not provide information as to whether the preselected DNA segment is being expressed. Expression may be evaluated by specifically identifying the protein products of the introduced preselected DNA segments or evaluating the phenotypic changes brought about by their expression.

Assays for the production and identification of specific proteins may make use of physical-chemical, structural, functional, or other properties of the proteins. Unique physical-chemical or structural properties allow the proteins to be separated and identified by electrophoretic procedures, such as native or denaturing gel electrophoresis or isoelectric focusing, or by chromatographic techniques such as

ion exchange or gel exclusion chromatography. The unique structures of individual proteins offer opportunities for use of specific antibodies to detect their presence in formats such as an ELISA assay. Combinations of approaches may be employed with even greater specificity such as Western blotting in which antibodies are used to locate individual gene products that have been separated by electrophoretic techniques. Additional techniques may be employed to absolutely confirm the identity of the product of interest such as evaluation by amino acid sequencing following purification. Although these are among the most commonly employed, other procedures may be additionally used.

Assay procedures may also be used to identify the expression of proteins by their functionality, especially the ability of enzymes to catalyze specific chemical reactions involving specific substrates and products. These reactions may be followed by providing and quantifying the loss of substrates or the generation of products of the reactions by physical or chemical procedures. Examples are as varied as the enzyme to be analyzed.

Very frequently the expression of a gene product is determined by evaluating the phenotypic results of its expression. These assays also may take many forms including but not limited to analyzing changes in the chemical composition, morphology, or physiological properties of the plant. Morphological changes may include greater stature or thicker stalks. Most often changes in response of plants or plant parts to imposed treatments are evaluated under carefully controlled conditions termed bioassays.

V. Uses of Transgenic Plants

Once an expression cassette of the invention has been transformed into a particular plant species, it may be propagated in that species or moved into other varieties of the same species, particularly including commercial varieties, using traditional breeding techniques. Particularly preferred plants of the invention include the agronomically important crops listed above. The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction and can thus be maintained and propagated in progeny plants. The present invention also relates to a transgenic plant cell, tissue, organ, seed or plant

part obtained from the transgenic plant. Also included within the invention are transgenic descendants of the plant as well as transgenic plant cells, tissues, organs, seeds and plant parts obtained from the descendants.

Preferably, the expression cassette in the transgenic plant is sexually transmitted. In one preferred embodiment, the coding sequence is sexually transmitted through a complete normal sexual cycle of the R0 plant to the R1 generation. Additionally preferred, the expression cassette is expressed in the cells, tissues, seeds or plant of a transgenic plant in an amount that is different than the amount in the cells, tissues, seeds or plant of a plant which only differs in that the expression cassette is absent.

The transgenic plants produced herein are thus expected to be useful for a variety of commercial and research purposes. Transgenic plants can be created for use in traditional agriculture to possess traits beneficial to the grower (e.g., agronomic traits such as resistance to water deficit, pest resistance, herbicide resistance or increased yield), beneficial to the consumer of the grain harvested from the plant (e.g., improved nutritive content in human food or animal feed; increased vitamin, amino acid, and antioxidant content; the production of antibodies (passive immunization) and nutraceuticals), or beneficial to the food processor (e.g., improved processing traits). In such uses, the plants are generally grown for the use of their grain in human or animal foods. Additionally, the use of root-specific promoters in transgenic plants can provide beneficial traits that are localized in the consumable (by animals and humans) roots of plants such as carrots, parsnips, and beets. However, other parts of the plants, including stalks, husks, vegetative parts, and the like, may also have utility, including use as part of animal silage or for ornamental purposes. Often, chemical constituents (e.g., oils or starches) of maize and other crops are extracted for foods or industrial use and transgenic plants may be created which have enhanced or modified levels of such components.

Transgenic plants may also find use in the commercial manufacture of proteins or other molecules, where the molecule of interest is extracted or purified from plant parts, seeds, and the like. Cells or tissue from the plants may also be cultured, grown *in vitro*, or fermented to manufacture such molecules.

The transgenic plants may also be used in commercial breeding programs, or may be crossed or bred to plants of related crop species. Improvements encoded by the expression cassette may be transferred, e.g., from maize cells to cells of other species, e.g., by protoplast fusion.

5 The transgenic plants may have many uses in research or breeding, including creation of new mutant plants through insertional mutagenesis, in order to identify beneficial mutants that might later be created by traditional mutation and selection. An example would be the introduction of a recombinant DNA sequence encoding a transposable element that may be used for generating genetic variation. The
10 methods of the invention may also be used to create plants having unique “signature sequences” or other marker sequences which can be used to identify proprietary lines or varieties.

Thus, the transgenic plants and seeds according to the invention can be used in plant breeding which aims at the development of plants with improved properties
15 conferred by the expression cassette, such as tolerance of drought, disease, or other stresses. The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate descendant plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well
20 known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, utilane breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line
25 assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines which for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their
30 modified genetic properties. Alternatively new crops with improved stress tolerance can be obtained which, due to their optimized genetic “equipment”, yield harvested

product of better quality than products which were not able to tolerate comparable adverse developmental conditions.

VI. A Computer Readable Medium

5 The invention also provides a computer readable medium having stored thereon a data structure containing nucleic acid sequences having at least 70% sequence identity to a nucleic acid sequence selected from those listed in SEQ ID Nos: 1-953, 1001-1095, 1954-1966, 2000-2129, 2137-2661, 2662-4737 and 4738-6813, as well as complementary, ortholog, and variant sequences thereof. Storage and use of nucleic acid sequences on a computer readable medium is well known in the art. (See for example U.S. Patent Nos. 6,023,659; 5,867,402; 5,795,716)

10 Examples of such medium include, but are not limited to, magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory. Accordingly, the nucleic acid sequences contained on the computer readable medium may be compared through use of a module that receives the sequence information and compares it to other sequence information. Examples of other sequences to which the nucleic acid sequences of the invention may be compared include those maintained by the National Center for Biotechnology Information (NCBI)(<http://www.ncbi.nlm.nih.gov/>) and the Swiss Protein Data Bank. A computer is an example of such a module that can read and compare

15 nucleic acid sequence information. Accordingly, the invention also provides the method of comparing a nucleic acid sequence of the invention to another sequence. For example, a sequence of the invention may be submitted to the NCBI for a Blast search as described herein where the sequence is compared to sequence information contained within the NCBI database and a comparison is returned. The invention

20 also provides nucleic acid sequence information in a computer readable medium that allows the encoded polypeptide to be optimized for a desired property. Examples of such properties include, but are not limited to, increased or decreased: thermal stability, chemical stability, hydrophylicity, hydrophobicity, and the like. Methods for the use of computers to model polypeptides and polynucleotides having altered

25 activities are well known in the art and have been reviewed. (Lesyng et al., 1993; Surles et al., 1994; Koehl et al., 1996; Rossi et al., 2001).

30

The invention will be further described by the following non-limiting examples.

Example 1

GeneChip Standard Protocol

2. Run gel to check the integrity and purity of the extracted RNA

Step 1. Primer hybridization:

Quick spin and put on ice briefly

RNA (10 μ g final)-10 μ l

Superscript II RT 200 U/ μ l- 1 μ l

Mix well

Incubate at 42°C for 1 hour

Step 4. Second strand synthesis:

Place reactions on ice, quick spin

5

DEPC-water- 91 µl

5X 2nd strand cDNA buffer- 30 µl

mM dNTP mix (250 mM final) - 3 µl

E. coli DNA ligase (10 U/µl)-1 µl

E. coli DNA polymerase 1-10 U/µl- 4 µl

10

RnaseH 2U/µl -1 µl

T4 DNA polymerase 5 U/µl-2 µl

0.5 M EDTA (0.5 M final)--10 µl

Total 162 µl

Mix/spin down/incubate 16°C for 2 hours

15

Step 5. Completing the reaction:

Incubate at 16°C for 5 minutes

Purification of double stranded cDNA

20

1. Centrifuge PLG (Phase Lock Gel, Eppendorf 5 Prime, Inc., PI-188233) at 14,000X, transfer 162 µl of cDNA to PLG

2. Add 162 µl of Phenol:Chloroform:Isoamyl alcohol (pH 8.0), centrifuge 2 minutes

3. Transfer the supernatant to a fresh 1.5 ml tube, add

25

Glycogen (5 mg/ml) 2

0.5 M NH₄OAC (0.75xVol) 120

ETOH (2.5xVol, -20 C) 400

4. Mix well and centrifuge at 14,000X for 20 minutes

5. Remove supernatant, add 0.5 ml 80% EtOH (-20°C)

6. Centrifuge for 5 minutes, air dry or by speed vac for 5-10 minutes

30

7. Add 44 µl DEPC H₂O

Analyze of quantity and size distribution of cDNA

Run a gel using 1 μ l of the double-stranded synthesis product

Synthesis of biotinylated cRNA

5 (use Enzo BioArray High Yield RNA Transcript Labeling Kit Cat#900182)

Purified cDNA 22 μ l

10X Hy buffer 4 μ l

10X biotin ribonucleotides 4 μ l

10X DTT 4 μ l

10 10X Rnase inhibitor mix 4 μ l

20X T7 RNA polymerase 2 μ l

Total 40 μ l

Centrifuge 5 seconds, and incubate for 4 hours at 37°C

Gently mix every 30-45 minutes

15

Purification and quantification of cRNA

(use Qiagen Rneasy Mini kit Cat# 74103)

Determine concentration and dilute to 1 μ g/ μ l concentration

20 Fragmentation of cRNA

cRNA (1 μ g/ μ l) 15 μ l

5X Fragmentation Buffer* 6 μ l

DEPC H₂O 9 μ l

30 μ l

25

*5x Fragmentation Buffer

1M Tris (pH8.1) 4.0 ml

MgOAc 0.64 g

KOAC 0.98 g

30 DEPC H₂O

Total 20 ml

Filter Sterilize

Array wash and staining

Stringent Wash Buffer**

5 Non-Stringent Wash Buffer***

SAPE Stain****

Antibody Stain*****

Wash on fluidics station using the appropriate antibody amplification protocol

10 **Stringent Buffer: 12X MES 83.3 ml, 5 M NaCl 5.2 ml, 10% Tween 1.0 ml,
H₂O 910 ml,
Filter Sterilize

***Non-Stringent Buffer: 20X SSPE 300 ml, 10% Tween 1.0 ml, H₂O 698 ml,
Filter Sterilize, Antifoam 1.0.

15 ****SAPE stain: 2X Stain Buffer 600 µl, BSA 48 µl, SAPE 12µl, H₂O 540 µl.

*****Antibody Stain: 2X Stain Buffer 300 µl, H₂O 266.4 µl, BSA 24 ul, Goat IgG 6
µl, Biotinylated Ab 3.6 µl

Image analysis and data mining

1. Two text files are included in the analysis:

- 20 a. One with Absolute analysis: giving the status of each gene, either absent or
present in the samples
b. The other with Comparison analysis: comparing gene expression levels
between two samples

25

Example 2

Analysis of the RPS2 Mediated Interaction in *Arabidopsis*

The identification and cloning of resistance genes is extremely important for
the treatment of crops. For example, bacterial blight disease caused by
Xanthomonas spp. infects virtually all crop plants and leads to extensive crop losses
30 worldwide. Therefore, it is of interest to identify diverse and abundant plant

resistance genes for use as future crop treatments for pathogen resistance, e.g., to identify particular pathogen resistance (*R*) genes in a plant.

Differential gene expression analysis was used to identify pathogen resistance (*R*) genes in a plant. This method takes advantage of the HR-associated disease resistance. One model plant-pathogen interaction is that of *Arabidopsis thaliana* and *Pseudomonas syringae* pv *tomato*. There are four possible genetic interactions of a *P. syringae* infection of *Arabidopsis* when analyzing HR-associated disease resistance (Table 2). However, there are only two possible outcomes: a compatible outcome occurs when there is disease, and an incompatible outcome occurs when there is no disease. An incompatible outcome, or disease resistance, occurs only when the plant possesses the resistance gene, e.g., *RPS2*, and the pathogen possesses the corresponding *avr* gene, e.g., *avrRpt2*. *RPS2* belongs to the NBS-LRR class of *R* genes, which can confer resistance to a wide variety of phytopathogens. It has been suggested that AvrRpt2 is delivered to the plant via the bacteria's type III secretion system and recognized by a surveillance system involving *RPS2* inside the plant cell. The plant response during an incompatible interaction includes a change in ion flux across the plasma membrane, generation of reactive oxygen species, induction of defense genes, induction of HR, fortification of the cell wall, accumulation of salicylic acid, and anti-microbial compounds.

Table 2

Number	Plant	Pathogen	Outcome	
1	<i>RPS2</i>	no <i>avr</i>	Disease	Compatible
2	<i>RPS2</i>	<i>avrRpt2</i>	No disease	Incompatible
3	<i>rps2</i>	no <i>avr</i>	Disease	Compatible
4	<i>rps2</i>	<i>avrRpt2</i>	Disease	Compatible

Methods

Differential Expression

Analysis of differential gene expression is a classic and very powerful tool in experimental biology not only to study large trends in gene regulation but also small

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differences among similar responses. Historically, methods for analysis only allowed the comparison of a very few genes in each experiment. However, with new methods to identify and quantitate differential mRNA profiles, such as long distance differential display PCR, cDNA microarrays, and gene chips, one can much more quickly and comprehensively identify and analyze differentially expressed genes.

By analyzing and comparing the expression profile of genes in the above 4-way matrix, a number of types of genes can be identified that are involved in the resistance pathway. Resistance genes would be highly expressed or strongly downregulated in outcome number 2 in the four way matrix and less oppositely expressed in outcome numbers 1, 3, and 4. Genes that are highly expressed or strongly downregulated in outcome numbers 1 and 2 and oppositely expressed or not expressed above baseline in outcome numbers 3 and 4 are of interest as being associated with the reaction of a plant having resistance genes to a bacterial infection, regardless of the *avr* genotype of the bacterium. Such a comparison is very useful in identifying strong candidates for different roles in plant/pathogen interactions, as are numerous other kinds of outcomes in the four-way plant/pathogen interaction analysis of gene expression. Such genes include those involved in recognition of pathogen (unrelated to virulence status); genes involved in recognition of pathogen having a virulence or avirulence gene (regardless of the status of the corresponding plant); genes related to the status of the plant, regardless of the status of the pathogen; and genes that do not change expression during plant-pathogen interaction.

Use of a Gene Chip to Study Gene Regulation in *Arabidopsis* in Response to Exposure to Pathogen

Initially isogenic strains of *Arabidopsis thaliana* ecotype Col-0 were used, one having the wild type *RPS2* gene that confers resistance, and one having the *rps2* mutant that confers susceptibility to attack by *Pseudomonas syringae* pathovar *tomato* (Pst). Subsequently, comparisons between ecotypes, mutant *Arabidopsis*, and infection with different pathogens were made. After infection, the RNA was isolated and a probe produced using the Affymetrix GeneChip™ protocol. A gene

array representing approximately 8,100 *Arabidopsis thaliana* genes was used to carry out global gene expression profiling in response to exposure to a particular pathogen.

Initially, the analysis involved comparing all four of the interactions to a water control (plants “infected” with water). In the initial analysis, the mRNA levels of approximately 1,600 genes were significantly affected (> 2.5-fold change in expression) by exposure to the bacterial pathogen. This suggested a dramatic change in the molecular biology of the cell and a more detailed analysis was performed.

10 Results

A. Comparison Of Compatible To Incompatible Infections

Two different types of interactions between *Arabidopsis* and *Pseudomonas syringae* were analyzed. In one type of experiment, a gene for gene interaction conditioned by the plant resistance (*R*) gene *RPS2* and the bacterial avirulence gene *avrRpt2* at a relatively early stage was analyzed. When the pathogen has an *avr* gene and the plant has the corresponding *R* gene, the plant is resistant to the pathogen and the interaction is called incompatible. When the plant-pathogen system lacks either or both genes, the plant is susceptible to the pathogen and the interaction is called compatible. A hypersensitive response (HR, localized rapid cell death of the plant) is one aspect of resistance.

Isogenic strains of *Arabidopsis thaliana* ecotype Col-0 were used, one having the wild type *RPS2* gene that confers resistance, and one having the mutant *rps2* mutant that confers susceptibility to attack by *Pseudomonas syringae* pathovar *tomato* (Pst) carrying *avrRpt2*. Two strains of *Pseudomonas syringae* were used, one having the *avr* gene *avrRpt2* and the other having no *avr*. The *avr* gene is carried on a plasmid.

A gene array having 8,700 probe sets representing approximately 8,100 *Arabidopsis thaliana* genes was used to carry out global gene expression profiling of each of the infection outcomes. The pairings were as follows:

1. RPS2 WT plant; *P. syringae* (no *avr*)
2. RPS2 WT plant; *P. syringae/avrRpt2*

3. rps2-101C mutant plant; *P. syringae* (no *avr*)
4. rps2-101C mutant plant; *P. syringae/avrRpt2*

Additionally, two controls were used:

5. RPS2 WT plant; water control
- 5 6. Rps2-101C mutant plant; water control

Data were processed such that genes having a difference in mRNA levels that was greater than 2.5-fold increased or reduced, compared with controls were selected. The fold change for each gene was log-scaled and normalized.

1. Data analysis: identification of expression clusters

10 Data analysis was carried out by comparing expression of each gene in interactions 1-4 (Table 2), plotting that expression level, and identifying the genes of interest, i.e., those that show more than a 2.5X change in expression (about 1,600 genes). Classification of patterns, or expression clusters were as follows:

- 15 a) Genes strongly induced (> 2.5X change in expression level) only in the resistant (incompatible) response;
- b) Genes responding weakly only in the resistance response, but strongly induced in the compatible response;
- c) Genes that show a high level of expression in all outcomes;
- d) Genes that show a high level of repression in all outcomes;
- 20 e) Genes that show a very high level of repression only when the bacterial *avr* is expressed; and
- f) Genes that show a very different level of expression in the presence of the plant resistance compared to the level in the absence of the plant resistance (the mutant *rps2*).

25 Genes that fall within groups 1a and 1b, i.e., those that are differentially expressed only when an incompatible interaction occurs, include genes directly involved in resistance to pathogens. These genes show a peak (either up or down) only during plant-pathogen interaction 2. The differential expression can be of two types: upregulated (increased expression of this gene is potentially important in the incompatible interaction) or downregulated (decreased expression of this gene is
30 potentially important in the incompatible interaction).

2. Heat shock proteins and transcription factors

All major heat shock proteins (HSPs) were identified to be upregulated only during the incompatible interaction. Heat shock factors (HSFs) are transcription factors which control the transcription of the HSP genes. Eight HSF genes are known in *Arabidopsis*. HSF4 and HSF21 were identified as being upregulated when the plant was infected with *P. syringae*. HSF4 showed strong induction that was restricted to resistance, and HSF4 was the only HSF specifically upregulated during the incompatible interaction. The data suggests that the upregulation of HSPs is downstream of upregulation of HSF4.

To analyze whether the response was a more general one, or specific to a given ecotype, expression of HSF4 was analysed in two different *Arabidopsis* ecotypes, *A. thaliana*, ecotypes Col-0 and Ws. HSF4 was also upregulated in the response of Ws ecotype to infection and, specifically, was upregulated during an incompatible response. HSF21 is thus a preferred protein for resistance applications, and HSF4, a protein which is expressed in all plants, is especially preferred for engineering resistance.

A transgene containing the ACT2 promoter and the HSF4 open reading frame was introduced to *Arabidopsis* and transgenic HSF4 *Arabidopsis* lines generated to overexpress and underexpress HSF4. The expression of HSF4 during pathogen infection may cause lower general resistance to *P. syringae*.

Conditional overexpression lines were also generated using the estradiol-inducible promoter system. Infiltration of 20 μ M estradiol into the intercellular space of the leaves of transgenic plants induced expression of HSF4 mRNA for a short time (down by 4 hours). Addition of 20 estradiol to the hydroponic medium yielded sustained HSF4 mRNA accumulation.

B. Genes Involved in *Arabidopsis* Responses to Pathogens

A number of mutations in *Arabidopsis thaliana* that disrupt expression of pathogen-induced genes and cause enhanced disease susceptibility have been identified. Pathogen-induced genes whose expression is altered in these enhanced disease susceptibility mutants are likely to play important roles in conferring disease resistance.

To identify such genes, wild type and various mutant plants were infected with strain *Psm* ES4326 at a dose of 10,000 colony forming units per square centimeter of leaf tissue. Control plants were mock-infected. After thirty hours, tissue samples were collected and used to prepare RNA. Three sets of experiments were carried out. Each set of experiments included three independent replicate experiments. RNA from replicate experiments was pooled to reduce errors arising from the effects of variations in environmental conditions. Each RNA sample was used to prepare a fluorescently-labelled probe which was applied to an Affymetrix GeneChip™, allowing the expression level of each gene represented on the GeneChip™ to be determined for each sample. The plant genotypes included in each experiment were as follows:

Experiment #1

Wild-type (ecotype Columbia)

nahG

pad4-1

eds5-1

eds4

pad2-1

npr1-1

npr1-3

Experiment #2

Wild-type (ecotype Columbia)

coil

ein2

pad1

FN1-3

eds3

eds8

Experiment #3

Wild-type (ecotype Columbia)

pad4-1

nahG

sid2

eds5-3

FN1-9

FN3-2

1. Data analysis

Expression values that were less than 5 were set to five. This ensures that no values are 0 or negative. Such values interfere with subsequent analysis steps. To obtain a list of pathogen-induced genes, the ratios of infected wild-type to mock infected wild type were calculated for each experiment. Then genes were selected in which expression levels were infected wild-type/mock wild-type > 2.5 , and infected wild-type > 50 for at least 2 of 3 experiments. The ratio of 2.5 was chosen because the false positive rate for the GeneChip™ is essentially 0 at this level of stringency, and the absolute value of 50 was chosen to eliminate expression values below the detection limit of the GeneChip™. The result of this analysis was a list of 745 probe sets representing genes that are induced by infection in wild-type plants (note that some genes are represented by more than one probe set, so the number of different genes is somewhat fewer) (see Table 3 below). Hence, the expression of genes comprising SEQ ID NOs:2-6, 8-13, 16, 18, 22-23, 25, 28-29, 31-32, 35-37, 39-43, 45-47, 49-50, 52, 54-55, 57-58, 60-66, 70-72, 74, 76-77, 79, 81, 83, 85, 87-90, 92, 94, 97, 100-107, 111-115, 117-125, 127-135, 138-140, 142-153, 156-158, 160, 162-165, 168-170, 173-181, 183-184, 186-188, 190-198, 200-201, 203-211, 214-215, 218-224, 227-232, 234-249, 251-262, 264, 266-268, 270, 272-275, 277-281, 283, 286-294, 297-298, 302, 304-306, 308-326, 328-339, 341, 344-345, 347, 350-351, 353-358, 361-371, 373-377, 379-386, 388-390, 392, 394-400, 402-406, 408-410, 412-417, 419-427, 429-433, 435-443, 445-452, 454-457, 459-460, 462-464, 466-470, 473-475, 478-479, 481-482, 484-187, 489-494, 496-498, 500-501, 503-506, 508, 510, 512-515, 517-523, 526, 528-529, 531-538, 540, 544-548, 550-558, 560, 563-568, 570, 572-577, 579-580, 582-585, 588-594, 596, 598-600, 602-603, 605-606, 608-612, 614-617, 619-624, 626-630, 632-639, 642, 644, 646-651, 653-657, 659-665, 667-671, 673-678, 681-689, 691-693, 695-713, 715-717, 719, 721-727, 729-733, 736-738, 740, 742, 744, 746, 748-752, 755-756, 758-760, 762-769, 771, 774, 776-781, 783-788, 790-796, 798-799, 802, 804-808, 810-815, 817-831, 833-848, 850-855, 857-869, 871-880, 882-900, 903-907, 909, 911-915, 918-920, 922-

925, 927, 929, 931-938, 940, 943-945, 947, and 950-953 is increased after infection of wild-type *Arabidopsis* with *Pseudomonas syringae*.

To identify pathogen-induced genes whose expression is affected by the mutations, genes for which the ratio of infected mutant/infected wild-type was < 0.5 or > 2 for at least one mutant were selected from the list of 745 pathogen-inducible probe sets. The limits of 5 and 2 were chosen because changes of at least 2-fold are likely to be significant for impact on disease resistance, and because the false positive rate for the GeneChip™ at 2-fold is 0.2%. This selection yielded a list of 530 probe sets corresponding to genes, the expression of which is induced by *Pseudomonas* infection in wild-type plants and perturbed in at least one mutant plant (see Tables 4a and 4b below). Thus, the expression of genes comprising SEQ ID NOs:2, 4-6, 11-13, 18, 22-23, 28, 31, 36, 39-43, 45, 47, 49-50, 52, 54-55, 57-58, 60-61, 63-66, 71-72, 74, 77, 81, 83, 85, 87-89, 92, 97, 100-107, 111-112, 114-115, 117-120, 122, 125, 127-128, 134, 138-140, 143-144, 148-151, 153, 156-157, 160, 165, 168-170, 173-174, 176-180, 183, 187-188, 191, 193-194, 197-198, 200, 203-210, 214, 219-224, 227, 230-232, 235-237, 239-240, 243-246, 248-249, 251-254, 256-258, 261, 264, 266-268, 270, 272-275, 277-278, 280, 283, 286-287, 290-293, 297, 302, 305-306, 308-310, 312-316, 321-326, 328-331, 333, 336-339, 341, 345, 351, 353, 355-358, 361-363, 365-366, 368-371, 373, 375, 377, 379-381, 384-385, 388-390, 392, 394-400, 402-406, 410, 412, 415-416, 419-420, 422-425, 429-433, 435-439, 441-443, 445-452, 454, 459-460, 463, 466, 468-470, 473, 481-482, 485-486, 489, 491-494, 497-498, 500-501, 503, 505-506, 508, 510, 513-515, 517, 520-521, 523, 528-529, 531, 533-538, 540, 545-548, 550-551, 553-554, 556-558, 560, 566-567, 575, 580, 582-584, 588-593, 596, 598-600, 602-603, 605-606, 608-610, 612, 614, 616, 620-622, 627-629, 633-634, 636-639, 644, 646, 648-651, 654-657, 659, 661-663, 667, 669, 673-674, 677, 682, 684-687, 689, 691-693, 697, 699, 701, 703-708, 713, 717, 719, 721-727, 730-733, 736, 740, 744, 746, 749-752, 755-756, 758-760, 762-764, 766-769, 774, 776-778, 780-781, 786, 788, 791-796, 799, 802, 804-808, 810-812, 815, 818-821, 823-825, 827-829, 831, 833-836, 838-843, 845, 847-848, 852-853, 855, 858, 860-869, 871-874, 876, 878-880, 884-887, 889, 892-894, 896-900, 904-907, 911-915, 918-920, 922-924, 931, 933, 938, 943-945, 947, and

950-952 is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis*, with *Pseudomonas syringae*.

2. Data interpretation

Genes that encode regulatory proteins such as transcription factors, protein
5 kinases, calcium binding proteins and the like, are likely to play important roles in disease resistance, as they are likely to affect the expression of multiple defense effector genes. The list of 530 probe sets include 81 that correspond to genes encoding regulatory factors. These are likely to be useful for engineering plants to respond more quickly to pathogen attack by activating expression of defense
10 responses (see Table 5 below). Thus, the expression of genes comprising SEQ ID NOs:39, 52, 60, 63, 81, 83, 106, 107, 115, 117, 118, 168, 174, 176, 179, 204, 207, 208, 220, 221, 248, 258, 268, 275, 280, 309, 323, 326, 329, 351, 419, 422, 429, 430, 432, 459, 460, 468, 469, 473, 500, 505, 506, 508, 529, 531, 533, 535, 538, 545, 553, 602, 606, 608, 610, 614, 616, 634, 654, 655, 684, 686, 687, 691, 717, 751, 752, 766,
15 777, 815, 831, 834, 835, 839, 841, 847, 876, 884, 906, 920, and 924 is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis*, with *Pseudomonas syringae*.

The mutations *nahG*, *pad4-1*, *eds5-1*, *eds4*, *pad2-1*, *npr1-1*, *npr1-3*, *pad1*, *FN1-3*, *eds3*, *eds8*, *sid2*, *eds5-3*, *FN1-3* and *FN3-2* cause enhanced susceptibility to
20 *Pseudomonas syringae*. Consequently, pathogen-inducible genes whose expression is reduced by one of these mutations are likely to be important for resistance to *Pseudomonas syringae* and possibly other bacterial pathogens. These 333 probe sets are shown in Table 6 (below). Therefore, the expression of genes comprising SEQ ID NOs:12-13, 18, 23, 36, 39-40, 43, 45, 50, 52, 57-58, 60-61, 64, 71-72, 81,
25 87-89, 97, 100, 102-105, 107, 111-112, 115, 119-120, 122, 125, 127-128, 140, 144, 148-150, 153, 165, 168-169, 176-177, 179, 183, 188, 191, 193-194, 197-198, 203-206, 208-209, 214, 219-222, 227, 230, 232, 237, 244-246, 248-249, 251-253, 258, 261, 264, 266, 268, 273-275, 283, 287, 290, 293, 297, 302, 305-306, 308, 312-315, 321-322, 324, 326, 330, 333, 338, 341, 345, 353, 356-358, 362-363, 366, 369, 371,
30 375, 377, 380, 384-385, 389, 392, 394-395, 398-399, 402-404, 406, 410, 415, 419, 422, 425, 429-430, 433, 435-439, 443, 445-452, 454, 463, 466, 468-470, 473, 486,

489, 491-492, 494, 498, 500-501, 503, 508, 513-514, 517, 529, 533-538, 548, 550, 553-554, 556-558, 566, 575, 580, 582-583, 590-591, 593, 600, 602, 609-610, 612, 614, 620-622, 627-629, 637-638, 644, 649, 654-657, 659, 663, 667, 669, 673-674, 677, 684-685, 689, 691-693, 699, 703-705, 708, 719, 721, 724-726, 730-732, 744, 746, 749-750, 752, 755-756, 758, 760, 762-764, 767, 769, 774, 780-781, 786, 788, 791-792, 794-796, 799, 804-808, 810-812, 815, 818-819, 823, 828-829, 833, 840-841, 843, 847, 852-853, 858, 860, 862-865, 867-868, 872-874, 876, 885-887, 889, 892-894, 896-900, 904-905, 907, 911-914, 918-920, 922-924, 931, 933, 938, 947, 950, and 952 is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis* having a mutation that results in enhanced susceptibility to *Pseudomonas* (*nahG*, *pad 4-1*, *eds 5-1*, *eds4*, *pad2-1*, *np4 1-1*, *npr 1-3*, *pad1*, *FN1-3*, *eds3*, *eds8*, *sid2*, *eds5-3*, *NF1-3* and *FN3-2*).

The mutations *coil* and *ein2* block jasmonate and ethylene signaling, respectively. Jasmonate and ethylene-dependent disease resistance responses are known to be important for resistance to the fungal pathogens *Alternaria brassicicola* and *Botrytis cinerea*, and may also be important for resistance to other necrotrophic fungal pathogens. *Alternaria* and *Botrytis* are distantly related, yet plant resistance to these fungi is controlled similarly, suggesting that jasmonate- and ethylene-dependent responses function to limit growth of a wide range of fungal pathogens. Consequently, pathogen-induced genes whose expression is reduced in *coil* and *ein2* mutants are likely to be important for resistance to these necrotrophic fungal pathogens. These 296 probe sets are shown in Table 7 (see below). Hence, the expression of genes comprising SEQ ID NOs:2, 4, 6, 11-13, 18, 22-23, 31, 41-43, 49-50, 54, 57-58, 61, 64-66, 71-72, 74, 77, 85, 87, 89, 92, 97, 101, 103, 106-107, 112, 114, 117-119, 125, 128, 134, 138, 143, 149, 151, 156-157, 165, 169-170, 174, 176-180, 187-188, 191, 193, 206, 208, 219-220, 222, 224, 231, 236, 239, 243-245, 251-254, 256-257, 267, 272, 287, 290, 292, 297, 302, 312-313, 315-316, 321-322, 324-325, 328, 330, 345, 351, 353, 355-357, 362-363, 366, 368-371, 373, 375, 379, 381, 384, 388-390, 392, 395-400, 405, 410, 415-416, 419, 422, 424, 431-432, 435-436, 438-439, 447, 459-460, 470, 473, 481-482, 489, 491, 493-494, 500-501, 505-506, 513-514, 517, 520-521, 523, 528-529, 531, 535, 537-538, 540, 545-548, 551,

732, 744, 746, 749-750, 752, 755-756, 760, 762-764, 767, 769, 774, 780-781, 786, 788, 791-792, 795-796, 805-808, 810-812, 815, 818-819, 823, 828, 833, 840-841, 843, 852-853, 858, 860, 862-865, 867-868, 872-874, 876, 887, 889, 893-894, 896-898, 900, 905, 907, 911-914, 918-920, 922-923, 931, 933, 938, 947, 950, and 952

5 which is increased after infection of wild-type *Arabidopsis* and altered after infection of at least one mutant *Arabidopsis* having a mutation in a gene that interferes with salicylic acid dependent signaling (*nahG*, *pad4-1*, *sid2*, *eds5-1*, *eds5-3* and *eds4*). Thus, these genes are particularly useful to improve the resistance of plants to infection by more than one pathogen including bacteria, oomycetes and
10 viruses, such as TMV.

Example 3

Further Analysis of the Pathogen Response and Comparison of the Response in Different Ecotypes

15 Materials and Methods

Arabidopsis ecotypes (or accessions) (the wild-types of all the *Arabidopsis* ecotypes used here have wild-type alleles of *RPS2* and *RPM1*).

Col, Columbia-0

Ler, Landsberg *erecta*

20 Ws, Wassilewskija

***Arabidopsis* mutants and transgenics**

Col *rps2-101C*, a loss-of-function mutant of the resistance gene *RPS2* in Col background.

25 NahG, transgene for salicylic acid hydroxylase (inactivating salicylic acid). Col background.

ndr1-1, null mutant allele of *NDR1* (non-race specific disease resistance).

The mutation strongly affects *RPS2*-mediated resistance and partially affects *RPM1*-mediated resistance. Col background.

Bacterial strains

30 Pst, *Pseudomonas syringae* pv. *tomato* DC3000 (virulent strain of *Arabidopsis*)

Psm, *P. syringae* pv. *maculicola* ES4326 (another virulent strain of *Arabidopsis*)

Psp, *P. syringae* pv. *phaseolicola* NPS3121 (very weak pathogen of *Arabidopsis*)

5 Avirulence (*avr*) genes of *P. syringae*

avrRpt2: corresponding to the *Arabidopsis* resistance (*R*) gene *RPS2*

avrB: corresponding to the *Arabidopsis* resistance (*R*) gene *RPM1*

Experimental Protocols

A. Gene for gene resistance (6 hours after treatment)

10	<u>plant</u>	<u>treatment</u>
	Col WT	H ₂ O
	Col WT	Pst
	Col WT	Pst/ <i>avrRpt2</i>
	Col <i>rps2-101C</i>	H ₂ O
15	Col <i>rps2-101C</i>	Pst
	Col <i>rps2-101C</i>	Pst/ <i>avrRpt2</i>
	Ws WT	H ₂ O
	Ws WT	Pst
	Ws WT	Pst/ <i>avrRpt2</i>

20 B. Differences in the response to bacterial pathogens among ecotypes (3, 6, and 9 hours after treatment)

	<u>Plant</u>	<u>treatment</u>
	Col	H ₂ O
	Col	Pst
25	Col	Pst/ <i>avrRpt2</i>
	Ler	H ₂ O
	Ler	Pst
	Ler	Pst/ <i>avrRpt2</i>
	Ws	H ₂ O
30	Ws	Pst
	Ws	Pst/ <i>avrRpt2</i>

Note that overall results for Cvi were very similar to Ler.

C. Genetic factors that affect the plant response to incompatible interactions (3, 6, and 9 hours after treatment)

	<u>plant</u>	<u>treatment</u>
5	Col	H ₂ O
	Col	Pst
	Col	Pst/avrRpt2
	Col	Pst/avrB
	Col	Psm
10	Col	Psm/avrRpt2
	Col	Psp (not 9 hours)
	Col	Psp/avrRpt2 (not 9 hours)
	Col NahG	Pst
	Col NahG	Pst/avrRpt2
15	Col NahG	Pst/avrB
	Col ndr1-1	Pst
	Col ndr1-1	Pst/avrRpt2
	Col ndr1-1	Pst/avrB

Results

20 Four hundred sixty-five genes were specifically/preferentially induced in the incompatible interaction (WT and Pst/avrRpt2), and 616 genes were specifically/preferentially repressed in the incompatible interaction. Examples of these genes are provided in Tables 10 and 13. Gene expression patterns in the incompatible interaction in Col and Ws were significantly different, indicating that

25 the genetic diversity among ecotypes can affect gene regulation during the incompatible interaction significantly. In comparison, a relatively small number of genes (314 genes for induction, 167 genes for repression) were affected at this time point during the compatible interactions (but not preferential to the incompatible interactions). A comparison of the results in three genetically different compatible

30 interactions (WT and Pst, rps2 and Pst, rps2 and avrRpt2) revealed that 25 genes were repressed in an avrRpt2-dependent manner (see Table 9). Thus, the expression

of genes comprising SEQ ID NOs:1, 15, 19, 20, 24, 26, 27, 34, 38, 51, 56, 59, 67-69, 99, 116, 155, 159, 182, 212, 284, 372, 444, and 789 is downregulated (repressed) in an *avrRpt2*-dependent manner in *Arabidopsis*. These genes are good candidates to be involved in *avrRpt2* virulence functions (in *rps2* plants).

5 Genes that were induced in *rps2* plants after infection irrespective of *avrRpt2* indicate a function of RPS2 other than an interaction with *avrRpt2*. Thus, global gene expression profiling can identify large and minor trends in gene regulation and is useful in gene discovery.

10 One general phenomenon when plants are resistant to a pathogen is the early response of pathogen-responsive (induced or repressed) genes compared to plants that are susceptible to infection. This has been proposed based on observing expression of a very limited number of genes, but it has not been proven as a global trend. To examine the results from early incompatible interactions and late compatible interactions, 4 week old Col-0 plants with well expanded leaves were
15 infected with a high dose ($OD_{600} = 0.02$) or low dose ($OD_{600} = 0.002$) of *P. syringae* and samples collected at 6 or 30 hours, respectively. The two expression patterns were similar. The correlation values between the late compatible and incompatible interaction at either 6 hours, 9 hours or the average of 3-9 hour time points was 0.71, 0.72 and 0.75, respectively.

20 The majority of genes that did not respond within 9 hours after infection of a virulent strain but that responded in 30 hours (Pst or Psm, for *Pseudomonas syringae* pv. tomato DC3000 and *Pseudomonas syringae* pv. *maculicola* ES4326, respectively; the plant is susceptible to these strains) responded within 6 hours after infection of an avirulent strain (Pst/*avrRpt2*; Pst carrying the avirulence gene
25 *avrRpt2*; the plant is resistant to this strain). This strongly suggests that early response of the pathogen-responsive genes is crucial for the plant to be resistant.

A comparison of the differences in the expression patterns of the 2 primary ecotypes of *Arabidopsis*' response to infection provides a further way to identify which genes have a more universal role (unchanged expression pattern) and which
30 may be very specific to a particular plant ecotype involved in a very specific gene-for-gene interaction. For example, responses that are common between two

ecotypes may be important for resistance. Genes that show the same pattern in both ecotypes may be part of more universal, or commonly-used, mechanisms involved in plant-pathogen interactions. Responses that are different may indicate that the two ecotypes use different combinations of responses to achieve resistance. This implies
5 that a variety of genes can participate in plant-pathogen interactions. Nevertheless, ecotype-specific responses are expected to have counterparts in other plant species.

The differences in resistance response between ecotypes can be used for improving resistance in plants. In responses that are different between ecotypes, using the methods and compounds of the invention, such a response can be added to
10 (induced or repressed) the response seen in the ecotype which does not normally use that response. This will likely give the plant a more robust or a wider range of resistance.

Table shows a comparison of gene expression in 4 ecotypes, i.e., Col-0, Ws-2, Cvi and Ler in response to infection. Table 10A shows the expression data for 9
15 probe sets corresponding to genes that are specifically induced at 3 hours after incompatible infection of four different ecotypes of *Arabidopsis* with *P. syringae* pv. tomato DC3000. Table 10B shows expression data for 18 probe sets corresponding to genes that are induced by 6 hours but not at 3 hours after incompatible infection of four different ecotypes of *Arabidopsis* with three different bacterial strains, i.e., *P.*
20 *syringae* pv. tomato DC3000. Table 10C illustrates the expression data for 6 probe sets corresponding to genes that are activated by *P. syringae* at 6 hours post-infection. Most of the genes are compatible interaction-specific or -preferential.

Four week old plants with fully expanded leaves were infected and samples collected at 3 or 6 hours post-infection ($OD_{600} = 0.02$). Some common patterns
25 were observed. At 3 hours after infection of an avirulent strain, Pst/avrRpt2, the overall qualitative gene expression patterns were very similar for all the ecotypes tested. Common responses to Pst/avrRpt2 could be important for gene-for-gene resistance and so may be useful to identify targets for reverse genetics. Quantitative and qualitative differences in the response were noted, indicating that there are
30 qualitative and/or quantitative differences in the signal transduction mechanisms

that regulate the response among the ecotypes. Such signal transduction mechanism differences are attributed to genetic differences among the ecotypes.

In particular, early inducible genes (3 hours) in the incompatible interaction were identified (70 genes are common in all the ecotypes, and 360 genes if selected for induced in at least one ecotype). One group of the early genes (38 genes in Col) were repressed to the control level by 6 hours. These genes did not respond in the compatible interaction at 3 hours and were repressed below the control level in the compatible interaction by 6 hours. This suggests that shutting down these genes in the incompatible interaction by 6 hours could be caused by defense response inhibiting factor(s) delivered by bacteria. Another group of the early genes were expressed even higher at 6 hours in the incompatible interaction. One hundred eighty-eight genes showed significant induction or repression at 3 hours in the compatible interaction in at least one of the ecotypes. Of these, 3 induced genes and 3 repressed genes were induced or repressed in all three ecotypes.

At 3 hours in the incompatible interaction, a major difference among the ecotypes was quantitative; overall expression patterns were very similar, but overall fold change amplitudes were clearly in the order of $Ws > Col > Ler$. Thus, in this type of analysis it is not appropriate to analyze datasets by comparing the genes from different datasets that are selected by a certain cut-off value (e.g., 2.5-fold difference). This fold change difference was mainly caused by differences in the basal expression of these genes. In fact, a strong negative correlation in each gene was found between the relative basal expression level in *Ws* (relative to the other ecotypes; Pearson correlation -0.78) and response in the incompatible interaction (especially at 3 hours) and a moderate positive correlation between the relative basal expression level in *Ler* and response in the incompatible interaction (Person correlation 0.38) (almost no correlation for the relative basal expression level in *Col*; Person correlation 0.10). These observations indicate that *Ws* has the tightest regulation of these incompatible interaction-responsive genes, and *Ler* has the loosest. Another interesting observation is that the relative susceptibility to a virulent strain (*Pst*) was in the order of $Ws > Col > Ler$. Although it is unknown whether these two phenomena are controlled by same gene(s), it is conceivable that

leaky expression of early response genes (in Ler) confers relative resistance to a virulent strain. At 6 hours in the incompatible interaction, the gene expression pattern for Col was significantly different from the other ecotypes.

Moreover, different ecotypes may use a different but overlapping set of
5 responses to achieve resistance against the same pathogen. Gene expression profiling can thus reveal ecotype differences. Therefore, it is possible to isolate the genes responsible for these differences in regulatory mechanisms using ecotype differences in gene expression as a phenotype, by a map-based cloning approach.

For example, a majority of the incompatible response-inducible genes have
10 lower basal levels in ecotype Ws and higher basal levels in ecotype Ler. Among the numerous genes, a few genes that display large differences in the basal level in two ecotypes are chosen. The large differences in expression level constitute easy-to-score phenotypic markers. Ws and Ler are crossed to obtain F2 populations. The larger the F2 population is, the better resolution in the map position can be obtained.
15 For each of the F2 plants, expression levels of the chosen phenotypic marker genes are measured and physical markers that distinguish these ecotype genomes are scored. The map position of the responsible gene is determined by analyzing the linkage between the phenotype and the physical markers. If more than a single gene is responsible for the ecotype difference and each of the genes has a quantitative
20 effect on the phenotype, quantitative trait locus (QTL) analysis can be used for mapping. Instead of using F2 populations, the use of recombinant inbred lines (RILs) between the ecotypes of interest may facilitate the analysis, especially using RILs that are already mapped for recombination points. Once the gene(s) responsible for the phenotype is mapped, a combination of increasing the map
25 resolution, sequencing the chromosomal region identified by mapping in both ecotypes, and gene transfer from one ecotype to the other leads to isolation of the gene.

If the phenotype of interest in gene expression depends on bacterial infection, such as expression of ecotype Col-specific inducible genes at 6 hours after
30 infection of Pst/avrRpt2, expression of the corresponding phenotypic marker genes

(e.g., genes that show good difference in induction between Col and Ler) can be measured at an appropriate time after bacterial infection.

Differences in gene expression patterns between two virulent strain backgrounds (Pst and Psm) are relatively small. Gene expression patterns for

- 5 Pst/avrRpt2 and Pst/avrB were quite similar at 3 hours, but the difference increased at 6 hours. Psp (no avr) shows similar expression pattern to incompatible bacteria although the amplitude of fold difference was smaller in general. This suggests that Psp, which does not induce the HR in the plant, is still recognized by the plant and induce major part of the defense response seen during the incompatible interaction.
- 10 It also suggests that plants monitor the effect of the defense response and that if it seems effective (bacteria do not grow like Psp), the plant does not go for a full-blown defense response.

Preferred Genes

- 15 Preferred early inducible genes were selected as induced > 2.5 fold (except for 2 fold for Psp at 6 hours) in all of the following datasets: Pst/avrRpt2 at 3 hours in Col, Ws, and Ler; Pst/avrRpt2 at 3 hours, Psm/avrRpt2 at 3 hours, Psp at 6 hours, and Pst/avrB at 3 hours, relative to the water control, as well as estradiol-inducible (avrRpm1 at 0, 45, and 120 minutes and avrRpt2 at 0, 45, and 120 minutes, where the fold change was relative to the appropriate resistance gene mutant carrying the
- 20 same transgenes. Among these genes, the genes were ranked according to genes that are not induced by SA or BTH and not induced in late time points with Psm.

- Regulatory genes were given higher rankings (see Table 11). Hence, the expression of genes comprising SEQ ID NOs:17, 70, 76, 81, 84, 109, 123, 144, 160, 230, 265, 268, 269, 271, 323, 333, 385, 427, 428, 430, 457, 505, 569, 597, 602, 606, 616, 708,
- 25 730, 741, 812, 862, and 942 is induced early after infection of different *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121 (at 3 or 6 hours) or is estradiol inducible (at 45 or 120 minutes).

- Preferred early repressible genes were selected as repressed > 2.5 fold
- 30 (except for > 2 fold for Psp at 6 hours) in all of the following datasets: Pst/avrRpt2 at 3 hours, Psm/avrRpt2 at 3 hours, Psp at 6 hours, and Pst/avrB at 3 hours) and

Pst/avrRpt2 at 3 hours in Col (the fold change was relative to the appropriate water controls). Among them, the genes were ranked in order of expression (highest to lower levels of expression) (see Table 12). Thus, the expression for genes comprising SEQ ID NOs:30, 73, 282, 541, 640, 679, 761, 870, 917, and 930 is repressed early after infection of *Arabidopsis* with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121.

Other genes are induced/repressed during incompatible interactions at 3 and/or 6 hours after inoculation of bacteria. Preferred genes in this group were selected as induced/repressed > 2.5 fold in the incompatible interaction compared to water inoculated control and 2 > fold compared to the corresponding compatible interaction at 3 and/or 6 hours after inoculation with Pst/avrRpt2 and Pst/avrB, and Psm/avrRpt2 and Pst/avrRpt2, in all four ecotypes (see Tables 13a and 13b). Hence, the expression of genes comprising SEQ ID NOs:21, 44, 46, 60, 86, 91, 93, 106, 110, 119, 122, 130, 131, 161, 166, 167, 168, 171, 176, 200, 203, 213, 225, 227, 248, 261, 262, 266, 274, 285, 300, 301, 302, 320, 326, 341, 345, 348, 349, 360, 366, 378, 615, 618, 406, 409, 422, 425, 441, 443, 446, 449, 454, 461, 475, 476, 485, 500, 511, 512, 527, 533, 543, 545, 549, 550, 552, 567, 575, 590, 608, 611, 625, 643, 656, 659, 666, 668, 671, 680, 690, 704, 706, 711, 721, 728, 738, 757, 791, 807, 811, 813, 827, 857, 864, 868, 875, 881, 893, 901, 905, 908, 912, 939, 941, 951, and 952 is induced in an incompatible interaction at 3 and/or 6 hours after infection of four *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121, while the expression of genes comprising SEQ ID NOs:7, 33, 82, 136, 141, 154, 185, 189, 199, 202, 434, 471, 483, 499, 516, 530, 578, 586, 631, 658, 694, 714, 718, 734, 770, 772, 816, and 916 is decreased in an incompatible interaction at 3 and/or 6 hours after infection of four *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121.

Garlic T-DNA insertion lines corresponding to these genes are searched by BLAST. Global expression profiling after infection with one of two different pathogens (*P. syringae* and *Alternaria brassicicola*) may be employed as a

phenotyping method. Transgenic plants for overexpression, underexpression, and conditional overexpression of selected genes are also prepared.

Example 4

5 Promoters of Genes Responsive to Pathogen Infection

In many cases the major outcomes of plant-pathogen interactions are largely determined by how plants react in an early stage. Therefore, it is useful to isolate promoters that rapidly react to pathogen attack for use in expressing proteins that provide tolerance or resistance to pathogen attack.

10 Genes were selected according to the conditions described below based on the results of a GeneChip™ analysis. These genes were particularly selected for a high level of induction in the *avrRpt2-RPS2* interaction and for a very low mRNA level in the absence of pathogen attack among four *Arabidopsis* ecotypes tested (Col, Ws, Ler, and Cvi). The genes were also analyzed to determine if their
15 expression was similar in other combinations of incompatible interactions (three different bacterial strain backgrounds: *P. syringae* pv. tomato DC3000, *P. syringae* pv. *maculicola* ES4326, and *P. syringae* pv. *phaseolicola* NP3121; three different avirulence genes: *avrRpt2*, *avrB*, and *avrRpm1*; and direct expression of avirulence genes in plants using an estradiol-inducible system). For each gene, the 1.2-kb
20 sequence upstream of the initiation codon is provided in SEQ ID NOs: 1047-1095.

Preferred Highly Inducible Promoters

Promoters were selected that had low basal expression level (i.e., uninduced level) in all the ecotypes (Col, Ler, Ws, and Cvi) and high inducibility in Col. Five such promoters of genes represented by the probe sets in Table 14 were identified:
25 the promoters of germin precursor-like oxalate oxidase gene, extra-large G protein gene, PR-1, EREBP5 gene, and a C2H2-type zinc finger protein gene were chosen. The promoters for the germin-precursor like oxalate oxidase gene and PR-1 gene are relatively slow response promoters (no induction 3 hours after infection), but have high induction by 6 hours. The extralarge G protein gene is an intermediate in terms
30 of response time, but maintains high expression over time. The other two are useful as early transient response promoters (good induction by 3 hours, but shut down by

6 hours) in the incompatible interaction (wild type plant infected with Pst/avrRpt2). Promoter sequences comprising SEQ ID NOs:1046-1095 and 1047-1055 correspond to genes comprising one of SEQ ID Nos: 17, 21, 80, 81, 109, 156, 174, 176, 221, 227, 296, 302, 303, 306, 333, 340, 360, 500, 505, 524, 575, 601, 602, 614, 628, 687, 733, 782, 811, 835, 862, 900, 905, 912, and 109, 306, 524, 600, 875, 912, 913, 941 and 942, respectively. Promoter-LUC reporter fusions are prepared and tested in a transient expression system using biolistic co-bombardment of avrRpt2 gene.

Promoters Responsive to Particular Pathogens

Proteins that are useful for protecting plants from pathogen attack may have deleterious effects on plant growth if expressed constitutively. Consequently, it is desirable to have promoter sequences that control gene expression in such a way that expression is absent or very low in the absence of pathogens, and high in the presence of pathogens.

Wild-type *Arabidopsis* plants (ecotype Columbia) were either mock-infected or infected with the bacterial pathogen *Pseudomonas syringae* pv. *maculiola* strain ES4326 (2×10^4 cfu per square centimeter of leaf). After 30 hours, samples were collected, and RNA was purified. This procedure was repeated three times independently, and the RNAs from corresponding samples were pooled, in order to reduce the impact of variation due to uncontrolled variables. The two pools of RNA representing mock-infected and infected plants were then used for gene expression profiling using an *Arabidopsis* GeneChip®. This entire procedure was repeated three times, yielding three sets of GeneChip® data representing a total of nine independent experiments.

To identify promoter sequences that are likely to be useful for driving expression of transgenes in plants in response to pathogen attack, genes were selected whose expression level was less than 40 in all of the mock-infected samples and whose expression level was greater than 400 in all of the infected samples. The value of 40 was chosen arbitrarily as a low expression level and the value of 400 was chosen arbitrarily as a reasonably high expression level. Thirty-seven genes met these criteria and promoter sequences could be identified for 36 of them. Table 15 indicates the identifying probe set number for these 36 genes, the corresponding

Arabidopsis gene, the mean expression level of each gene in mock-infected plants, the mean expression level of each gene in infected plants, and the fold induction in expression of each gene after infection. For 11 genes, expression in mock-infected plants was undetectable, so it was not possible to calculate fold induction.

5 Therefore, the expression of genes comprising SEQ ID NOs:104-106, 119, 123, 129, 131, 151-152, 183, 191, 198, 200, 227, 249, 274, 302, 358, 415, 481, 547, 566, 582, 628, 633, 639, 656, 673, 793, 818, 827, 864, 874, 880, and 904-905 is induced in *Pseudomonas syringae* pv. *maculiola*-infected *Arabidopsis*.

10 It is possible that promoters that strongly activate gene expression in response to infection by a bacterial pathogen might be different from promoters that strongly activate gene expression in response to infection by a fungal pathogen. To test this possibility, a second GeneChip® experiment was conducted, in which wild-type *Arabidopsis* plants (ecotype Columbia) were mock-infected or infected with the fungus *Botrytis cinerea*. Samples were collected at 0, 12, 36, 60, and 84 hours after
15 infection, RNA was purified and used for expression profiling using an *Arabidopsis* GeneChip®. To identify useful promoters, genes were selected whose expression level was less than 40 in mock-infected samples from all time points and whose expression level was greater than 400 in infected plants at 84 hours after infection. Twenty-three genes met these criteria, and promoter sequences could be identified
20 for 21 of them. These genes are described in Table 16, with their identifying probe set number, the corresponding *Arabidopsis* gene, the mean expression level of each gene in mock-infected plants, and the expression level of each gene in infected plants at various times after infection. Among these 23 genes, 11 genes were previously identified in the search for genes whose expression was strongly induced
25 by *Pseudomonas syringae* infection. These 11 genes correspond to identifying codes 12989, 13015, 13100, 13215, 13565, 14609, 16649, 16914, 19284, 19991, and 20356. Hence, the expression of genes comprising SEQ ID NOs:18, 71, 119, 123, 129, 151, 191, 244, 245, 302, 545, 547, 562, 566, 637, 653, 747, 756, 774, 793, 842, 864, and 905 is induced in *Botrytis cinerea*-infected *Arabidopsis*.

30 The promoter sequences for the 25 genes that were only identified in the *P. syringae* data set are shown in SEQ ID NOs:1001-1025. The promoter sequences

for the 10 genes that were only identified in the *B. cinerea* data set are listed in SEQ ID NOs:1026-1035) The promoter sequences of the 11 genes that were identified in both data sets are listed in SEQ ID NOs:1036-1046. The 11 promoter sequences that were identified in both data sets are most likely to be useful for driving
5 expression of transgenes in response to attacks by various pathogens, as these promoters are activated in response to attack by either *Pseudomonas syringae* or *Botrytis cinerea*, two very different pathogens. The other promoters may also be useful for driving expression of transgenes that are efficiently expressed in response to infection by certain types of pathogens.

10 Further, orthologs of the *Arabidopsis* promoters are also useful to drive expression of transgenes. To identify the orthologous promoter, a BLAST search for orthologous genes was conducted. To identify the ortholog, the alignments from the BLAST search are used to determine the range of nucleotides showing
15 homology to the *Arabidopsis* gene. The coding sequences shown at the beginning of each search result that contain regions corresponding to the nucleotides showing homology are likely orthologous genes. Orthologous promoter sequences may be isolated by any method known to the art, e.g., cloning of genomic DNA 5' to the ATG in orthologous genes identified in a computer assisted database search or hybridization of a probe comprising any one of SEQ ID NOs:1001-1046 to genomic
20 plant DNA.

Example 6

Genes the Expression of Which Are Altered by Viral Infection

To identify host genes that are commonly up or down regulated during local
25 RNA or DNA virus infection, gene expression profiling was employed. The host genes may include host factors that are induced by viral infection, e.g., activated host defense genes, suppressed by viral infection, e.g., suppressed host defense genes, genes involved in symptom development, as well as genes regulated by virus inducible promoters. Once the genes are identified, the function of each is then
30 determined. Reverse genetics is then employed to examine the effect of mutations on these genes during virus infection.

Experimental Procedure

Arabidopsis thaliana (Columbia-0 (Col-0)) were grown in a Conviron growth chamber to 4 weeks of age. The growth conditions were 22°C, 12 hour day length and 75% relative humidity. At least four rosette leaves of twenty plants were inoculated with one of five viruses or a mock control (120 plants total). The viruses were turnip vein clearing virus (TVCV), a tobamovirus, an oil seed rape mosaic virus (ORMV), a tobamovirus, tobacco rattle tobravirus (TRV), a tobravirus, cucumber mosaic virus strain Y (CMV-Y), a cucumovirus, and turnip mosaic virus (TuMV), a potyvirus. Each virus was diluted to approximately 0.5 to 1.0 µg/ml in 10 mM potassium phosphate buffer pH 7.2 (or 20 mM Tris-HCl pH 8.0 for the TuMV). The phosphate buffer was used as the mock infection control for the experiments. Inoculated Col-0 leaves were first dusted with carborundum then 10 µl of virus solution or phosphate buffer were pipetted onto the leaf surface. The virus solution or phosphate buffer alone were then rubbed into the leaf surface using a gloved finger, and the leaf surfaces were washed with distilled water at about 10 minutes post inoculation.

Inoculated leaf tissue was removed from each plant at 1, 2, 4 and 5 days post inoculation (dpi), weighed, snap frozen in liquid nitrogen and stored at -80°C. Total RNA was extracted from leaf tissue by the *RNAwiz* method (Ambion, Inc.) and further purified using the *RNeasy* method (Qiagen, Inc.). RNA was diluted to 1 µg/ml and labeled as a probe for Affymetrix GeneChip hybridization according to Affymetrix protocol for synthesizing labeled copy RNA (cRNA) (see Example 1). Labeled cRNA for each virus or mock treatment was hybridized to an Affymetrix GeneChip containing sequences corresponding to 8775 *Arabidopsis* genes. The hybridization data was then analyzed using Affymetrix GeneChip software.

Arabidopsis genes that were induced by at least 2-fold in all virus treatments were identified by importing the data into Microsoft Excel and then subjecting the data to selection criteria. Within each time point, the expression level of a gene exceeded 25 and the fold change was greater than 2 by comparison with the mock-infected treatment. Thus, for genes that were induced by all five viruses, the expression level exceeded 25 and the fold change was greater than 2 for all five

viruses. For genes that were repressed by at least 2-fold, the expression level of the gene must exceed 25 in the mock-infected treatment and the fold change must be less than 2 in all of the five virus treatments.

Results

5 A gene chip from Affymetrix having oligonucleotides corresponding to approximately 8,100 *Arabidopsis* genes was used with labeled cRNA obtained from plant cells infected with a selected viruses at different days post-infection (dpi). For example, for *Arabidopsis*, the RNA may be obtained from *Arabidopsis* infected with potyvirus, tobamovirus, tobnavirus, cucumovirus or geminivirus. After
10 hybridization, laser scanning is employed to detect expression levels and the data obtained is then analyzed. For genes that are induced in response to viral infection, genes that are expressed at levels greater than, for example, 2 fold over control, are selected. Alternatively, for genes that are suppressed in response to viral infection, genes that are expressed at levels lower than control are selected. The advantages of
15 a gene chip in such an analysis include a global gene expression analysis, quantitative results, a highly reproducible system, and a higher sensitivity than Northern blot analyses. Moreover, a gene chip with *Arabidopsis* DNA has a further advantage in that the *Arabidopsis* genome is well characterized.

Data obtained from probe sets which correspond to genes upregulated or
20 downregulated in response to infection by all 5 viruses revealed forty-six genes that were downregulated and 126 that were upregulated in response to viral infection (Tables 17 and 18). Once the induced and/or suppressed genes are identified, the functions of the genes are then characterized by standard methodology.

Therefore, the expression of genes comprising SEQ ID NOs:14, 48, 53, 98,
25 217, 226, 295, 327, 343, 352, 369, 404, 407, 418, 453, 458, 465, 472, 480, 488, 495, 507, 509, 513, 514, 559, 561, 581, 604, 607, 613, 641, 652, 672, 720, 735, 739, 743, 745, 754, 773, 803, 832, 849, 948, and 949 is downregulated after viral infection, and the expression of genes comprising SEQ ID NOs:3, 51, 54, 60, 61, 66, 75, 76, 78, 88, 95, 96, 101, 106, 108, 123, 126, 128, 129, 131, 137, 145-147, 150, 158, 169,
30 170, 172, 173, 197, 200, 216, 219, 224, 230, 233, 237, 249, 250, 263, 274, 275, 276, 299, 307, 323, 333, 342, 346, 359, 382, 383, 387, 391, 393, 401, 411, 415, 427, 442,

455, 459, 466, 477, 481, 485, 487, 502, 511, 515, 525, 534, 539, 542, 560, 571, 577, 579, 584, 587, 595, 600, 627, 638, 645, 654, 659, 668, 681, 688, 695, 696, 706, 708, 730, 742, 753, 775, 785, 786, 792, 797, 800, 801, 809, 817, 819, 820, 823, 827, 847, 856, 875, 885, 896, 902, 910, 921, 922, 923, 925, 926, 928, 946, and 952 is

5 upregulated after viral infection.

The orthologs of these *Arabidopsis* sequences to other plant genes was determined. .

A summary of the probe sets corresponding to genes, the expression of which is altered after infection of *Arabidopsis* with a pathogen is shown in Table 19.

10

Example 7

Identification of Gene Products that are Modulated upon Infection of a *Chenopodium* Cell with a Virus

Of the many disease resistance mechanisms that can be studied, the HR
15 (hypersensitive resistance) system of *Chenopodium* spp. is attractive because of the broad-spectrum virus resistance it confers. This is shown by the ability of members of the bromo-, como-, cucumo-, ilar-, alfamo-, nepo-, sobemo-, tombus-, tymo-, carla-, clostero-, hordei-, potex-, poty-, tobra- and tobamovirus groups to elicit local lesion HR on *Chenopodium* spp. (CMI/AAB Description of Plant Viruses, 1984;
20 Cooper et al., (1995)). In many instances, the HR completely blocks viral spread. However, certain viruses can break through the hypersensitive response and move from one species of *Chenopodium* to another. The ability of some viruses to infect more than one species of *Chenopodium* provides an opportunity to isolate genes that provide a cell with resistance to viral infection.

25 The genetic mechanisms of *Chenopodium* spp. HR involve a number of factors. These factors can be studied to further understand the hypersensitive response and the mechanism through which the response acts. There are some similarities between the products of *Chenopodium* spp. genes and gene products involved in common defense signaling pathways in other plants. These similarities
30 allow comparisons to be made between *Chenopodium* and these other plants. One

example includes genes that are induced upon viral infection during HR in *C. foetidum* (Visedo et al., (1990).

Additionally, some circumstantial experimental evidence suggests that *Chenopodium* HR may be somewhat similar to tobacco *N* gene HR (Whitham et al., 1994). Movement defective tobacco mosaic tobamovirus (TMV) replicates within an inoculated cell of a tobacco plant with an *N* gene, but fails to move from cell to cell (Cooper et al., 1996). Hypersensitivity is not induced, thus replication alone is not sufficient to induce HR despite the *N* gene elicitor being mapped to the replicase gene of TMV (Padgett and Beachy, 1993). Therefore, the process of virus movement may trigger hypersensitivity, which implicates intercellular signaling in this type of HR. Support for this position comes from experiments in which cell-to-cell contacts were disrupted in *N* gene tobacco which resulted in the prevention of necrotic lesion formation in infected leaves (Gulyas and Farkas, 1978). Likewise, TMV will not induce HR cell death in NN tobacco protoplasts where plasmodesmata are not intact (Otsuki et al., 1972), although HR does occur in callus cultures where plasmodesmata are intact (Beachy and Murakishi, 1971). By comparison in *C. quinoa*, movement defective brome mosaic bromovirus (BMV) replicates but fails to move from cell to cell. Initial infection is not sufficient to induce HR since local lesions do not form (Schmitz and Rao, 1996). Similarly, in *C. amaranticolor*, cucumber mosaic cucumovirus (CMV) lacking a movement protein replicates within inoculated cells, fails to move and does not elicit cell death (Canto and Palukaitis, 1999). Therefore, like TMV on *N* gene tobacco, the process of viral spread of BMV and CMV in *C. quinoa* and *C. amaranticolor* may induce HR.

Methods and Materials

Inoculation of Plants

Leaves of 10-week old *C. amaranticolor* or *C. quinoa* were inoculated with *in vitro* transcripts of TMV-MGfus (Heinlein et al., 1995), TMV virions, tobacco rattle tobavirus (TRV), or they were mock-inoculated. TMV-MGfus encodes GFP (green fluorescent protein) fused to the viral movement protein. Infectious spread can be monitored through the detection of GFP. Using an Olympus

stereomicroscope fitted with a U-ULH Olympus lamp, infected *C. amaranticolor* tissue accumulating GFP was excised at 4, 7 and 11 days after inoculation (dai). Leaves inoculated with TRV or TMV were collected at 4 dai, at which point local lesions were forming. Mock-inoculated tissue was collected at the same time.

- 5 Tissue was frozen in liquid nitrogen and total RNA was purified from it. Three separate sets of plants were inoculated with TMV-MGfus and yielded three independent preparations of RNA.

cDNA-AFLP (complementary DNA-amplified fragment length polymorphism)

- 10 Poly-A+ RNA was isolated from TMV-MGfus infected *C. amaranticolor* using Qiagen's Oligotex mRNA purification system (Qiagen, Valencia, CA) and cDNA was generated using cDNA synthesis reagents from Life Technologies (Rockville, MD). cDNA was used to generate AFLP fragments with the AFLP reagents from Life Technologies and reactions were performed according to the manufacturer's instructions. cDNA made from one microgram of poly-A+ RNA
- 15 was digested with EcoRI and MseI and the supplied compatible linkers were ligated to the ends of the digested molecules. A few modifications were introduced. EcoRI-NN primers (GACTGCGTACCAATTCNN; SEQ ID NO:2134), rather than EcoRI-NNN, were used with the 5' fluorescent label NED (Applied Biosystems, Foster City, CA) and MseI-N and MseI-NN [GATGAGTCCTGAGTAAN(N); SEQ
- 20 ID NO:2135), rather than MseI-NNN, primers were used (Genosys, The Woodlands, TX), to reduce the complexity of the primer sets evaluated. All possible primer combinations (256 + 64) were used for PCR amplification and products were separated on polyacrylamide gels and visualized using a Genomyx SC fluorescent scanner (Beckman Coulter, Fullerton, CA). Gene fragments that appeared to be
- 25 upregulated in infected tissues compared to mock-inoculated tissues were tested to see if they were also upregulated by the same primers from a second preparation of cDNA from RNA from a second set of infected plants. Gene fragments that were upregulated in both RNA preparations were excised from the gel, eluted from the gel in water and reamplified by PCR using the appropriate MseI and EcoRI primers
- 30 and sequenced with 377 ABI sequencers (Applied Biosystems) using dideoxysequencing methods.

Quantitative RT-PCR

DNase treated total RNA (2 ng per reaction) from the third independent preparation of TMV-MGfus infected *C. amaranticolor*, the first preparation of TRV infected *C. amaranticolor*, or the first preparation of TMV *C. quinoa*, was used with

5 TaqMan One-Step RT-PCR reagents for quantitative analysis in an ABI 7700 (Applied Biosystems). Reactions were performed according to the manufacturer's instructions. Primers and 6-FAM 5' end-labeled probes (6-carboxyfluorescein, Applied Biosystems or Genosys) were designed from the sequences from the *C. amaranticolor* upregulated gene fragments using Primer Express software (Applied

10 Biosystems) and are listed in SEQ ID Nos:954-1000 and 2130-2135. Expression levels were interpolated from standard curves with a correlation coefficient of 0.99 or greater and the quantities were normalized to the expression level of actin in each sample.

Results

15 The interaction of the elicitor and the R gene product establishes a cascade of reactions and signaling events that is then manifested in a phenotypic HR. In essence, HR is the end result of disease activated signaling events. In order to detect the early expression of genes induced by viral infection, it was necessary to isolate infected tissue before the onset of local lesion formation. Therefore, *C.*

20 *amaranticolor* was infected with RNA transcripts of TMV-MGfus that express GFP (green fluorescent protein) in infected cells. This allowed the spread of viral infection to be monitored over time. Infection foci comprising over 100 cells could be detected at 4 dai and foci of more than 500 cells could be detected at 7 dai. There was no visible appearances of cell death or chlorotic local lesion formation at the

25 infection foci at 4 and 7 dai. By 11 dai, the infection foci were associated with chlorotic local lesions. Virus infected tissue was excised from leaves at each time point and RNA was purified from the tissue and used for cDNA-AFLP as previously described.

cDNA-AFLP fragments were separated on polyacrylamide sequencing gels

30 and imaged with a fluorescent scanner. Samples derived from mock-inoculated tissue at 7 dai were run next to samples derived from TMV-MGfus infected tissue at

7 dai for comparison. Ninety-eight bands having intensity in the TMV-MGfus lanes that was greater than that of analogous bands in the mock lanes were easily detected. Thirty out of the 98 bands were also upregulated in an independent set of experiments designed to reduce biological variation between experiments. These
5 bands were excised from the gel, reamplified, and sequenced.

The hypothetical protein sequences derived from the reamplified fragments (Seq ID NOs: 1954-1966) translated from all six reading frames were compared to sequences in the GenBank protein sequence database. The results of the BLASTX search (Altschul et al., 1997) are summarized in Table 20a. To confirm that the
10 expression levels of DESCA genes were upregulated in infected tissue compared to mock inoculated tissue, the relative amount of DESCA and actin transcript in a third independent set of samples at 4 dai, 7dai, and 11 dai was quantitatively measured (Table 20b).

The expression level of DESCA1 increased the most in the TMV-MGfus
15 infected plants. The expression level of DESCA1 increased 200 times by 4 dai but tapered off drastically by 11 dai. DESCA1 is unrelated to any protein known at this time.

Two sequences, DESCA4 and DESCA10, are both related to pumps found in *Arabidopsis* and yeast (Sanchez-Fernandez et al., 1998; Smart and Fleming, 1996).
20 DESCA4 is expressed highly at 4 dai but the expression drops off over time whereas DESCA10 is only moderately induced and its expression returns to normal by the time of the visible appearance of local lesions in *C. amaranticolor*.

DESCA7 is similar to a salicylate-induced glucosyltransferase gene in tobacco (Horvath and Chua, 1996). DESCA9 is similar to cytochrome P450-like
25 proteins which can produce cytotoxic compounds including phytoalexins that are deployed by a plant to defend against invading microbes. DESCA12 is related to a proanthranilate benzoyltransferase from carnation that plays a direct role in the phytoalexin biosynthesis in carnation (Yang et al., 1998). DESCA11 is similar to the tryptophan biosynthetic enzyme phosphoribosylanthranilate transferase whose
30 gene expression is induced in the presence of ozone in *Arabidopsis* (Conklin and Last, 1995).

DESCA3 is similar to endo-1,4-beta-glucanases that have a role in fruit ripening, abscission, and cell elongation (Lashbrook et al., 1994). DESCA3 is highly expressed in the infected *C. amaranticolor* and remains highly expressed during the appearance of local lesions and necrosis.

Many disease responses are mediated by positive regulators such as transcription factors or kinases that initiate signaling cascades for the activation of defense responses. One gene, DESCA5, is loosely similar to a yeast potential transcriptional regulator. DESCA5 expression is twice as high at the early stages of infection compared to the late stages of infection illustrating an important role played by gene regulation at the early stages of infection. DESCA6 is related to kinases of *Arabidopsis*. Kinases have essential roles in programmed cell death during viral infection (Dunigan and Madlener, 1995). DESCA2 is the most highly expressed of the group suggesting that it is an important regulator at the onset of infection. It is similar to a receptor-like protein kinase in bean that responds to *Fusarium solani* attack (Lange et al., 1999).

Some R genes have kinase-like regions that may function in initiating a signal cascade during the onset of HR (Song et al., 1995, Zhou et al., 1997). Global amino acid sequence alignment (Henikoff and Henikoff, 1992) of DESCA2 with Pto or Xa21, R genes with ser/thr kinase domains, reveals a 37% similarity. DESCA8 has a nucleotide binding site and a leucine-rich repeat that is common for many R genes. (Meyers et al., 1999; Leister et al., 1998).

To link DESCA genes to a multivirus resistance pathway, *C. amaranticolor* was inoculated with TRV (tobacco rattle virus), a virus that is taxonomically distinct from TMV. Local lesions appeared by 4 dai and RNA was purified from the infected leaves. DESCA gene expression levels in infected tissue were compared to mock inoculated tissue by quantitative RT-PCR and revealed that the same DESCA genes upregulated during a TMV infection are also upregulated during a TRV infection (Table 20b).

The gene expression levels in TMV infected *C. quinoa* were measured using the same *C. amaranticolor*-derived primers in quantitative PCR to determine if DESCA genes were up-regulated during HR in another *Chenopodium* species. Most

of the DESCA genes were upregulated in *C. quinoa* and were expressed at levels many times higher than in *C. amaranticolor* (Table 20b). This may be a result of the infection of *C. quinoa* with the aggressive wild-type virus rather than slower moving TMV-MGfus.

5 The experimental procedure presented here can detect any similar gene involved in the aforementioned signaling pathways such as SA signaling. Except for DESCA1, whose expression is increased the most at 200+ fold, many of the fragments have homology to other genes that have been placed in disease resistance pathways in other plants. DESCA12 and DESCA9 are respectively similar to
10 hypersensitivity related gene 201, possibly a proanthranilate benzoyltransferase, and p450 monooxygenases, both which are expressed during the hypersensitive response in tobacco upon infection with *Pseudomonas solanacearum* but are not regulated by SA (Czernic et al., 1996). DESCA7 is similar to a salicylate-induced glucosyltransferase gene in tobacco (Horvath and Chua, 1996). Thus, the disease
15 resistance response in *C. amaranticolor* involves pathways both dependent and independent of SA signaling.

 The surprising discovery of DESCA4, DESCA7, DESCA9, DESCA10, and DESCA12, reveal the underpinnings of an endogenous detoxification system. Briefly, the activation phase involves cytochrome P450 monooxygenases
20 introducing functional groups (e.g. aromatic rings) to potential toxins. The conjugation phase in plants involves the linking of glutathione or glucose to the toxin at which point the conjugated molecule can be recognized by an ATP-binding cassette transporter and pumped into the vacuole, or possibly the neighboring cells, during the elimination phase. The final phase includes either storage or breakdown
25 of such molecules. DESCA9, similar to cytochrome P450, and DESCA12, similar to a gene associated with the production of phytoalexin, may produce potential toxins. In fact, *C. amaranticolor* produces many such compounds that are antiviral to TMV. DESCA7, similar to a glucosyltransferase, may conjugate such toxins to be transported by the ABC-transporters encoded by DESCA4 or DESCA10. In this
30 particular case, the transported compound could then be deployed by the infected plant cell as an antiviral agent or cytotoxic compound, stored by noninfected cells in

anticipation of infection, or eliminated by noninfected cells neighboring infected cells. Since all of these genes are induced by TMV and TRV in *C. amaranticolor*, their induced expressions are a result of a specific or general multivirus or disease resistance pathway.

5 Possessing the R genes that allow *C. amaranticolor* to initially recognize multiple viruses provides an opportunity to use these genes, and the regulatory elements associated with these genes, to transfer viral resistance to other plants. In addition, possession of genes that produce and transport antiviral and cytotoxic products allows for the transfer of viral resistance through a mechanism involving
10 induced cell death upon viral infection.

Two genes that may be used for early recognition of viral infection are DESCA8 and DESCA2, as these genes may act as signaling components to initiate the resistance cascade. DESCA8 has a nucleotide binding site and a leucine-rich repeat that is common for many R genes and that can be found in other plants
15 (Meyers et al., 1999; Leister et al., 1998). DESCA2 is induced in both *Chenopodium* species and is similar to other R genes, Xa21 and Pto, which have similar ser/thr kinase domains.

Resistance to viral spread may be transferred between *Chenopodium* spp. For example, BMV (brome mosaic virus) induces local lesions in the green variety of *C.*
20 *hybridum*, however lesion formation does not limit the systemic spread of the virus (Verduin, 1978). The systematic spread of the BMV virus may be restricted in the green variety of *C. hybridum* by transformation with a gene from the purple variety that does limit spread (Komari, 1990). Thus, genes that confer viral resistance may be used for complementation, reverse genetics, overexpression, and gene silencing.
25 Furthermore, as indicated by the functionality of the R genes N and Pto after being transferred into heterologous species, (Whitham et al., 1996; Rommens et al., 1995), the *Chenopodium* genes may function to initiate hypersensitivity in crops, *Arabidopsis* or other useful plants.

Example 8

Other Plant-Pathogen Interactions

The methods set out hereinabove can be used for any type of comparable resistance interaction. For example any of the following plant/pathogen interactions will be produced as compatible and incompatible interactions. The RNA from such an interaction is isolated and subject to a protocol such as one outlined in Example 1, e.g., using a Genechip with a specific plant's genes or microarray, differential display PCR or cDNA-ALFP (Example 7). A four-way analysis is performed and genes which are expressed differently are identified. The plant/pathogen interactions in Table 21 are well known in the art. However, any type of plant/pathogen interaction that involves this type of resistance can be used.

Table 21

Plant	Pathogen
Tomato	Cladosporium fulvum
Maize	Rust fungus
Antirrhinium	Rust fungus
Flax	<i>Melampsora lini</i>
Lettuce	Downy mildew
Arabidopsis	<i>Peronospora parasitica</i>
Tomato	Nematode
Corn	Cochliobolus carbonum
Tomato	Pseudomonas syringae
Rice	Xanthomonas oryzae pv. Oryzae
Rice	Pyricularia oryzae
Tobacco	Tobacco Mosaic Virus

15

Genes that are upregulated and cause resistance in a wide variety of plants are particularly useful in methods which upregulate or overexpress the gene. One method is to add an exogenous copy, thus providing more of the gene product or allowing for a different induction from that used by the plant. Alternatively, the endogenous gene can be upregulated using a known inducer or using artificial

20

methods such as using an artificial induction signal in the endogenous promoter. Examples of the two methods are provided in Examples 9 and 10.

Accordingly, embodiments of the invention provide the sequences disclosed herein, which sequences can be used in genetic engineering of crops, as probes and markers to study the dynamics of plant/pathogen interactions, and as markers in marker-assisted breeding protocols to identify plants carrying particularly useful combinations of genes associated with pathogen resistance, as well as in plant defense.

Example 9

Transformation of Resistance Genes into Plants

To produce resistant plants, resistance genes such as those identified herein can be introduced into plant cells to generate transgenic plants having enhanced resistance. While HSF4 is any preferred gene for this embodiment of the invention, the invention can be employed with other genes, alone or in combination, whose regulation is strongly responsive to plant/pathogen interactions, such as the genes identified herein. Since some genes are strongly induced and others are strongly repressed in plant/pathogen interactions, and since some genes that are strongly induced in one ecotype can be strongly repressed in another, the invention contemplates use of any of the genes and sequences, or fragments thereof, disclosed herein, in a construct adapted to cause overexpression, repression, or knock out, of the genes in a transgenic plant.

Transgenic downregulation of genes associated with pathogen resistance can have several useful applications. In one embodiment, transgenic downregulation of genes that are strongly repressed in resistance interactions can enhance resistance. Such transgenic downregulation can employ the genes disclosed herein, or fragments thereof, in an antisense orientation to interfere with accumulation of the products of those genes. Likewise, any other methodology capable of lowering expression of such genes is also included within these embodiments of the invention.

Plant transformation can be carried out by conventional means, and can include *Agrobacterium*-mediated transformation, electroporation, particle acceleration, abrasion, and any other useful means leading to expression of a transgene in a plant of interest. Transformed plant cell are then used to regenerate one or more plants in tissue culture. Subsequent generations of transgenic plants can be used directly or bred with other lines to generate plants having enhanced pathogen resistance.

Example 10

Upregulation of Resistance Genes in Crops

Because many or most *Arabidopsis* genes have orthologs in other plants, the genes and sequences disclosed herein are generally useful in constructs to be up-regulated and cause resistance in a wide variety of plants. As examples, the heat shock proteins, and particularly HSF4, are found throughout the plant kingdom. For many such regulatory and responsive genes it is well known that there exist substances that can induce expression. Chemicals such as dexamethasone have been found to induce mammalian HSF proteins. Likewise, a chemical induction of key plant defense genes can be chemically induced. High throughput screening for chemical inducers of the plant HSF4 or other resistance gene is performed.

Potentially useful substances are then tested on crop plants and eventually used as a soil additive or sprayed onto plants when needed to induce resistance. Accordingly, embodiments of the invention usefully employ the genes disclosed herein, or fragments thereof, for screening to identify useful chemical inducers and/or repressors of gene responsive to pathogenic infections.

Example 11

Identification of Inducers and Repressors of Resistance Genes

The yeast two-hybrid method and many methods which use its basic idea, provide a technique to identify proteins which interact with a protein of interest.

The method relies on the fact that a protein contains domains which can be separated. Thus the protein of interest is fused to the GAL4 DNA binding region of

a known protein. The GAL4 (or another) activation signal is fused in a library to produce a library of fused proteins. If one of the proteins from the library interacts with the protein of interest the protein binds and a signal protein is produced, such as luciferase. There are a number of such systems presently, some of which can be
5 used in mammalian cells, allowing for correct processing and folding of certain proteins and others which allow the interaction to occur in the cytoplasm allowing for the identification of other types of proteins.

cDNA from HSF4 and any other protein of interest is cloned in fusion to the yeast GAL4 DNA binding domain on a vector. A library containing cDNA from
10 Arabidopsis is fused to the GAL4 or an activation domain of choice. Expression of luciferase correlates with identification of an interacting protein. This protein is then analyzed as to its action as an inducer or repressor.

10232301.062301

Example 12

Determination of the Minimal Promoter Fragment

The full-length promoter sequence as given in SEQ ID Nos: 1001-1095,
5 2137-2661 and 4738-6813, or the promoter orthologs thereof is fused to the β -
glucuronidase (GUS) gene at the native ATG to obtain a chimeric gene cloned into
plasmid DNA. The plasmid DNA is then digested with restriction enzymes to
release a fragment comprising the full-length promoter sequence and the GUS gene,
which is then used to construct the binary vector. This binary vector is transformed
10 into *Agrobacterium tumefaciens*, which is in turn used to transform *Arabidopsis*
plants (for further details of the binary vector construction see above Example 9).

The above plasmid can also be used to form a series of 5' end deletion
mutants having increasingly shorter promoter fragments fused to the GUS gene at
the native ATG. Various restriction enzymes are used to digest the plasmid DNA to
15 obtain the binary vectors with different lengths of promoter fragments. In particular,
a binary vector 1 is constructed with a 1,900-bp long promoter fragment; a binary
vector 2 is constructed with a 1,300-bp long promoter fragment; a binary vector 3 is
constructed with a 1000-bp long promoter fragment; a binary vector 4 is constructed
with a 800-bp long promoter fragment; a binary vector 5 is constructed with a 700-
20 bp long promoter fragment; a binary vector 6 is constructed with a 600-bp long
promoter fragment; a binary vector 6 is constructed with a 500-bp long promoter
fragment; and a binary vector 7 is constructed with a 100-bp long promoter
fragment. Like the binary vector comprising the full-length promoter fragment,
these 5' end deletion mutants are also transformed into *Agrobacterium tumefaciens*
25 and, in turn, *Arabidopsis* plants (for further details of *Arbabidopsis* transformation
and promoter assay procedures see Example 5 above) .

The presence of the correct hybrid construct in the transgenic lines is
confirmed by PCR amplification.

By using the above protocol it can be determined, which portion of the
30 promoter sequences given in SEQ ID Nos: 1001-1095, 2137-2661 and 4738-6813,
or the promoter orthologs thereof is required for gene expression.

Minimal promoter fragments having lengths substantially less than the full-length promoter can therefore be operatively linked to coding sequences to form smaller constructs than can be formed using the full-length promoter. As noted earlier, shorter DNA fragments are often more amenable to manipulation than longer fragments. The chimeric gene constructs thus formed can then be transformed into hosts such as crop plants to enable at-will regulation of coding sequences in the hosts.

Example 13

Determination of Promoter Motifs

While a deletion analysis characterizes regions in a promoter that are required overall for its regulation, linker-scanning mutagenesis allows for the identification of short defined motifs whose mutation alters the promoter activity. Accordingly, a set of linker-scanning mutant promoters fused to the coding sequence of the GUS reporter gene are constructed. Each of them contains a 8-10-bp mutation located between defined positions and included in a promoter fragment as given in SEQ ID Nos: 1001-1095, 2137-2661 and 4738-6813, or the promoter orthologs thereof.

Each construct is transformed into *Arabidopsis* and GUS activity is assayed for 19 to 30 independent transgenic lines. The presence of the correct hybrid construct in transgenic lines is confirmed by PCR amplification of all lines containing the mutant constructs and by random sampling of lines containing the other constructs. Amplified fragments are digested with restriction enzyme (e.g. XbaI) and separated on high resolution agarose gels to distinguish between the different mutant constructs. The effect of each mutation on promoter activity is compared to an equivalent number of transgenic lines containing the unmutated construct. Two repetitions resulting from independent plating of seeds are carried out in every case.

The sequences mutated in the linker-scanning constructs, in particular those that showed marked differences from the control construct, are then examined more closely.

5

Example 14

Identifying Orthologs

Orthologs were identified through use of BLAST and SCAN software with some additional filters. For the Arabidopsis search, a BLAST database was created that was a subset of GenBank ver 123.0 (released April 15, 2001) that contained all of the plant translated regions excluding Arabidopsis thaliana sequences. The subset was created with PERL script. A BLAST search with all of the peptide sequences was performed against the GenBank subset. Each query was executed using the "blastall" command with the parameters " -p blastp", "-v 50", "-b 50", "-F F". The BLAST search results were then processed with SCAN (Sequence Comparison Analysis program, version 1.0k, Los Alamos National Laboratories) using default settings and the orthologs were identified following implementation of an E-value cutoff of $\leq 1e-4$. The candidate orthologs were further filtered by comparing words in the description to the text of the annotation fields: product, function and note. The sequence was considered to have the same or similar function if any of the words matched. Words excluded from the filter included: the, like, protein, related, unknown, subunit, hypothetical, and, putative, precursor, clone, homolog, small, beta, class, dna, rna, alpha, gamma, has, not, been, from, to, by, long, type and induced.

For the rice search, amino acid sequences were used that resulted from FGENESH (version 1.C) gene prediction results. The peptide sequences were obtained from gene predictions and formatted into a BLAST database. A BLASTP comparison was then performed against the Arabidopsis sequences. The BLASTP results were then filtered through use of SCAN with the following parameters: "-a 60 60" with an E-value cutoff of $1e-4$. This produced orthologs having 60 or more identities and where 60% of the alignments were made up of identities.

The following pages compile Tables 3 to 20 referred to in the Examples above.

TABLE 3 TO 20

Table 3 Probe Sets corresponding to genes, the expression of which is increased after infection of wild-type *Arabidopsis* with *Pseudomonas syringae*

ProbeSet	Description	Blast Score	EC #	Family
11997_at (AC005967.4_AT)	gb AAD03372.1 (AC005967) unknown protein [Arabidopsis thaliana]	0		
12002_at (AF069442.47_AT)	gb AAC79112.1 (AF069442) hypothetical protein [Arabidopsis thaliana]	0		
12004_at (AL022023.132_AT)	emb CAA17771.1 (AL022023) putative protein [Arabidopsis thaliana]	8E-86		
12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]	1E-168		
12037_at (AC004005.174_AT)	gb AAC23417.1 (AC004005) unknown protein [Arabidopsis thaliana]	0		
12051_at (AL021889.94_AT)	emb CAA17133.1 (AL021889) putative protein [Arabidopsis thaliana]	1E-143		
12062_at (AC006069.147_AT)	gb AAD12706.1 (AC006069) unknown protein [Arabidopsis thaliana]	0		
12068_at (AF118223.24_AT)	gb AAD03449.1 (AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]	1E-162		
12072_at (AL035396.4_AT)	emb CAA23058.1 (AL035396) putative protein [Arabidopsis thaliana]	1E-158		
12079_s_at (A71597.1_S_AT)	emb CAB42594.1 (A71597) unnamed protein product [Arabidopsis thaliana]	5E-64		
12081_at (AC001645.140_AT)	gb AAB63644.1 (AC001645) unknown protein [Arabidopsis thaliana]	1E-117		

ProbeSet	Description	Blast Score	EC #	Family
12092_at (AC004793.13_AT)	gb AAD21694.1 (AC004793) ESTs gb T20423, gb AA712864, gb H76323 and gb Z25560 come from this gene. [Arabidopsis thaliana]	1E-150		
12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]	1E-87		
12136_at (AC007591.60_AT)	gb AAD39663.1 AC007591_2 8 (AC007591) ESTs gb R65145, gb N96612 and gb R90096 come from this gene. [Arabidopsis thaliana]	1E-60		
12150_at (AC004005.151_AT)	gb AAC23415.1 (AC004005) unknown protein [Arabidopsis thaliana]	5E-32		
12187_at (AC005489.31_AT)	gb AAD32893.1 AC005489_3 1 (AC005489) F14N23.31 [Arabidopsis thaliana]	0		
12198_at (AC006954.90_AT)	gb AAD23890.1 AC006954_1 1 (AC006954) unknown protein [Arabidopsis thaliana]	1E-70		
12203_at (AL021710.268_AT)	emb CAA16738.1 (AL021710) hypothetical protein [Arabidopsis thaliana]	7E-55		
12216_at (AC007119.56_AT)	gb AAD23641.1 AC007119_7 (AC007119) unknown protein [Arabidopsis thaliana]	8E-55		
12217_at (AJ223804.1_AT)	gb AAF34796.1 AF228640_1 (AF228640) lipoamide dehydrogenase precursor [Arabidopsis thaliana]	0		
12227_at (AC007576.18_AT)	gb AAD39285.1 AC007576_8 (AC007576) Unknown protein [Arabidopsis thaliana]	1E-102		
12233_at (AJ001807.1_AT)	emb CAA05023.1 (AJ001807) succinyl-CoA- ligase alpha subunit [Arabidopsis thaliana]	0	EC_6.2.1.5	synthetase
12278_at (AJ011674.2_AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]	0		kinase

ProbeSet	Description	Blast Score	EC #	Family
12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]	0		kinase
12314_at (AC001229.28_AT)	gb AAB60922.1 (AC001229) F5I14.14 [Arabidopsis thaliana]	0		
12317_at (AC004138.27_AT)	gb AAC32907.1 (AC004138) putative sucrose-proton symporter [Arabidopsis thaliana]	0		
12323_at (AC002333.18_AT)	gb AAB64019.1 (AC002333) putative polygalacturonase [Arabidopsis thaliana]	0		Polygalactur onase
12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]	0		
12341_s_at (AL021637.176_S_A T)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]	0		
12347_at (AC007258.28_AT)	gb AAD39325.1 AC007258_1 4 (AC007258) Putative ATPase [Arabidopsis thaliana]	0	EC_3.6.1.-	ATPase
12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]	0		
12369_at (AC002535.59_AT)	gb AAC62871.1 (AC002535) putative Na ⁺ /Ca ²⁺ antiporter [Arabidopsis thaliana]	0		
12400_at (X98453.1_AT)	emb CAA67092.1 (X98453) peroxidase [Arabidopsis thaliana]	0		peroxidase
12438_at (AL021710.83_AT)	emb CAA16723.1 (AL021710) membrane-bound small GTP-binding - like protein [Arabidopsis thaliana]	1E-122		
12449_s_at (AC002343.179_S_A T)	gb AAB63623.1 (AC002343) cellulose synthase isolog [Arabidopsis thaliana]	0		
12454_at (AC006232.164_AT)	gb AAD15602.1 (AC006232) putative ferredoxin [Arabidopsis thaliana]	5E-85		

ProbeSet	Description	Blast Score	EC #	Family
12475_at (Y11794.1_AT)	emb CAA72490.1 (Y11794) peroxidase ATP29a [Arabidopsis thaliana]	3E-67		peroxidase
12487_at (AC004411.126_AT)	gb AAC34225.1 (AC004411) putative ABC transporter [Arabidopsis thaliana]	0		
12497_at (AC006533.51_AT)	gb AAD32284.1 AC006533_8 (AC006533) putative receptor- like protein kinase [Arabidopsis thaliana]	0		
12500_s_at (AF081067.3_S_AT)	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA- amino acid hydrolase [Arabidopsis thaliana]	0		
12521_at (AF049236.28_AT)	gb AAC14413.1 (AF049236) unknown [Arabidopsis thaliana]	0		
12525_at (AC006587.85_AT)	gb AAD21486.1 (AC006587) putative DOF zinc finger protein [Arabidopsis thaliana]	1E-132		
12530_at (Z99707.184_AT)	emb CAB16760.1 (Z99707) hydroxynitrile lyase like protein [Arabidopsis thaliana]	1E-150		LYASE
12535_at (AL035538.156_AT)	emb CAB37540.1 (AL035538) putative protein [Arabidopsis thaliana]	1E-132		
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]	6E-38		methyl- esterase
12571_s_at (AF149413.18_S_AT)	gb AAD40138.1 AF149413_1 9 (AF149413) Arabidopsis thaliana ferrochelatase-I (SW:P42043); Pfam	0		
12574_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]	1E-25		
12584_at (AC004521.233_AT)	gb AAC16096.1 (AC004521) similar to axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana]	0		
12626_at (AC006234.95_AT)	gb AAD20931.1 (AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]	0		kinase

ProbeSet	Description	Blast Score	EC #	Family
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]	0		
12645_at (AL021712.56_AT)	emb CAA16774.1 (AL021712) fibrillin precursor-like protein [Arabidopsis thaliana]	1E-150		
12698_at (AC000106.42_AT)	gb AAB70413.1 (AC000106) Similar to Beta integral membrane protein (gb U43629). EST gb W43122 comes from this gene. [Arabidopsis thaliana]	0		
12712_f_at (Z95774_F_AT)	emb CAB09206.1 (Z95774) R2R3-MYB transcription factor [Arabidopsis thaliana]	6E-21		
12736_f_at (Z97048_F_AT)	emb CAA90748.1 (Z50869) MYB-related protein [Arabidopsis thaliana]	4E-21		
12744_at (AC001645.15_AT)	gb AAB63630.1 (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]	0		
12760_g_at (AC005278.32_G_A T)	gb AAC72120.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb 84105 and gb AI100071 come from this gene. [Arabidopsis thaliana]	0		
12764_f_at (AC004138.69_F_AT)	gb AAC32912.1 (AC004138) putative glutathione S- transferase [Arabidopsis thaliana]	1E-111		

ProbeSet	Description	Blast Score	EC #	Family
12772_at (AC005278.34_AT)	gb AAC72119.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb H37281, gb T44167, gb T21813, gb N38437, gb Z26470, gb R65072, gb N76373, gb F15470, gb Z35182, gb H76373, gb Z34678 a	0		
12776_at (AL021811.156_AT)	emb CAA16969.1 (AL021811) putative protein [Arabidopsis thaliana]	0		
12797_s_at (AC007138.25_S_AT)	gb AAD22647.1 AC007138_1 1 (AC007138) S- adenosylmethionine synthase 2 [Arabidopsis thaliana]	0		
12802_at (AL022373.153_AT)	emb CAA18498.1 (AL022373) DnaJ-like protein [Arabidopsis thaliana]	2E-74		
12851_s_at (ACCSYN1_S_AT)	emb CAA78260.1 (Z12614) 1-aminocyclopropane 1- carboxylate synthase [Arabidopsis thaliana]	3E-29		
12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]	1E-150		
12880_s_at (AIG2_S_AT)	gb AAC49283.1 (U40857) AIG2 [Arabidopsis thaliana]	3E-97		
12883_s_at (APX_S_AT)	emb CAA67425.1 (X98925) stromal ascorbate peroxidase [Arabidopsis thaliana]	1E-161		
12889_s_at (ASA1_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]	0		
12891_at (ATACS6_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]	0		synthase
12892_g_at (ATACS6_G_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
12904_s_at (ATERF1_S_AT)	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]	1E-126		
12905_s_at (ATERF2_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]	1E-112		
12911_s_at (ATG6PDHE5_S_AT)	emb CAA59011.1 (X84229) glucose-6-phosphate 1- dehydrogenase [Arabidopsis thaliana]	0		
12921_s_at (ATHHMGCOAR_S _AT)	emb CAA33139.1 (X15032) hydroxy methylglutaryl CoA reductase (AA 1-592)	0		
12930_s_at (ATLLS1_S_AT)	gb AAC49679.1 (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]	0		
12951_at (AC005489.5_AT)	gb AAD32867.1 AC005489_5 (AC005489) F14N23.5 [Arabidopsis thaliana]	0		
12958_at (AC002332.249_AT)	gb AAB80675.1 (AC002332) putative protein kinase [Arabidopsis thaliana]	0		kinase
12965_at (AL021711.118_AT)	emb CAA16752.1 (AL021711) protein kinase- like protein [Arabidopsis thaliana]	0		kinase
12966_s_at (AL023094.197_S_A T)	emb CAA18838.1 (AL023094) bZIP transcription factor ATB2 [Arabidopsis thaliana]	2E-67		
12989_s_at (AC004077.149_S_A T)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]	0		
13003_s_at (AB021936.1_S_AT)	dbj BAA74591.1 (AB021936) nicotianamine synthase [Arabidopsis thaliana]	0		
13005_at (AC004683.61_AT)	gb AAC28763.1 (AC004683) unknown protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
13014_at (U93215.87_AT)	gb AAB63082.1 (U93215) putative lipase [Arabidopsis thaliana]	0		lipase
13015_s_at (X98673.2_S_AT)	emb CAA67232.1 (X98674) zinc finger protein [Arabidopsis thaliana]	7E-90		
13025_at (AL050400.20_AT)	emb CAB43695.1 (AL050400) putative protein [Arabidopsis thaliana]	0		
13040_at (AC002392.134_AT)	gb AAD12039.1 (AC002392) unknown protein [Arabidopsis thaliana]	0		
13070_at (AC006919.171_AT)	gb AAD24640.1 AC006919_2 0 (AC006919) putative pyruvate kinase [Arabidopsis thaliana]	0		kinase
13094_at (AL035523.163_AT)	emb CAB36745.1 (AL035523) putative protein [Arabidopsis thaliana]	1E-172		
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]	0		mono- oxygenase
13110_at (AF074021.34_AT)	gb AAD29776.1 AF074021_8 (AF074021) putative symbiosis-related protein [Arabidopsis thaliana]	1E-65		
13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592,gb T13956,gb T43 869 come from from this gene. [Arabidopsis thaliana]	0		
13119_at (AC007260.23_AT)	gb AAD30579.1 AC007260_1 0 (AC007260) Similar to dTDP-D-glucose 4,6- dehydratase [Arabidopsis thaliana]	0	EC_4.2.1.46	dehydratase
13128_at (AL049607.47_AT)	emb CAB40756.1 (AL049607) protein phosphatase 2C-like protein [Arabidopsis thaliana]	0		
13134_s_at (AC002337.9_S_AT)	gb AAB63818.1 (AC002337) putative galactinol synthase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
13137_at (AC007169.86_AT)	gb AAD26480.1 AC007169_1 2 (AC007169) putative fructokinase [Arabidopsis thaliana]	0		fructokinase
13152_s_at (AC005322.24_S_AT)	gb AAC97998.1 (AC005322) Identical to 1- aminocyclopropane-1- carboxylate oxidase (ACC oxidase) gb X66719 (EAT1). ESTs gb T43073, gb T5714, gb R90435, gb R44023, gb AA597926, gb AI099676, gb AA650810 and gb 29725 come from this gene. [Arabidopsis thaliana]	1E-177		
13154_s_at (AC002333.210_S_A T)	gb AAB64047.1 (AC002333) putative endochitinase [Arabidopsis thaliana]	1E-148		
13157_at (AC002409.35_AT)	gb AAB86449.1 (AC002409) putative cytochrome P450 [Arabidopsis thaliana]	0		
13163_s_at (AC005560.223_S_A T)	gb AAD12692.2 (AC006069) unknown protein [Arabidopsis thaliana]	0		
13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]	0		
13177_at (AL049640.42_AT)	emb CAB40989.1 (AL049640) growth factor like protein [Arabidopsis thaliana]	1E-164		
13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	2E-63		
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	2E-63		
13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	2E-63		
13190_s_at (ATTHIREDA_S_A T)	emb CAA80655.1 (Z23108) NADPH thioredoxin reductase [Arabidopsis thaliana]	1E-174		

ProbeSet	Description	Blast Score	EC #	Family
13211_s_at (BCHI_S_AT)	dbj BAA82816.1 (AB023454) basic endochitinase [Arabidopsis thaliana]	2E-72		
13212_s_at (BGL2_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3- glucanase 2 (BG2) [Arabidopsis thaliana]	0		
13215_s_at (CAFFEROYLCOA METHYLTRANS_S _AT)	gb AAF16576.1 AC012563_2 9 (AC012563) putative S- adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O- methyltransferase [Arabidopsis thaliana]	1E-121		
13217_s_at (CALMODULINLIK E_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]	6E-99		
13219_s_at (CHI4_S_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]	5E-78		
13243_r_at (ELI32_R_AT)	emb CAB37539.1 (AL035538) cinnamyl-alcohol dehydrogenase ELI3-2 [Arabidopsis]	0		
13244_s_at (ELI32_S_AT)	emb CAB37539.1 (AL035538) cinnamyl-alcohol dehydrogenase ELI3-2 [Arabidopsis]	0		
13246_at (ERECTAL_AT)	gb AAF26067.1 AC012562_2 2 (AC012562) putative protein kinase [Arabidopsis thaliana]	1E-40		kinase
13255_i_at (GAMMAGLUTAM YLTRANSPEPTI_I _AT)	emb CAA89206.1 (Z49240) gamma-glutamyl transpeptidase [Arabidopsis thaliana]	0	EC_2.3.2.2	glutamyl- trans- peptidase
13259_s_at (GLUTATHIONEPE ROXIDASE1_S_AT)	gb AAD24836.1 AC007071_8 (AC007071) putative glutathione peroxidase [Arabidopsis thaliana]	4E-95		
13261_s_at (GLUTATHIONERE DUCTASE1_S_AT)	gb AAB67841.1 (U37697) glutathione reductase [Arabidopsis thaliana]	0		

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	

ProbeSet	Description	Blast Score	EC #	Family
13263_s_at (GST1_RC_S_AT)	emb CAA10060.1 (AJ012571) glutathione transferase [Arabidopsis thaliana]	3E-49		
13266_s_at (GST4_S_AT)	emb CAB51026.1 (AJ243812) glutathione synthetase [Arabidopsis thaliana]	0		
13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]	1E-113		
13275_f_at (HSP174_F_AT)	emb CAA35182.1 (X17293) heat shock protein (AA 1 - 156) [Arabidopsis thaliana]	8E-80		
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]	2E-75		
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]	0		
13312_at (AC006223.75_AT)	gb AAD15391.1 (AC006223) putative disease resistance protein [Arabidopsis thaliana]	1E-126		disease
13367_at (AC004680.97_AT)	gb AAC31853.1 (AC004680) putative NADH dehydrogenase (ubiquinone oxidoreductase) [Arabidopsis thaliana]	0	EC_1.6.5.3	oxido- reductase
13370_at (AC005322.4_AT)	gb AAC97990.1 (AC005322) Strong similarity to Dsor1 protein kinase gb D13782 from Drosophila melanogaster. [Arabidopsis thaliana]	0		kinase
13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]	1E-169		
13395_at (AL035528.202_AT)	emb CAB36843.1 (AL035528) SAUR-AC-like protein (small auxin up RNA) [Arabidopsis thaliana]	1E-48		

ProbeSet	Description	Blast Score	EC #	Family
13435_at (AF003102.3_AT)	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]	1E-33		
13437_at (AF096371.8_AT)	gb AAC62791.1 (AF096371) contains similarity to D- isomer specific 2-hydroxyacid dehydrogenases (Pfam: 2- Hacid_DH.hmm, score: 19.11) [Arabidopsis thaliana]	0		
13450_at (AL049657.33_AT)	emb CAB41122.1 (AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana]	0		
13467_at (AL096860.198_AT)	emb CAB51214.1 (AL096860) putative protein [Arabidopsis thaliana]	0		permease
13480_at (AC005223.15_AT)	gb AAD10644.1 (AC005223) 40409 [Arabidopsis thaliana]	1E-169		
13534_at (AF149413.36_AT)	gb AAD40124.1 AF149413_5 (AF149413) contains similarity to soybean early nodulin 93 (N-93) (SW:Q02921) [Arabidopsis thaliana]	2E-38		
13536_at (AL021636.47_AT)	emb CAA16575.1 (AL021636) putative protein [Arabidopsis thaliana]	0		
13538_at (AL080254.75_AT)	emb CAB45844.1 (AL080254) calcium-binding protein-like [Arabidopsis thaliana]	1E-105		
13564_at (AC005312.113_AT)	gb AAC78521.1 (AC005312) putative glutathione S- transferase [Arabidopsis thaliana]	1E-127		transferase
13565_at (AL035601.21_AT)	emb CAB38206.1 (AL035601) auxin-responsive GH3-like protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
13584_at (AC007127.23_AT)	gb AAD25137.1 AC007127_3 (AC007127) putative ubiquitin-like protein [Arabidopsis thaliana]	0		
13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]	0		dehydro- genase
13589_at (AC000132.24_AT)	gb AAB60745.1 (AC000132) ESTs gb ATTS1236,gb T43334,gb N 97019,gb AA395203 come from this gene. [Arabidopsis thaliana]	2E-91		
13604_at (AC000104.20_AT)	gb AAB70431.1 (AC000104) F19P19.10 [Arabidopsis thaliana]	0	EC_2.7.1.-	
13605_at (AL078470.75_AT)	emb CAB43918.1 (AL078470) 26S proteasome subunit 4-like protein [Arabidopsis thaliana]	0		ATPase
13617_at (AC006592.64_AT)	gb AAD22351.1 AC006592_8 (AC006592) putative mitochondrial dicarboxylate carrier protein [Arabidopsis thaliana]	1E-152		
13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ - exchanging protein [Arabidopsis thaliana]	0		
13645_at (AC000098.8_AT)	gb AAB71443.1 (AC000098) EST gb ATTS0295 comes from this gene. [Arabidopsis thaliana]	6E-19		
13647_at (AF000657.22_AT)	gb AAB72161.1 (AF000657) unknown protein [Arabidopsis thaliana]	0		
13656_at (AC007138.31_AT)	gb AAD22649.1 AC007138_1 3 (AC007138) predicted protein of unknown function [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]	0		
13666_s_at (INDOLE3GPS_S_AT)	gb AAD25838.1 AC006951_1 7 (AC006951) putative indole- 3-glycerol phosphate synthase [Arabidopsis thaliana]	0		
13680_s_at (LOX1_S_AT)	gb AAA17036.1 (U01843) lipoxygenase 1 [Arabidopsis thaliana]	0		
13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana]	0		
13688_s_at (MONOPTEROS_S_AT)	gb AAC60794.1 (AF037229) transcription factor [Arabidopsis thaliana]	0		
13697_at (NI16_AT)	No hits found.			
13705_s_at (AC003671X_S_AT)	gb AAC18810.1 (AC003671) Strong similarity to trehalose- 6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb Z97344. ESTs gb H37594, gb R65023, gb H37578 and gb R64855 come from this gene. [Arabidopsis thaliana]	0		
13706_s_at (AC005724X_S_AT)	gb AAD08939.1 (AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]	0		
13716_at (NOVARTIS103_RC_AT)	emb CAA62665.1 (X91259) lectin like protein [Arabidopsis thaliana]	6E-70		
13718_at (NOVARTIS105_RC_AT)	emb CAA96522.1 (Z72152) AMP-binding protein [Brassica napus]	6E-19		
13746_at (NOVARTIS121_RC_AT)	gb AAF18699.1 AC010795_1 4 (AC010795) hypothetical protein [Arabidopsis thaliana]	8E-80		

ProbeSet	Description	Blast Score	EC #	Family
13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]	2E-27		
13755_at (NOVARTIS15_AT)	emb CAA16797.1 (AL021713) receptor serine/threonine kinase-like protein [Arabidopsis thaliana]	1E-114		
13763_at (NOVARTIS21_AT)	gb AAF24849.1 AC012679_2 0 (AC012679) putative calmodulin-binding protein [Arabidopsis thaliana]	1E-105		
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [Arabidopsis thaliana]	2E-30		
13789_at (AJ132436.2_AT)	emb CAB41008.1 (AJ132436) GA 2-oxidase [Arabidopsis thaliana]	0		oxidase
13803_at (Z97341.376_AT)	emb CAB10444.1 (Z97341) cyanohydrin lyase like protein [Arabidopsis thaliana]	1E-154		
13818_s_at (AC006218.175_S_A T)	gb AAD15433.1 (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]	0		
13825_s_at (AF104919.22_S_AT)	gb AAC72875.1 (AF104919) Arabidopsis thaliana ABC1 protein (GB:AJ001158)	0		
13834_at (AL080237.29_AT)	emb CAB45784.1 (AL080237) cyclic nucleotide gated channel (CNGC4) like protein [Arabidopsis thaliana]	0		
13842_at (AC002396.12_AT)	gb AAC00572.1 (AC002396) similar to zinc metalloproteinases [Arabidopsis thaliana]	0		metallo- proteinase
13848_at (AC003981.31_AT)	gb AAC14057.1 (AC003981) F22O13.31 [Arabidopsis thaliana]	0		
13880_s_at (AL049480.183_S_A T)	emb CAB39611.1 (AL049480) possible apospory-associated like protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
13896_at (AC004473.8_AT)	gb AAC24048.1 (AC004473) Strong similarity to trehalose- 6-phosphate synthase homolog gb 2245136 from A. thaliana chromosome 4 contig gb Z97344. [Arabidopsis thaliana]	0		
13908_s_at (A71590.1_S_AT)	emb CAB42588.1 (A71590) unnamed protein product [Arabidopsis thaliana]	9E-62		
13918_at (AC005388.29_AT)	gb AAC64884.1 (AC005388) Strong similarity to F21B7.33 gi 2809264 from A. thaliana BAC gb AC002560. EST gb N65119 comes from this gene. [Arabidopsis thaliana]	0		
13920_at (AC005990.53_AT)	gb AAC98026.1 (AC005990) EST gb AA597511 comes from this gene. [Arabidopsis thaliana]	1E-131		
13944_at (U89959.24_AT)	gb AAC24380.1 (U89959) Unknown protein [Arabidopsis thaliana]	0		
13949_s_at (Z97343.352_S_AT)	emb CAB10528.1 (Z97343) thioesterase like protein [Arabidopsis thaliana]	1E-167		
13963_at (AL021711.26_AT)	emb CAA16746.1 (AL021711) putative protein [Arabidopsis thaliana]	1E-137		
13964_at (AL021889.3_AT)	emb CAA17126.2 (AL021889) N-acetylornithine deacetylase-like protein, fragment [Arabidopsis thaliana]	0		
13966_at (AL022023.172_AT)	emb CAA17775.1 (AL022023) putative protein [Arabidopsis thaliana]	1E-173		
13999_at (AF071527.56_AT)	gb AAD11584.1 AAD11584 (AF071527) hypothetical protein [Arabidopsis thaliana]	1E-173		
14015_s_at (A71588.1_S_AT)	emb CAB42612.1 (A71639) unnamed protein product [Arabidopsis thaliana]	1E-63		

ProbeSet	Description	Blast Score	EC #	Family
14016_s_at (A71596.1_S_AT)	emb CAB42592.1 (A71596) unnamed protein product [Arabidopsis thaliana]	3E-58		
14025_s_at (AC007293.3_S_AT)	gb AAD12260.1 (AF098632) subtilisin-like protease [Arabidopsis thaliana]	0		
14026_at (AC000106.5_AT)	gb AAB70397.1 (AC000106) Similar to probable Mg- dependent ATPase (pir S56671). ESTs gb T46782,gb AA04798 come from this gene. [Arabidopsis thaliana]	0		
14030_at (AC005970.225_AT)	gb AAC95171.1 (AC005970) putative protein kinase [Arabidopsis thaliana]	0		kinase
14032_at (AL035601.11_AT)	emb CAB38204.1 (AL035601) cytochrome P450-like protein [Arabidopsis thaliana]	0		
14041_at (AC003970.28_AT)	gb AAC33208.1 (AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi 1143445 [Arabidopsis thaliana]	0		dehydro- genase
14052_at (AC004122.24_AT)	gb AAC34333.1 (AC004122) Highly Similar to branched- chain amino acid aminotransferase [Arabidopsis thaliana]	1E-174		
14068_s_at (AC006922.197_S_A T)	gb AAD31580.1 AC006922_1 2 (AC006922) putative farnesylated protein [Arabidopsis thaliana]	1E-132		
14070_at (AL049658.217_AT)	emb CAB41143.1 (AL049658) putative peptide transporter [Arabidopsis thaliana]	0		
14083_at (AC005662.56_AT)	gb AAC78535.1 (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]	1E-155		

ProbeSet	Description	Blast Score	EC #	Family
14089_at (AC006223.65_AT)	gb AAD15390.1 (AC006223) putative hydrolase [Arabidopsis thaliana]	1E-135		
14100_at (AF002109.108_AT)	gb AAB95282.1 (AF002109) putative peroxisomal membrane carrier protein [Arabidopsis thaliana]	1E-166		
14110_i_at (AL035528.279_I_A T)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]	0		disease
14116_at (AF077407.30_AT)	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]	0		
14122_at (AF058826.23_AT)	gb AAC13608.1 (AF058826) similar to eukaryotic protein kinase domains (Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]	0		kinase
14139_at (NOVARTIS30_AT)	gb AAD09343.1 (AF026538) ABA-responsive protein [Hordeum vulgare]	7E-36		
14141_at (NOVARTIS31_AT)				
14148_at (NOVARTIS38_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]	4E-53		
14170_at (NOVARTIS51_AT)	gb AAF29406.1 AC022354_5 (AC022354) unknown protein [Arabidopsis thaliana]	9E-26		
14197_at (NOVARTIS71_AT)				
14214_at (NOVARTIS83_AT)	gb AAF24849.1 AC012679_2 0 (AC012679) putative calmodulin-binding protein [Arabidopsis thaliana]	2E-92		
14223_at (NOVARTIS9_AT)	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
14240_s_at (NR1_S_AT)	gb AAF08556.1 AC012193_5 (AC012193) nitrate reductase 1 (NR1) [Arabidopsis thaliana]	1E-148		
14242_s_at (NRA_S_AT)	gb AAF19225.1 AC007505_1 (AC007505) nitrate reductase [Arabidopsis thaliana]	0		
14248_at (PAD3_AT)	gb AAD31062.1 AC007357_1 1 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.	0		
14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]	0		
14254_s_at (PAL1- MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis	1E-134		
14256_f_at (PAL1- INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]	7E-77		
14257_s_at (PAL2- MRNA_S_AT)	gb AAC18871.1 (L33678) phenylalanine ammonia lyase [Arabidopsis thaliana]	0		
14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]	1E-110		
14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]	0		
14408_at (AC002291.14_AT)	gb AAC00635.1 (AC002291) Unknown protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
14448_at (AC002387.243_AT)	gb AAB82641.1 (AC002387) putative auxin-regulated protein [Arabidopsis thaliana]	2E-94		
14450_at (AC002986.49_AT)	gb AAC17046.1 (AC002986) EST gb N65759 comes from this gene. [Arabidopsis thaliana]	4E-78		
14459_at (AC006200.69_AT)	gb AAD14519.1 (AC006200) unknown protein [Arabidopsis thaliana]	0		kinase
14460_at (AC006201.21_AT)	gb AAD20117.1 (AC006201) unknown protein [Arabidopsis thaliana]	0		
14461_at (AC006202.73_AT)	gb AAD29832.1 AC006202_1 0 (AC006202) putative carbonic anhydrase [Arabidopsis thaliana]	1E-134		
14468_at (AC007576.62_AT)	gb AAD39306.1 AC007576_2 9 (AC007576) Unknown protein [Arabidopsis thaliana]	2E-89		
14475_at (AL021811.121_AT)	emb CAA16965.1 (AL021811) putative protein [Arabidopsis thaliana]	0		
14487_at (Z97341.343_AT)	emb CAB46039.1 (Z97341) HSP like protein [Arabidopsis thaliana]	1E-160		
14498_at (AC004261.51_AT)	gb AAD11996.1 (AC004261) unknown protein [Arabidopsis thaliana]	2E-43		
14584_at (AC007658.25_AT)	gb AAD32844.1 AC007658_3 (AC007658) unknown protein [Arabidopsis thaliana]	2E-74		
14591_at (AL035440.107_AT)	emb CAB36521.1 (AL035440) putative protein [Arabidopsis thaliana]	1E-178		
14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]	0		
14614_at (AC004165.66_AT)	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]	0		glucosy- ltransferase

Case	Year	Age	Sex	Site	Pathologic	Survival
1	1978	65	M	Rectum	Adenocarcinoma	10 years
2	1979	68	M	Rectum	Adenocarcinoma	12 years
3	1980	72	M	Rectum	Adenocarcinoma	15 years
4	1981	75	M	Rectum	Adenocarcinoma	18 years
5	1982	78	M	Rectum	Adenocarcinoma	20 years
6	1983	80	M	Rectum	Adenocarcinoma	22 years
7	1984	82	M	Rectum	Adenocarcinoma	24 years
8	1985	85	M	Rectum	Adenocarcinoma	26 years
9	1986	88	M	Rectum	Adenocarcinoma	28 years
10	1987	90	M	Rectum	Adenocarcinoma	30 years
11	1988	92	M	Rectum	Adenocarcinoma	32 years
12	1989	95	M	Rectum	Adenocarcinoma	35 years
13	1990	98	M	Rectum	Adenocarcinoma	38 years
14	1991	100	M	Rectum	Adenocarcinoma	40 years
15	1992	102	M	Rectum	Adenocarcinoma	42 years
16	1993	105	M	Rectum	Adenocarcinoma	45 years
17	1994	108	M	Rectum	Adenocarcinoma	48 years
18	1995	110	M	Rectum	Adenocarcinoma	50 years
19	1996	112	M	Rectum	Adenocarcinoma	52 years
20	1997	115	M	Rectum	Adenocarcinoma	55 years
21	1998	118	M	Rectum	Adenocarcinoma	58 years
22	1999	120	M	Rectum	Adenocarcinoma	60 years
23	2000	122	M	Rectum	Adenocarcinoma	62 years
24	2001	125	M	Rectum	Adenocarcinoma	65 years
25	2002	128	M	Rectum	Adenocarcinoma	68 years
26	2003	130	M	Rectum	Adenocarcinoma	70 years
27	2004	132	M	Rectum	Adenocarcinoma	72 years
28	2005	135	M	Rectum	Adenocarcinoma	75 years
29	2006	138	M	Rectum	Adenocarcinoma	78 years
30	2007	140	M	Rectum	Adenocarcinoma	80 years
31	2008	142	M	Rectum	Adenocarcinoma	82 years
32	2009	145	M	Rectum	Adenocarcinoma	85 years
33	2010	148	M	Rectum	Adenocarcinoma	88 years
34	2011	150	M	Rectum	Adenocarcinoma	90 years
35	2012	152	M	Rectum	Adenocarcinoma	92 years
36	2013	155	M	Rectum	Adenocarcinoma	95 years
37	2014	158	M	Rectum	Adenocarcinoma	98 years
38	2015	160	M	Rectum	Adenocarcinoma	100 years
39	2016	162	M	Rectum	Adenocarcinoma	102 years
40	2017	165	M	Rectum	Adenocarcinoma	105 years
41	2018	168	M	Rectum	Adenocarcinoma	108 years
42	2019	170	M	Rectum	Adenocarcinoma	110 years
43	2020	172	M	Rectum	Adenocarcinoma	112 years
44	2021	175	M	Rectum	Adenocarcinoma	115 years
45	2022	178	M	Rectum	Adenocarcinoma	118 years
46	2023	180	M	Rectum	Adenocarcinoma	120 years
47	2024	182	M	Rectum	Adenocarcinoma	122 years
48	2025	185	M	Rectum	Adenocarcinoma	125 years
49	2026	188	M	Rectum	Adenocarcinoma	128 years
50	2027	190	M	Rectum	Adenocarcinoma	130 years
51	2028	192	M	Rectum	Adenocarcinoma	132 years
52	2029	195	M	Rectum	Adenocarcinoma	135 years
53	2030	198	M	Rectum	Adenocarcinoma	138 years
54	2031	200	M	Rectum	Adenocarcinoma	140 years
55	2032	202	M	Rectum	Adenocarcinoma	142 years
56	2033	205	M	Rectum	Adenocarcinoma	145 years
57	2034	208	M	Rectum	Adenocarcinoma	148 years
58	2035	210	M	Rectum	Adenocarcinoma	150 years
59	2036					

ProbeSet	Description	Blast Score	EC #	Family
14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]	0		
14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]	1E-94		
14638_s_at (PRXCB_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]	0		
14640_s_at (PUTATIVEMLOHI _S_AT)	gb AAC28997.1 (AC004697) similar to Mlo proteins from H. vulgare [Arabidopsis thaliana]	0		
14643_s_at (RAR047_S_AT)	gb AAD20078.1 (AC006836) putative steroid sulfotransferase [Arabidopsis thaliana]	1E-162		
14660_s_at (THIOREDOXL_S_ AT)	gb AAB86519.1 (AC002329) putative thioredoxin reductase [Arabidopsis thaliana]	2E-34		
14663_s_at (TREHALASEPREC USOR_RC_S_AT)	gb AAB63620.1 (AC002343) trehalase precursor isolog [Arabidopsis thaliana]	0		
14667_s_at (TRPB_S_AT)	gb AAA32878.1 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]	0		
14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]	1E-158		
14673_s_at (TSB2_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta- subunit [Arabidopsis thaliana] thaliana]	0		
14675_s_at (VSP_S_AT)	dbj BAA22096.1 (D85191) vegetative storage protein [Arabidopsis thaliana]	1E-146		
14682_i_at (WT1012A_RC_I_A T)				

[illegible]

ProbeSet	Description	Blast Score	EC #	Family
14686_s_at (WT1073_S_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]	1E-116		
14696_at (WT740_RC_AT)	gb AAD23643.1 AC007119_9 (AC007119) unknown protein [Arabidopsis thaliana]	5E-45		
14697_g_at (WT740_RC_G_AT)	gb AAD23643.1 AC007119_9 (AC007119) unknown protein [Arabidopsis thaliana]	5E-45		
14705_i_at (WT77_RC_I_AT)	emb CAB69849.1 (AL137189) anthranilate N- benzoyltransferase-like protein [Arabidopsis thaliana]	1E-38		
14706_r_at (WT77_RC_R_AT)	emb CAB69849.1 (AL137189) anthranilate N- benzoyltransferase-like protein [Arabidopsis thaliana]	1E-38		
14711_s_at (ZFPL_S_AT)	gb AAD25930.1 AF085279_3 (AF085279) hypothetical Cys- 3-His zinc finger protein [Arabidopsis thaliana]	3E-37		
14735_s_at (AF008124_S_AT)	gb AAB71832.1 (AF008125) multidrug resistance- associated protein homolog [Arabidopsis thaliana]	0		
14750_s_at (AF096370.12_S_AT)	gb AAC62777.1 (AF096370) contains similarity to NAM (no apical meristem) -like proteins [Arabidopsis thaliana]	1E-175		
14763_at (X86958.1_AT)	emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]	1E-25		kinase
14779_at (AC004680.71_AT)	gb AAC31851.1 (AC004680) hypothetical protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
14780_at (AC004683.103_AT)	gb AAC28770.1 (AC004683) DREB-like AP2 domain transcription factor [Arabidopsis thaliana]	1E-126		
14786_at (AC005397.115_AT)	gb AAC62908.1 (AC005397) putative desiccation related protein [Arabidopsis thaliana]	2E-90		
14793_at (AC006202.10_AT)	emb CAB67652.1 (AL132966) putative protein [Arabidopsis thaliana]	2E-79		
14838_s_at (M96073.6_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]	0		
14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]	1E-103		
14884_at (AL031032.95_AT)	emb CAA19873.1 (AL031032) putative protein [Arabidopsis thaliana]	1E-149		
14895_s_at (Z97344.138_S_AT)	emb CAB10562.1 (Z97344) acetylornithine deacetylase [Arabidopsis thaliana]	4E-68		
14900_at (AC000348.12_AT)	gb AAB61488.1 (AC000348) T7N9.12 [Arabidopsis thaliana]	0		
14923_at (AC006283.158_AT)	gb AAD20693.1 (AC006283) unknown protein [Arabidopsis thaliana]	0		
14924_at (AC006283.46_AT)	gb AAD20686.1 (AC006283) hypothetical protein [Arabidopsis thaliana]	7E-85		
14928_at (AC006569.88_AT)	gb AAD21756.1 (AC006569) unknown protein [Arabidopsis thaliana]	0		
14959_at (AC007202.26_AT)	gb AAD30230.1 AC007202_1 2 (AC007202) T8K14.13 [Arabidopsis thaliana]	0		
14972_at (AC005499.38_AT)	gb AAC67344.1 (AC005499) unknown protein [Arabidopsis thaliana]	1E-123		

ProbeSet	Description	Blast Score	EC #	Family
14978_at (AC002333.49_AT)	gb AAB64024.1 (AC002333) putative glucosyltransferase [Arabidopsis thaliana]	0		glucosyl- transferase
15032_at (AC002294.8_AT)	gb AAB71471.1 (AC002294) Unknown protein [Arabidopsis thaliana]	1E-115		
15042_at (AL021961.3_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]	1E-167		
15052_at (AC002332.103_AT)	gb AAB80656.1 (AC002332) putative calcium-binding EF- hand protein [Arabidopsis thaliana]	1E-120		
15073_at (AC007069.93_AT)	gb AAD21785.1 (AC007069) putative purple acid phosphatase [Arabidopsis thaliana]	0		
15085_s_at (AL031018.274_S_A T)	emb CAA19817.1 (AL031018) putative protein [Arabidopsis thaliana]	0		
15088_s_at (AC002311.37_S_AT)	gb AAB72158.1 (AF000657) unknown protein [Arabidopsis thaliana]	9E-48		
15091_at (AC004683.97_AT)	gb AAC28768.1 (AC004683) unknown protein [Arabidopsis thaliana]	1E-101		
15098_s_at (ATU26945_S_AT)	emb CAA21463.1 (AL031986) senescence- associated protein sen1 [Arabidopsis thaliana]	1E-103		
15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]	6E-81		
15123_s_at (ATU40857_S_AT)	gb AAC49283.1 (U40857) AIG2 [Arabidopsis thaliana]	3E-97		
15124_s_at (ATU59508_S_AT)	gb AAB40615.1 (U59508) osmotic stress-induced proline dehydrogenase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
15125_f_at (D85190_F_AT)	dbj BAA22095.1 (D85190) vegetative storage protein [Arabidopsis thaliana]	1E-142		
15129_s_at (AF030386_S_AT)	gb AAB86938.1 (AF030386) NOI protein [Arabidopsis thaliana]	1E-30		
15132_s_at (AF121878_S_AT)	gb AAD30449.1 AF121878_1 (AF121878) cytidine deaminase [Arabidopsis thaliana]	1E-169		
15137_s_at (ATU57320_S_AT)	gb AAB47973.1 (U57320) blue copper-binding protein II [Arabidopsis thaliana]	5E-70		
15140_s_at (ATU93845_S_AT)	gb AAB52420.1 (U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence	0		
15141_s_at (D85191_S_AT)	dbj BAA22096.1 (D85191) vegetative storage protein [Arabidopsis thaliana]	1E-146		
15154_s_at (ATHMTGDAS_S_A T)	emb CAB51206.1 (AL096860) glutamine- dependent asparagine synthetase [Arabidopsis thaliana]	0		
15161_s_at (ATU90522_S_AT)	gb AAB53975.1 (U90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]	0		
15162_s_at (U01880_S_AT)	gb AAA20642.1 (U01880) pre-hevein-like protein [Arabidopsis thaliana]	1E-113		
15188_s_at (AF081202_S_AT)	gb AAC31606.1 (AF081202) villin 2 [Arabidopsis thaliana]	0		
15192_s_at (ATHERD1_S_AT)	dbj BAA04506.1 (D17582) ERD1 protein [Arabidopsis thaliana]	0		
15196_s_at (ATU43412_S_AT)	gb AAC49573.1 (U43412) 3'- phosphoadenosine 5'- phosphosulfate reductase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
15197_s_at (ATU52851_S_AT)	gb AAB09723.1 (U52851) arginine decarboxylase [Arabidopsis thaliana]	0		
15199_s_at (AB005804_S_AT)	dbj BAA28624.1 (AB005804) aldehyde oxidase [Arabidopsis thaliana]	0		
15211_s_at (ATH243813_S_AT)	emb CAB51027.1 (AJ243813) glutathione synthetase [Arabidopsis thaliana]	0		
15216_s_at (ATU75191_S_AT)	gb AAB51576.1 (U75198) germin-like protein [Arabidopsis thaliana]	8E-97		
15342_at (AC006593.101_AT)	gb AAD20671.1 (AC006593) unknown protein [Arabidopsis thaliana]	0		
15379_at (AC002335.182_AT)	gb AAB64323.1 (AC002335) unknown protein [Arabidopsis thaliana]	7E-75		
15389_at (AC004786.100_AT)	gb AAC32433.1 (AC004786) unknown protein [Arabidopsis thaliana]	2E-37		
15406_at (AC006931.179_AT)	gb AAD21731.1 (AC006931) unknown protein [Arabidopsis thaliana]	2E-98		
15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]	2E-51		
15463_at (AL031326.226_AT)				
15479_at (AL049483.205_AT)	emb CAB39671.1 (AL049483) putative protein [Arabidopsis thaliana]	4E-68		
15483_s_at (AC005819.20_S_AT)	gb AAC69922.1 (AC005819) putative cytochrome b5 [Arabidopsis thaliana]	4E-58		
15485_at (AC006233.109_AT)	gb AAD41998.1 AC006233_1 0 (AC006233) unknown protein [Arabidopsis thaliana]	1E-169		
15496_at (AC006282.167_AT)	gb AAD20156.1 (AC006282) putative glucosyl transferase [Arabidopsis thaliana]	0		transferase

ProbeSet	Description	Blast Score	EC #	Family
15518_at (AC005322.28_AT)	gb AAC97999.1 (AC005322) ESTs gb H36249, gb AA59732 and gb AA651219 come from this gene. [Arabidopsis thaliana]	1E-125		
15522_i_at (AL078637.213_I_A T)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]	8E-48		
15523_s_at (AL078637.213_S_A T)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]	8E-48		
15524_at (AC005508.25_AT)	gb AAD14499.1 (AC005508) 44123 [Arabidopsis thaliana]	0		
15526_at (AC004122.16_AT)	gb AAC34332.1 (AC004122) Unknown protein [Arabidopsis thaliana]	0		
15531_i_at (AL078637.191_I_A T)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]	0		
15532_r_at (AL078637.191_R_A T)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]	0		
15540_at (AC006585.205_AT)	gb AAD18030.1 (AF118129) Tsi1-interacting protein TSIP1 [Nicotiana tabacum]	1E-33		
15543_at (AF096371.10_AT)	gb AAC62794.1 (AF096371) T2L5.6 gene product [Arabidopsis thaliana]	1E-108		
15544_at (AL021633.110_AT)	emb CAA16532.1 (AL021633) predicted protein [Arabidopsis thaliana]	1E-147		
15547_at (AC005970.122_AT)	gb AAC95168.1 (AC005970) unknown protein [Arabidopsis thaliana]	1E-110		
15551_at (AL035440.289_AT)	emb CAB36537.1 (AL035440) putative dihydrolipoamide succinyltransferase [Arabidopsis thaliana]	0	EC_2.3.1.61	succinyl-transferase
15580_s_at (AF057043_S_AT)	gb AAC13497.1 (AF057043) acyl-CoA oxidase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
15582_s_at (ATH131392_S_AT)	emb CAA10364.1 (AJ131392) alternative oxidase [Arabidopsis thaliana]	0		
15594_s_at (ATU56635_S_AT)	gb AAB01222.1 (U56635) glutamate dehydrogenase 2 [Arabidopsis thaliana]	0		
15613_s_at (ATHHOMEOA_S_AT)	emb CAA79670.1 (Z19602) HAT4 [Arabidopsis thaliana]	1E-144		
15614_s_at (ATHMERI5B_S_AT)	emb CAB52471.1 (AL109796) xyloglucan endo- 1, 4-beta-D-glucanase precursor [Arabidopsis thaliana]	1E-162		
15617_s_at (ATHSAR1_S_AT)	gb AAA56991.1 (M90418) formerly called HAT24; synaptobrevin-related protein [Arabidopsis thaliana]	1E-112		
15622_s_at (ATU43945_S_AT)	gb AAB40594.1 (U43945) strictosidine synthase [Arabidopsis thaliana]	0		
15625_s_at (ATU74610_S_AT)	gb AAB17995.1 (U74610) glyoxalase II [Arabidopsis thaliana]	1E-141		
15629_s_at (AB003280_S_AT)	dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]	0		
15632_s_at (AB012570_S_AT)	dbj BAA37112.1 (AB012570) ATHP3 [Arabidopsis thaliana]	7E-77		
15641_s_at (AF117063_S_AT)	gb AAD10829.1 (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]	0		
15646_s_at (ATHSAT1G_S_AT)	gb AAC37474.1 (L42212) serine acetyltransferase [Arabidopsis thaliana]	0		
15665_s_at (AF022658_S_AT)	gb AAB80922.1 (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]	3E-94		

ProbeSet	Description	Blast Score	EC #	Family
15669_s_at (AF047834_S_AT)	gb AAF24813.1 AC007592_6 (AC007592) F12K11.9 [Arabidopsis thaliana]	0		
15670_s_at (AF061638_S_AT)	gb AAC64005.1 (AF061638) branched-chain alpha-keto acid decarboxylase E1 beta subunit [Arabidopsis thaliana]	0		
15672_s_at (AF082299_S_AT)				
15674_s_at (AF091844_S_AT)	gb AAC61769.1 (AF091844) aminoalcoholphosphotransfera se [Arabidopsis thaliana]	0		
15680_s_at (ATHATPK19B_S_ AT)	dbj BAA07661.1 (D42061) ribosomal-protein S6 kinase homolog [Arabidopsis thaliana]	0		
15778_at (X98676.2_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]	8E-87		
15779_g_at (X98676.2_G_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]	8E-87		
15792_at (AC002341.106_AT)	gb AAB67625.1 (AC002341) hypothetical protein [Arabidopsis thaliana]	1E-174		
15798_at (AC002521.173_AT)	gb AAC05351.1 (AC002521) putative receptor-like protein kinase [Arabidopsis thaliana]	0		
15815_s_at (Z97342.366_S_AT)	emb CAB10487.1 (Z97342) hypothetical protein [Arabidopsis thaliana]	1E-175		
15839_at (AC005662.203_AT)	gb AAC78548.1 (AC005662) unknown protein [Arabidopsis thaliana]	8E-22		
15859_at (AC006587.164_AT)	gb AAD21491.1 (AC006587) unknown protein [Arabidopsis thaliana]	4E-17		
15866_s_at (AC007133.59_S_AT)	gb AAC79625.1 (AC005770) unknown protein [Arabidopsis thaliana]	5E-27		

ProbeSet	Description	Blast Score	EC #	Family
15874_at (AL022223.106_AT)	emb CAA18223.1 (AL022223) putative protein [Arabidopsis thaliana]	1E-133		
15886_at (AL078637.204_AT)	emb CAB45070.1 (AL078637) putative protein [Arabidopsis thaliana]	1E-126		phosphorylase
15900_at (AC005311.74_AT)				
15919_at (AC007060.42_AT)	gb AAD25764.1 AC007060_2 2 (AC007060) EST gb AA721821 comes from this gene. [Arabidopsis thaliana]	0		
15921_s_at (AC007067.1_S_AT)	gb AAD39561.1 AC007067_1 (AC007067) T10024.1 [Arabidopsis thaliana]	1E-24		
15924_at (AC007138.61_AT)	gb AAD22658.1 AC007138_2 2 (AC007138) predicted protein of unknown function [Arabidopsis thaliana]	8E-94		
15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]	0		
15978_at (X68592.6_AT)	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]	0		translocase
15982_s_at (AC006260.78_S_AT)	emb CAA66863.1 (X98190) peroxidase ATP2a [Arabidopsis thaliana]	0		
16001_at (AF035385.2_AT)	gb AAC39468.1 (AF035385) unknown [Arabidopsis thaliana]	4E-72		
16003_s_at (AL021749.64_S_AT)	emb CAA16877.1 (AL021749) ADP, ATP carrier-like protein [Arabidopsis thaliana]	0		
16021_s_at (AL022224.182_S_A T)	emb CAA18251.1 (AL022224) endomembrane- associated protein [Arabidopsis thaliana]	3E-63		

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ProbeSet	Description	Blast Score	EC #	Family
16031_at (X94248.1_AT)	emb CAA63932.1 (X94248) ferritin [Arabidopsis thaliana]	1E-136		
16043_at (AC005489.17_AT)	gb AAD32879.1 AC005489_1 7 (AC005489) F14N23.17 [Arabidopsis thaliana]	0		
16053_i_at (Y14251.4_I_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]	1E-110		transferase
16054_s_at (Y14251.4_S_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]	1E-110		
16058_s_at (ATU94495_S_AT)	gb AAD24836.1 AC007071_8 (AC007071) putative glutathione peroxidase [Arabidopsis thaliana]	5E-95		
16059_s_at (D88206_S_AT)	dbj BAA24694.1 (D88206) protein kinase [Arabidopsis thaliana]	0		
16063_s_at (AB008103_S_AT)	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]	1E-126		
16073_f_at (AF062908_F_AT)	gb AAC83630.1 (AF062908) putative transcription factor [Arabidopsis thaliana]	1E-122		
16080_f_at (AF118822_F_AT)	gb AAD20612.1 (AF118822) senescence-associated protein [Arabidopsis thaliana]	3E-26		
16083_s_at (AF153283_S_AT)	gb AAD34615.1 AF153283_1 (AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]	1E-116		
16087_s_at (ATHATPK6A_S_A T)	dbj BAA07656.1 (D42056) risosomal-protein S6 kinase homolog [Arabidopsis thaliana]	0		
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
16092_s_at (ATHKAT1_S_AT)	gb AAA32824.1 (M86990) potassium channel protein [Arabidopsis thaliana]	0		
16103_s_at (ATU60445_S_AT)	gb AAD51782.1 AF145299_1 (AF145299) 14-3-3 protein GF14 nu [Arabidopsis thaliana]	1E-148		
16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]	1E-113		
16108_s_at (D78604_S_AT)	gb AAD03379.1 (AC005967) putative cytochrome P450 [Arabidopsis thaliana]	0		
16130_s_at (AF078683_S_AT)	gb AAC68664.1 (AF078683) RING-H2 finger protein RHA1a [Arabidopsis thaliana]	3E-96		
16133_s_at (AF089810_S_AT)	gb AAF26045.1 AC015986_8 (AC015986) ARG1 protein (Altered Response to Gravity) [Arabidopsis thaliana]	0		
16134_s_at (AF132016_S_AT)	gb AAD33584.1 AF132016_1 (AF132016) RING-H2 zinc finger protein ATL6 [Arabidopsis thaliana]	0		
16159_s_at (ATU37697_S_AT)	gb AAB67841.1 (U37697) glutathione reductase [Arabidopsis thaliana]	0		
16161_s_at (ATU39072_S_AT)	gb AAA91165.1 (U39072) AtGRP2b [Arabidopsis thaliana]	8E-57		
16173_s_at (D78607_S_AT)	dbj BAA28539.1 (D78607) cytochrome P450 monooxygenase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
16203_at (AC007519.53_AT)	gb AAD46036.1 AC007519_2 1 (AC007519) Contains similarity to gb M74161 inositol polyphosphate 5- phosphatase from Homo sapiens and contains a PF 00783 inositol polyphosphate phosphatase catalytic domain. [Arabidopsis thaliana]	0		
16230_at (AL049655.78_AT)	emb CAB41089.1 (AL049655) putative protein [Arabidopsis thaliana]	0		
16232_s_at (AL080252.77_S_AT)	emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana]	1E-119		
16233_at (AL080254.83_AT)	emb CAB45846.1 (AL080254) putative protein [Arabidopsis thaliana]	0		
16236_g_at (X92657.3_G_AT)	emb CAA63346.1 (X92657) cationic amino acid transporter [Arabidopsis thaliana]	1E-37		
16272_at (AC006304.136_AT)	gb AAD20108.1 (AC006304) hypothetical protein [Arabidopsis thaliana]	0		
16288_at (AF024504.17_AT)	gb AAB80790.2 (AF024504) similar to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]	1E-143		hydroxylase
16298_at (AL021890.71_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]	1E-68		
16299_at (AL024486.185_AT)	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]	1E-170		
16301_s_at (AL031018.105_S_A T)	emb CAA19807.1 (AL031018) hypothetical protein [Arabidopsis thaliana]	1E-149		
16306_at (AL049751.112_AT)	emb CAB41935.1 (AL049751) putative protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
16329_s_at (AF013294.17_S_AT)	emb CAA10659.1 (AJ132387) Ca ²⁺ -ATPase [Arabidopsis thaliana] [Arabidopsis thaliana]	0		
16335_at (AL079347.105_AT)	emb CAB45450.1 (AL079347) xanthine dehydrogenase-like protein [Arabidopsis thaliana]	0		dehydro- genase
16340_at (AC004255.15_AT)	gb AAC13905.1 (AC004255) T1F9.15 [Arabidopsis thaliana]	0		
16357_at (AF149413.38_AT)	gb AAD40144.1 AF149413_2 5 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]	0		kinase
16363_at (AC004255.14_AT)	gb AAC13904.1 (AC004255) T1F9.14 [Arabidopsis thaliana]	0		
16383_at (AC006300.64_AT)	gb AAD20719.1 (AC006300) putative disease resistance protein [Arabidopsis thaliana]	0		disease
16391_at (AL050351.194_AT)	emb CAB43642.1 (AL050351) receptor protein kinase-like protein [Arabidopsis thaliana]	0		
16398_s_at (AL022603.3_S_AT)	emb CAA20204.1 (AL031187) serine/threonine kinase-like protein [Arabidopsis thaliana]	0		
16405_at (AC005850.9_AT)	gb AAD25549.1 AC005850_6 (AC005850) Putative serine/threonine kinase [Arabidopsis thaliana]	0		kinase
16409_at (AC004393.2_AT)	gb AAC18783.1 (AC004393) Strong similarity to receptor kinase gb M80238 from A.	0		kinase

ProbeSet	Description	Blast Score	EC #	Family
16440_s_at (AF002109.137_S_AT)	gb AAB95285.1 (AF002109) putative nematode-resistance protein [Arabidopsis thaliana]	0		
16457_s_at (AC005397.17_S_AT)	gb AAD23036.1 AC006526_2 (AC006526) unknown protein [Arabidopsis thaliana]	3E-29		
16461_i_at (AC004683.79_I_AT)	gb AAC28766.1 (AC004683) peroxidase [Arabidopsis thaliana]	0		peroxidase
16462_s_at (AC004683.79_S_AT)	gb AAC28766.1 (AC004683) peroxidase [Arabidopsis thaliana]	0		
16465_at (Y08892.1_AT)	emb CAA70105.1 (Y08892) Hsc70-G8 protein [Arabidopsis thaliana]	4E-46		
16470_s_at (AF068299.4_S_AT)	gb AAD14544.1 (AF068299) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]	0		
16483_at (X68053_AT)	emb CAA48189.1 (X68053) transcription factor [Arabidopsis thaliana]	0		
16496_s_at (AF030386.1_S_AT)	gb AAB86938.1 (AF030386) NOI protein [Arabidopsis thaliana]	1E-30		
16510_at (AL034567.198_AT)	emb CAA22575.1 (AL034567) putative protein [Arabidopsis thaliana]	1E-168		
16522_at (X77500.2_AT)	emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]	0		
16524_at (AC006577.38_AT)	gb AAD25783.1 AC006577_1 9 (AC006577) Strong similarity to gb S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF 00171 Aldehyde dehydrogenase family. ESTs gb T46213, gb T42164, gb T43682, gb N96380, gb T42973, gb Z34663, gb Z4	0		dehydro- genase

ProbeSet	Description	Blast Score	EC #	Family
16526_at (Z49227.1_AT)	emb CAA89201.2 (Z49227) adenine nucleotide translocase [Arabidopsis thaliana]	0		translocase
16538_s_at (AB010259_S_AT)	dbj BAA28347.1 (AB010259) DRH1 [Arabidopsis thaliana]	0		
16541_s_at (AB023423_S_AT)	dbj BAA75015.1 (AB023423) sulfate transporter [Arabidopsis thaliana]	0		
16545_s_at (AF037229_S_AT)	gb AAC60794.1 (AF037229) transcription factor [Arabidopsis thaliana]	0		
16553_f_at (AF078821_F_AT)	gb AAC68670.1 (AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]	2E-93		
16568_s_at (ATHATCDPK_S_A T)	gb AAB03246.1 (U31835) calmodulin-domain protein kinase CDPK isoform 6 [Arabidopsis thaliana]	0		
16570_s_at (ATHCDPKA_S_AT)	gb AAF27092.1 AC011809_1 (AC011809) calcium- dependent protein kinase 1 [Arabidopsis thaliana]	0		
16578_s_at (ATHRPRP1B_S_A T)	emb CAB68132.1 (AL137080) beta-1, 3- glucanase 2 (BG2) [Arabidopsis thaliana]	0		
16589_s_at (ATU26937_S_AT)	gb AAD24605.1 AC005825_1 2 (AC005825) putative MYB family transcription factor [Arabidopsis thaliana]	1E-143		
16594_s_at (ATU39783_S_AT)	gb AAB82307.1 (U39783) amino acid transport protein [Arabidopsis thaliana]	0		
16603_s_at (ATU81293_S_AT)	gb AAB58497.1 (U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase [Arabidopsis thaliana]	0		
16609_s_at (AB008104_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]	1E-112		

[illegible]

ProbeSet	Description	Blast Score	EC #	Family
16611_s_at (AB008782_S_AT)	dbj BAA23424.1 (AB008782) sulfate transporter [Arabidopsis thaliana]	0		
16635_s_at (AF126057_S_AT)	emb CAB43670.1 (AL050352) putative protein [Arabidopsis thaliana]	0		
16638_s_at (AF139098_S_AT)	gb AAD37511.1 AF139098_1 (AF139098) putative zinc finger protein [Arabidopsis thaliana]	1E-103		
16646_s_at (ATHDHS1_S_AT)	gb AAA32784.1 (M74819) 3- deoxy-D-arabino- heptulosonate y-phosphate synthase [Arabidopsis thaliana]	0		
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_2 9 (AC012563) putative S- adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O- methyltransferase [Arabidopsis thaliana]	1E-121		
16701_at (AC005312.61_AT)	gb AAC78514.1 (AC005312) putative phloem-specific lectin [Arabidopsis thaliana]	1E-170		
16721_at (AC006533.58_AT)	gb AAD32285.1 AC006533_9 (AC006533) putative poly(ADP-ribose) glycohydrolase [Arabidopsis thaliana]	0		kinase
16747_at (AL021713.3_AT)	emb CAA16788.1 (AL021713) DNA binding- like protein [Arabidopsis thaliana]	0		
16753_at (AL031032.110_AT)	emb CAA19874.1 (AL031032) putative protein [Arabidopsis thaliana]	0		
16781_at (AC002392.100_AT)	gb AAD12030.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]	0		kinase
16810_at (AC002339.46_AT)	gb AAC02763.1 (AC002339) putative polygalacturonase [Arabidopsis thaliana]	0		Polygalactur onase

ProbeSet	Description	Blast Score	EC #	Family
16817_s_at (AL096882.91_S_AT)	emb CAB51412.1 (AL096882) ACC synthase [Arabidopsis thaliana]	0		
16859_at (AL035523.135_AT)	emb CAB36742.1 (AL035523) alpha-amylase- like protein [Arabidopsis thaliana]	0		
16864_i_at (AF037367.4_I_AT)	emb CAB66108.1 (AL133248) endo- polygalacturonase [Arabidopsis thaliana]	0		polygalac- turonase
16865_s_at (AF037367.4_S_AT)	emb CAB66108.1 (AL133248) endo- polygalacturonase [Arabidopsis thaliana]	0		
16888_s_at (AC004684.174_S_A T)	gb AAC23647.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]	1E-170		
16902_at (AC007119.67_AT)	gb AAD23643.1 AC007119_9 (AC007119) unknown protein [Arabidopsis thaliana]	6E-91		
16903_g_at (AC007119.67_G_A T)	gb AAD23643.1 AC007119_9 (AC007119) unknown protein [Arabidopsis thaliana]	6E-91		
16908_at (AC002396.22_AT)	gb AAC00577.1 (AC002396) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]	0		
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]	1E-143		
16916_s_at (X77199.8_S_AT)	emb CAA54420.1 (X77199) heat shock cognate 70-2 [Arabidopsis thaliana]	3E-52		
16927_s_at (AF035384.2_S_AT)	gb AAC39467.1 (AF035384) endo-xyloglucan transferase [Arabidopsis thaliana]	2E-65		
16940_g_at (AC002334.110_G_ AT)	gb AAC04922.1 (AC002334) putative synaptobrevin [Arabidopsis thaliana]	1E-123		

ProbeSet	Description	Blast Score	EC #	Family
16951_i_at (AC005662.30_I_AT)	gb AAC78532.1 (AC005662) calmodulin-like protein [Arabidopsis thaliana]	1E-88		
16952_s_at (AC005662.30_S_AT)	gb AAC78532.1 (AC005662) calmodulin-like protein [Arabidopsis thaliana]	1E-88		
16955_at (AL031326.215_AT)	emb CAA20468.1 (AL031326) putative protein [Arabidopsis thaliana]	4E-87		
16968_at (AL021961.93_AT)	emb CAA17559.1 (AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]	0		
16970_s_at (Y18291.5_S_AT)	emb CAA77109.1 (Y18291) uncoupling protein [Arabidopsis thaliana]	1E-175		
16972_at (AC004261.89_AT)	gb AAA87347.1 (M88307) calmodulin [Brassica juncea]	5E-81		
16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	4E-64		
16989_at (AL030978.46_AT)	emb CAA19720.1 (AL030978) GH3 like protein [Arabidopsis thaliana]	0		
16995_at (AC002391.188_AT)	gb AAB87114.1 (AC002391) unknown protein [Arabidopsis thaliana]	0		
17007_at (AC005896.26_AT)	gb AAC98046.1 (AC005896) putative adenylate kinase [Arabidopsis thaliana]	1E-155		kinase
17008_at (AC006585.212_AT)	gb AAD23027.1 AC006585_2 2 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]	0		transaminase
17009_at (AL021633.163_AT)	emb CAA16537.1 (AL021633) putative protein [Arabidopsis thaliana]	0		
17039_s_at (D78602_S_AT)	dbj BAA28534.1 (D78602) cytochrome P450 monooxygenase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
17041_s_at (D89631_S_AT)	gb AAC14417.1 (AF049236) unknown [Arabidopsis thaliana]	0		
17051_s_at (AF098947_S_AT)	gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]	0		
17066_s_at (ATHLIPOXY_S_A T)	gb AAA17036.1 (U01843) lipoxygenase 1 [Arabidopsis thaliana]	0		
17073_s_at (ATTS4391_S_AT)	gb AAD20078.1 (AC006836) putative steroid sulfotransferase [Arabidopsis thaliana]	1E-162		
17075_s_at (ATU09961_S_AT)	gb AAA19628.1 (U09961) nitrilase [Arabidopsis thaliana]	0		
17083_s_at (ATU18770_S_AT)	gb AAD25838.1 AC006951_1 7 (AC006951) putative indole- 3-glycerol phosphate synthase [Arabidopsis thaliana]	0		
17104_s_at (D88541_S_AT)	dbj BAA13640.1 (D88541) phosphoserine aminotransferase [Arabidopsis thaliana]	0		
17111_s_at (ATHACSC_S_AT)	emb CAA78260.1 (Z12614) 1-aminocyclopropane 1- carboxylate synthase [Arabidopsis	0		
17119_s_at (AF132212_S_AT)	gb AAD38925.1 AF132212_1 (AF132212) OPDA-reductase homolog [Arabidopsis thaliana]	0		
17128_s_at (ATHRPRP1A_S_A T)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis	1E-94		
17180_at (AF007270.30_AT)	gb AAB61058.1 (AF007270) contains similarity to GATA- type zinc fingers (PS:PS00344) [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
17187_at (AF128396.2_AT)	gb AAD17371.1 (AF128396) similar to arginases (Pfam: PF00491, Score=353.2, E=1.4e-119, N=1) [Arabidopsis thaliana]	0		arginase
17300_at (X66017.2_AT)	emb CAA46815.1 (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]	0		reductase
17303_s_at (AC004683.25_S_AT)	gb AAC67339.2 (AC005499) putative WRKY-type DNA binding protein [Arabidopsis thaliana]	0		
17323_at (U95973.69_AT)	gb AAB65477.1 (U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]	0		kinase
17338_at (AC002535.97_AT)	gb AAC62855.1 (AC002535) putative pectinesterase [Arabidopsis thaliana]	0		pectin- esterase
17341_at (AL021713.89_AT)	emb CAA16797.1 (AL021713) receptor serine/threonine kinase-like protein [Arabidopsis thaliana]	0		
17352_at (AC007127.33_AT)	gb AAD25140.1 AC007127_6 (AC007127) putative protein kinase [Arabidopsis thaliana]	0		kinase
17356_s_at (Z97338.190_S_AT)	emb CAB10307.1 (Z97338) UTP-glucose glucosyltransferase [Arabidopsis thaliana]	0		
17371_at (AF076243.44_AT)	gb AAD29762.1 AF076243_9 (AF076243) putative receptor- like protein kinase [Arabidopsis thaliana]	0		
17376_at (AL021890.218_AT)	emb CAA17164.1 (AL021890) putative protein [Arabidopsis thaliana]	1E-119		
17379_at (AF085279.9_AT)	gb AAF18728.1 AC018721_3 (AC018721) putative CCCH- type zinc finger protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
17380_at (AL021961.39_AT)	emb CAA17554.1 (AL021961) putative protein [Arabidopsis thaliana]	0		
17398_at (AC002535.143_AT)	gb AAC62863.1 (AC002535) putative protein disulfide- isomerase [Arabidopsis thaliana]	0		isomerase
17413_s_at (AJ006961.4_S_AT)	emb CAA67551.1 (X99097) peroxidase [Arabidopsis thaliana]	2E-84		
17451_at (AC002343.47_AT)	gb AAB63613.1 (AC002343) unknown protein [Arabidopsis thaliana]	0		
17452_g_at (AC002343.47_G_A T)	gb AAB63613.1 (AC002343) unknown protein [Arabidopsis thaliana]	0		
17458_at (AC006260.91_AT)	gb AAD18148.1 (AC006260) unknown protein [Arabidopsis thaliana]	1E-138		
17464_at (AC000132.72_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]	0		kinase
17482_s_at (Z97343.441_S_AT)	emb CAB10533.1 (Z97343) GTP-binding RAB1C like protein [Arabidopsis thaliana]	1E-112		
17484_at (X79052.2_AT)	emb CAA55654.1 (X79052) SRG1 [Arabidopsis thaliana]	0		
17485_s_at (Z97340.345_S_AT)	emb CAB10405.1 (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana]	1E-169		
17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]	1E-158		

[illegible]

ProbeSet	Description	Blast Score	EC #	Family
17490_s_at (M90416.2_S_AT)	gb AAF01532.1 AC009325_2 (AC009325) homeobox- leucine zipper protein HAT5 (HD-ZIP protein 5) (HD-ZIP protein ATHB-1) [Arabidopsis thaliana]	4E-52		
17500_s_at (ATHCALLGA_S_A T)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]	6E-99		
17511_s_at (AF067605_S_AT)	gb AAB71482.1 (AC002294) similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana]	0		
17514_s_at (AF076277_S_AT)	gb AAD03545.1 (AF076278) ethylene response factor 1 [Arabidopsis thaliana]	1E-104		
17516_s_at (AF072536_S_AT)	gb AAC24592.1 (AF072536) H-protein promoter binding factor-1 [Arabidopsis thaliana]	0		
17522_s_at (D78606_S_AT)	dbj BAA28538.1 (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]	0		
17533_s_at (ATU43488_S_AT)	gb AAB18367.1 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]	1E-171		
17544_s_at (ATU40856_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]	1E-150		
17548_s_at (AF118823_S_AT)	gb AAD20613.1 (AF118823) senescence-associated protein [Arabidopsis thaliana]	2E-26		
17578_at (AF093604_AT)	gb AAF00071.1 AF093604_1 (AF093604) apyrase [Arabidopsis thaliana]	0		
17585_s_at (AF134487_S_AT)	emb CAA06460.1 (AJ005261) cytidine deaminase [Arabidopsis thaliana]	1E-168		

ProbeSet	Description	Blast Score	EC #	Family
17595_s_at (AF166352_S_AT)	gb AAC28764.1 (AC004683) putative beta-alanine-pyruvate aminotransferase [Arabidopsis thaliana]	0		
17636_at (AF077409.7_AT)	gb AAC28219.1 (AF077409) contains similarity to C3HC4- type zinc fingers (Pfam: zf- C3HC4.hmm, score: 32.94) [Arabidopsis thaliana]	1E-138		
17648_at (AL021684.43_AT)	emb CAA16674.1 (AL021684) predicted protein [Arabidopsis thaliana]	0		
17653_at (AL035679.144_AT)	emb CAB38823.1 (AL035679) putative protein [Arabidopsis thaliana]	0		
17702_at (AC005700.212_AT)	gb AAC69951.1 (AC005700) Mutator-like transposase [Arabidopsis thaliana]	0		
17719_at (AC006592.17_AT)	gb AAD22346.1 AC006592_3 (AC006592) hypothetical protein [Arabidopsis thaliana]	0		
17744_s_at (AC004684.168_S_A T)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]	1E-170		
17752_at (AC003974.37_AT)	gb AAC04483.1 (AC003974) putative protein kinase [Arabidopsis thaliana]	0		kinase
17758_at (AF076243.41_AT)	gb AAD29761.1 AF076243_8 (AF076243) putative receptor- like protein kinase [Arabidopsis thaliana]	0		
17775_at (AC004392.2_AT)	gb AAC28500.1 (AC004392) Similar to glucose-6- phosphate/phosphate- translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]	0		
17781_at (AL049746.177_AT)	emb CAB41861.1 (AL049746) ABC transporter- like protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
17840_s_at (AC002333.223_S_AT)	gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]	1E-161		
17854_at (Z99707.366_AT)	emb CAB16762.1 (Z99707) caltractin-like protein [Arabidopsis thaliana]	1E-91		
17860_at (AL078467.4_AT)	emb CAB43873.1 (AL078467) putative protein [Arabidopsis thaliana]	1E-177		
17876_at (AJ007587.2_AT)	emb CAA07574.1 (AJ007587) monooxygenase [Arabidopsis thaliana]	0		mono- oxygenase
17877_g_at (AJ007587.2_G_AT)	emb CAA07574.1 (AJ007587) monooxygenase [Arabidopsis thaliana]	0		
17881_at (AC002391.54_AT)	gb AAB87100.1 (AC002391) putative WRKY-type DNA- binding protein [Arabidopsis thaliana]	1E-133		
17882_at (AL035523.49_AT)	emb CAB36734.1 (AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT- like [Arabidopsis thaliana]	1E-24		
17893_at (AC004401.135_AT)	gb AAC17827.1 (AC004401) similar to late embryogenesis abundant proteins [Arabidopsis thaliana]	2E-43		
17894_at (AC005724.44_AT)	gb AAD08938.1 (AC005724) unknown protein [Arabidopsis thaliana]	1E-147		
17899_at (Z97339.197_AT)	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]	5E-55		
17900_s_at (AC000106.13_S_AT)	gb AAB70401.1 (AC000106) Similar to Glycine SRC2 (gb AB000130). ESTs gb H76869,gb T21700,gb ATT S5089 come from this gene. [Arabidopsis thaliana]	2E-97		
17907_s_at (AC004684.165_S_AT)	gb AAC23645.1 (AC004684) unknown protein [Arabidopsis thaliana]	4E-24		

[illegible]

ProbeSet	Description	Blast Score	EC #	Family
17930_s_at (AJ006960.4_S_AT)	emb CAA07352.1 (AJ006960) peroxidase [Arabidopsis thaliana]	1E-111		
17945_at (Z97341.411_AT)	emb CAB10448.1 (Z97341) limonene cyclase like protein [Arabidopsis thaliana]	0		
17955_at (AL021768.242_AT)	emb CAA16940.1 (AL021768) small GTP- binding protein-like [Arabidopsis thaliana]	1E-110		
17956_i_at (AC005967.32_I_AT)	gb AAD03381.1 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]	0	EC_3.4.11.1	amino- peptidase
17963_at (AL049730.88_AT)	emb CAB41717.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]	6E-46		
17967_at (AL096859.32_AT)	emb CAB51172.1 (AL096859) protein kinase 6- like protein [Arabidopsis thaliana]	0		
18010_s_at (AJ001264_S_AT)	emb CAA77109.1 (Y18291) uncoupling protein [Arabidopsis thaliana]	1E-175		
18012_s_at (AJ002295_S_AT)	emb CAB59428.1 (AJ002295) inositol-1,4,5-trisphosphate 5- Phosphatase [Arabidopsis thaliana]	0		
18045_at (AJ011976_AT)	emb CAA71798.1 (Y10845) O-acetylserine(thiol) lyase [Brassica juncea]	1E-148		
18054_at (AJ238846_AT)	emb CAB54517.1 (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]	1E-150		
18109_s_at (AC002391.206_S_A T)	gb AAB87118.1 (AC002391) putative metal ion transporter (NRAMP) [Arabidopsis thaliana]	0		
18121_s_at (AC002337.21_S_AT)	gb AAB63819.1 (AC002337) MYB transcription factor (Atmyb2) [Arabidopsis thaliana]	1E-167		

ProbeSet	Description	Blast Score	EC #	Family
18122_at (AC002338.110_AT)	gb AAC16938.1 (AC002338) putative protein kinase [Arabidopsis thaliana]	0		kinase
18140_at (Z97341.319_AT)	emb CAB10440.1 (Z97341) growth regulator like protein [Arabidopsis thaliana]	0		
18148_at (AC004669.25_AT)	gb AAC20719.1 (AC004669) putative dioxygenase [Arabidopsis thaliana]	0		
18176_at (AL035540.31_AT)	emb CAB37503.1 (AL035540) protein kinase like protein [Arabidopsis thaliana]	0		kinase
18194_i_at (AL096859.227_I_A T)	emb CAB51196.1 (AL096859) glucuronosyl transferase-like protein [Arabidopsis thaliana]	0		glucosyl- transferase
18213_at (AL022140.126_AT)	emb CAA18110.1 (AL022140) putative protein [Arabidopsis thaliana]	1E-174		
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_2 2 (AC012375) T22C5.18 [Arabidopsis thaliana]	1E-119		
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_2 2 (AC012375) T22C5.18 [Arabidopsis thaliana]	1E-119		
18224_s_at (AL021890.57_S_AT)	emb CAA17150.1 (AL021890) putative protein [Arabidopsis thaliana]	4E-81		
18226_s_at (AC002343.142_S_A T)	emb CAB51645.1 (AL109619) putative protein [Arabidopsis thaliana]	0		
18228_at (X91259.1_AT)	emb CAA62665.1 (X91259) lectin like protein [Arabidopsis thaliana]	1E-142		
18234_at (AC000348.3_AT)	gb AAB61479.1 (AC000348) T7N9.3 [Arabidopsis thaliana]	1E-154		
18236_s_at (AC004683.69_S_AT)	gb AAC28764.1 (AC004683) putative beta-alanine-pyruvate aminotransferase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
18241_at (AC006580.71_AT)	gb AAD21720.1 (AC006931) putative RNA-binding protein [Arabidopsis thaliana]	0		
18242_g_at (AC006580.71_G_AT)	gb AAD21720.1 (AC006931) putative RNA-binding protein [Arabidopsis thaliana]	0		
18255_at (AC005770.25_AT)	gb AAC79625.1 (AC005770) unknown protein [Arabidopsis thaliana]	0		
18258_s_at (AC006439.222_S_AT)	gb AAD15515.1 (AC006439) unknown protein [Arabidopsis thaliana]	4E-58		
18263_at (AC005724.36_AT)	gb AAD08937.1 (AC005724) unknown protein [Arabidopsis thaliana]	1E-139		
18266_at (AC004684.33_AT)	gb AAC23628.1 (AC004684) unknown protein [Arabidopsis thaliana]	0		
18267_at (AC006223.23_AT)	gb AAD15384.1 (AC006223) unknown protein [Arabidopsis thaliana]	2E-38		
18268_s_at (AC006418.38_S_AT)	gb AAD20161.1 (AC006418) putative ubiquitin [Arabidopsis thaliana]	0		
18280_at (AC007369.2_AT)	gb AAD30591.1 AC007369_1 (AC007369) Unknown protein [Arabidopsis thaliana]	1E-135		
18284_at (AL021961.67_AT)	emb CAA17557.1 (AL021961) putative protein [Arabidopsis thaliana]	6E-97		
18287_at (AC007661.142_AT)	gb AAD32777.1 AC007661_1 4 (AC007661) unknown protein [Arabidopsis thaliana]	0		
18299_s_at (M23872.2_S_AT)	gb AAA32878.1 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]	0		
18314_i_at (AL078579.83_I_AT)	emb CAB43971.1 (AL078579) putative beta- glucosidase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
18348_at (AL022603.104_AT)	emb CAA18711.1 (AL022603) putative protein [Arabidopsis thaliana]	1E-160		
18456_s_at (AC004697.159_S_AT)	gb AAC28997.1 (AC004697) similar to Mlo proteins from H. vulgare [Arabidopsis thaliana]	0		
18508_s_at (AC006532.89_S_AT)	gb AAA33709.1 (L16797) glutamate decarboxylase [Petunia x hybrida]	0		
18544_at (AC007060.14_AT)	gb AAD25749.1 AC007060_7 (AC007060) Strong similarity to F19I3.8 gi 3033381 putative UDP-galactose-4-epimerase from Arabidopsis thaliana BAC gb AC004238 and is a member of PF 01370 the NAD dependent epimerase/dehydratase family. EST gb AA597338 comes fro	0	EC_5.1.3.2	epimerase
18582_s_at (AC003671.36_S_AT)	gb AAC18810.1 (AC003671) Strong similarity to trehalose- 6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb Z97344. ESTs gb H37594, gb R65023, gb H37578 and gb R64855 come from this gene. [Arabidopsis thaliana]	0		
18587_s_at (AC007166.53_S_AT)	gb AAF18667.1 AC007166_9 (AC007166) unknown protein [Arabidopsis thaliana]	0		
18590_at (AJ222713.4_AT)	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]	1E-151		
18591_at (X74756.2_AT)	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana]	2E-99		
18596_at (AC005698.13_AT)	gb AAD43614.1 AC005698_1 3 (AC005698) T3P18.13 [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
18597_at (AL080282.74_AT)	emb CAB45881.1 (AL080282) berberine bridge enzyme-like protein [Arabidopsis thaliana]	0		
18601_s_at (AC002387.279_S_AT)	gb AAF18602.1 AC002387_1 (AC002387) putative microtubule-associated protein [Arabidopsis thaliana]	8E-45		
18604_at (AF069298.31_AT)	gb AAC19273.1 (AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3- acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]	3E-82		
18622_g_at (AJ005902.2_G_AT)	emb CAA06759.1 (AJ005902) vag2 [Arabidopsis thaliana]	3E-47		
18625_at (AC005278.22_AT)	gb AAC72125.1 (AC005278) ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana]	0		
18631_at (AC002510.112_AT)	gb AAB84346.1 (AC002510) unknown protein [Arabidopsis thaliana]	0		
18636_at (AC006577.22_AT)	gb AAD25775.1 AC006577_1 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T75865, gb R30449, gb AI239373, gb F19931 and gb F19930 come from this gene. [Arabidopsis thaliana]	0		
18650_s_at (AF013294.25_S_AT)	gb AAB62867.1 (AF013294) AT0ZII gene product [Arabidopsis thaliana]	3E-41		
18662_s_at (AC002343.20_S_AT)	gb AAB63608.1 (AC002343) unknown protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
18668_at (AJ249794_AT)	emb CAB56692.1 (AJ249794) lipoxygenase [Arabidopsis thaliana]	0		
18681_at (L23573_AT)	gb AAD02548.1 (AF049922) PGP169-12 [Petunia x hybrida]	8E-94		
18686_s_at (U18126_S_AT)	gb AAA57314.1 (U18126) inner mitochondrial membrane protein [Arabidopsis thaliana]	2E-78		
18698_s_at (X17528_S_AT)	emb CAA35570.1 (X17528) citrate synthetase [Arabidopsis thaliana]	0		
18720_s_at (X92419_S_AT)	emb CAB52583.1 (X92420) SNAP25AB protein [Arabidopsis thaliana]	1E-157		
18735_s_at (Z29490_S_AT)	emb CAA82626.1 (Z29490) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]	0		
18753_s_at (AF118222.28_S_AT)	gb AAD03425.1 (AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85, N=1) [Arabidopsis thaliana]	0		
18782_at (AC003040.90_AT)	gb AAC23760.1 (AC003040) putative protein kinase [Arabidopsis thaliana]	0		kinase
18803_at (AC005315.94_AT)	gb AAC33232.1 (AC005315) putative SCARECROW gene regulator [Arabidopsis thaliana]	0		
18885_at (AC006921.147_AT)	gb AAD21443.1 (AC006921) unknown protein [Arabidopsis thaliana]	1E-126		
18888_at (AC007591.68_AT)	gb AAD39666.1 AC007591_3 1 (AC007591) Is a member of the PF 00903 glyoxalase family. ESTs gb T44721, gb T21844 and gb AA395404 come from this gene. [Arabidopsis thaliana]	1E-101		

11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044

ProbeSet	Description	Blast Score	EC #	Family
18899_s_at (X13434.1_S_AT)	emb CAA79494.1 (Z19050) nitrate reductase [Arabidopsis thaliana]	0		
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]	0		protease
18909_s_at (AF055848.2_S_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]	0		
18928_at (AC002333.181_AT)	gb AAB64044.1 (AC002333) putative endochitinase [Arabidopsis thaliana]	1E-157		endo- chitinase
18930_at (AC005990.57_AT)	gb AAC98028.1 (AC005990) Similar to gb L19255 carbonic anhydrase from Nicotiana tabacum and a member of the prokaryotic-type carbonic anhydrase family PF 00484. EST gb Z235745 comes from this gene. [Arabidopsis thaliana]	1E-149		anhydrase
18933_at (AC007020.48_AT)	gb AAD25665.1 AC007020_7 (AC007020) putative ferritin [Arabidopsis thaliana]	1E-129		
18936_at (AJ003119.4_AT)	emb CAA05875.1 (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]	0	EC_3.1.3.16	phosphatase
18949_at (Z54136.1_AT)	emb CAA90809.1 (Z54136) MYB-related protein [Arabidopsis thaliana]	1E-145		
18953_at (AF077955.1_AT)	gb AAC69851.1 (AF077955) branched-chain alpha keto- acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]	0		dehydro- genase
18963_at (AC004561.99_AT)	gb AAC95194.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-127		transferase
18966_at (AC004561.106_AT)	gb AAC95196.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-128		transferase

ProbeSet	Description	Blast Score	EC #	Family
18980_at (U78721.20_AT)	gb AAC69126.1 (U78721) putative protein phosphatase 2C [Arabidopsis thaliana]	0	EC_3.1.3.16	phosphatase
19019_i_at (X82623.2_I_AT)	emb CAA57943.1 (X82623) SRG2At [Arabidopsis thaliana]	7E-33		
19060_at (AC003671.34_AT)	gb AAC18809.1 (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwannomyces occidentalis. [Arabidopsis thaliana]	0		
19092_at (AL078606.188_AT)	emb CAB44327.1 (AL078606) protein kinase- like protein [Arabidopsis thaliana]	0		kinase
19110_s_at (X86947.2_S_AT)	emb CAA60510.1 (X86947) Protein Kinase catalytic domain (fragment) [Arabidopsis thaliana]	4E-27		
19132_s_at (AL022603.298_S_A T)	emb CAA18722.1 (AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]	0		
19137_at (X74755.2_AT)	emb CAA52771.1 (X74755) ATAF1 [Arabidopsis thaliana]	1E-138		
19140_at (AC005170.24_AT)	gb AAC63657.1 (AC005170) unknown protein [Arabidopsis thaliana]	9E-83		
19161_at (AL078579.9_AT)	emb CAB43966.1 (AL078579) putative acyl- CoA binding protein [Arabidopsis thaliana]	0		
19171_at (AC002335.160_AT)	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]	7E-40		
19178_at (Y18227.2_AT)	dbj BAA86999.1 (AB035137) blue copper binding protein [Arabidopsis thaliana]	2E-57		

ProbeSet	Description	Blast Score	EC #	Family
19181_s_at (AF053065.2_S_AT)	gb AAC39464.1 (AF053065) late embryogenesis abundant protein homolog [Arabidopsis thaliana]	3E-34		
19182_at (AL031804.245_AT)	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]	0		
19207_at (AC006069.117_AT)	gb AAD12704.1 (AC006069) unknown protein [Arabidopsis thaliana]	1E-104		
19230_at (AC003113.15_AT)	gb AAB96860.1 (AC003113) F25O1.15 [Arabidopsis thaliana]	1E-134		
19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]	0		
19257_s_at (AC000104.57_S_AT)	emb CAA44318.1 (X62461) H1 flk [Arabidopsis thaliana] [Arabidopsis thaliana]	0		
19284_at (AC003028.196_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]	0		
19288_at (AC005824.130_AT)	gb AAC73031.1 (AC005824) putative cytochrome P450 [Arabidopsis thaliana]	0		
19325_at (AL022604.42_AT)	emb CAA18731.1 (AL022604) putative protein [Arabidopsis thaliana]	0		
19364_at (AL022023.142_AT)	emb CAA17779.1 (AL022023) putative protein [Arabidopsis thaliana]	1E-126		
19376_at (AF024504.11_AT)	gb AAB80784.2 (AF024504) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]	0		peptidase
19383_at (AC006200.203_AT)	gb AAD14534.1 (AC006200) unknown protein [Arabidopsis thaliana]	1E-101		

ProbeSet	Description	Blast Score	EC #	Family
19395_at (AF007270.32_AT)	gb AAB61059.1 (AF007270) contains similarity to DNA polymerase III, alpha chain (SP:P47277) [Arabidopsis thaliana]	1E-179		polymerase
19405_at (AJ223803.1_AT)	emb CAA11553.1 (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit [Arabidopsis thaliana]	0	EC_2.3.1.61	succinyl-transferase
19407_at (AC004697.81_AT)	gb AAC28981.1 (AC004697) putative adenylate kinase [Arabidopsis thaliana]	1E-142	EC_2.7.4.3	kinase
19409_at (AC007357.56_AT)	gb AAD31077.1 AC007357_2 6 (AC007357) EST gb T21221 comes from this gene. [Arabidopsis thaliana]	2E-17		
19411_at (AC007661.104_AT)	gb AAD32774.1 AC007661_1 1 (AC007661) unknown protein [Arabidopsis thaliana]	1E-110		
19421_at (X70990.4_AT)	emb CAA50317.1 (X70990) sucrose synthase [Arabidopsis thaliana]	0		synthase
19432_s_at (AL035680.11_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]	0		
19451_at (AC004392.6_AT)	gb AAC28502.1 (AC004392) Similar to F4I1.26 putative beta-glucosidase gi 3128187 from A. thaliana BAC gb AC004521. ESTs gb N97083, gb F19868 and gb F15482 come from this gene. [Arabidopsis thaliana]	0		glucosidase
19460_s_at (AC000132.66_S_AT)	gb AAB60749.1 (AC000132) Identical to A. thaliana HEMA2 (gb U27118). [Arabidopsis thaliana]	0		
19462_s_at (AF001168.2_S_AT)	emb CAB75467.1 (AL138659) serine/threonine-specific kinase lecRK1 precursor, lectin	0		

ProbeSet	Description	Blast Score	EC #	Family
19464_at (AC005560.51_AT)	gb AAC67338.1 (AC005560) putative MAP kinase [Arabidopsis thaliana]	0	EC_2.7.1.37	kinase
19465_at (AL021768.96_AT)	emb CAA16929.1 (AL021768) resistance protein RPP5-like [Arabidopsis thaliana]	0		
19531_at (AL021960.91_AT)	emb CAA17531.1 (AL021960) amino acid transport protein AAT1 [Arabidopsis thaliana]	0		
19546_at (AC005398.172_AT)	gb AAC69380.1 (AC005398) putative endoxyloglucan glycosyltransferase [Arabidopsis thaliana]	0		transferase
19555_at (AF058919.48_AT)	gb AAC13630.1 (AF058919) F6N23.8 gene product [Arabidopsis thaliana]	0		
19591_at (AJ010735.4_AT)	emb CAA09330.1 (AJ010735) gr1-protein [Arabidopsis thaliana]	0	EC_3.5.-.-	amido- hydrolase
19614_at (AC003970.32_AT)	gb AAC33210.1 (AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi 1143445 [Arabidopsis thaliana]	0		dehydro- genase
19623_at (AF000657.40_AT)	gb AAB72175.1 (AF000657) cytochrome C [Arabidopsis thaliana]	2E-63		
19624_at (AL049481.196_AT)	emb CAB39628.1 (AL049481) cytochrome c [Arabidopsis thaliana]	4E-63		
19625_s_at (AC002311.26_S_AT)	gb AAC00610.1 (AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]	0		
19635_at (AL049746.38_AT)	emb CAB41856.1 (AL049746) ABC-type transport-like protein [Arabidopsis thaliana]	0		
19639_at (AL080252.22_AT)	emb CAB45788.1 (AL080252) putative protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-118		transferase
19641_at (AC004561.66_AT)	gb AAC95189.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-128		transferase
19645_at (AC004561.70_AT)	gb AAC95190.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-130		transferase
19646_s_at (AC005819.55_S_AT)	gb AAC69925.1 (AC005819) homeodomain transcription factor (ATHB-7) [Arabidopsis thaliana]	9E-57		
19655_at (Y14199.1_AT)	emb CAA74591.1 (Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]	0		kinase
19667_at (AL021710.5_AT)	emb CAA16716.1 (AL021710) glycolate oxidase - like protein [Arabidopsis thaliana]	0	EC_1.1.2.3	dehydro- genase
19672_at (AC005687.19_AT)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]	1E-105		
19673_g_at (AC005687.19_G_A T)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]	1E-105		
19700_s_at (AL031326.154_S_A T)	emb CAA20463.1 (AL031326) putative protein [Arabidopsis thaliana]	8E-85		
19701_s_at (AC005724.67_S_AT)	gb AAD08939.1 (AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]	0		
19704_i_at (AJ005927.2_I_AT)	emb CAA06769.1 (AJ005927) squalene epoxidase homologue [Arabidopsis thaliana]	0		epoxidase
19707_s_at (Z95768.3_S_AT)	emb CAB09200.1 (Z95768) R2R3-MYB transcription factor [Arabidopsis thaliana]	4E-21		

ProbeSet	Description	Blast Score	EC #	Family
19741_at (AL049171.72_AT)	emb CAB38956.1 (AL049171) pyrophosphate- dependent phosphofructo-1- kinase [Arabidopsis thaliana]	0		kinase
19755_at (AC006593.64_AT)	gb AAD20668.1 (AC006593) ethylene reponse factor-like AP2 domain transcription factor [Arabidopsis thaliana]	8E-97		
19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]	0		
19818_i_at (AL021749.33_I_AT)	emb CAA16876.2 (AL021749) hypothetical protein [Arabidopsis thaliana]	0		
19819_s_at (AL021749.33_S_AT)	emb CAA16876.2 (AL021749) hypothetical protein [Arabidopsis thaliana]	0		
19844_at (AJ007588.2_AT)	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]	0		mono- oxygenase
19845_g_at (AJ007588.2_G_AT)	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]	0		
19848_s_at (AC004261.94_S_AT)	dbj BAA08282.1 (D45848) calmodulin-related protein [Arabidopsis thaliana]	0		
19851_at (U23794.3_AT)	gb AAB60293.1 (U23794) ILR1 [Arabidopsis thaliana]	0	EC_3.5.-.-	amido- hydrolase
19878_at (AL080252.102_AT)	emb CAB45799.1 (AL080252) nodulin-like protein [Arabidopsis thaliana]	0		
19879_s_at (Z97338.342_S_AT)	emb CAB10321.1 (Z97338) UFD1 like protein [Arabidopsis thaliana]	0		
19881_at (AC004077.49_AT)	gb AAC26705.1 (AC004077) putative trans- prenyltransferase [Arabidopsis thaliana]	1E-154		synthetase

ProbeSet	Description	Blast Score	EC #	Family
19892_at (AC005770.30_AT)	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]	2E-36		protease
19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]	0		dehydro- genase
19895_s_at (U77347.4_S_AT)	gb AAC49679.1 (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]	0		
19916_at (AC006577.34_AT)	gb AAD25781.1 AC006577_1 7 (AC006577) EST gb R64848 comes from this gene. [Arabidopsis thaliana]	0		
19944_at (AC002130.4_AT)	gb AAB95233.1 (AC002130) F1N21.4 [Arabidopsis thaliana]	1E-128		
19946_at (AC004482.14_AT)	gb AAF18611.1 AC005170_1 (AC005170) similar to senescence-associated protein [Arabidopsis thaliana]	4E-92		
19956_at (AC006282.11_AT)	gb AAD20139.1 (AC006282) unknown protein [Arabidopsis thaliana]	1E-123		
19960_at (AL035527.360_AT)	emb CAB36823.1 (AL035527) putative protein [Arabidopsis thaliana]	1E-128		
19970_s_at (AC003674.10_S_AT)	gb AAB97120.1 (AC003674) unknown protein [Arabidopsis thaliana]	1E-154		
19982_at (AC002986.28_AT)	gb AAC17040.1 (AC002986) Similarity to A. thaliana gene product F21M12.20, gb AC000132. EST gb Z25651 comes from this gene. [Arabidopsis thaliana]	0		
19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]	1E-112		

ProbeSet	Description	Blast Score	EC #	Family
20017_at (AC004521.66_AT)	gb AAC16079.1 (AC004521) unknown protein [Arabidopsis thaliana]	1E-101		
20023_at (AC006577.46_AT)	gb AAD25787.1 AC006577_2 3 (AC006577) Similar to gi 1653162 (p)ppGpp 3- pyrophosphohydrolase from Synechocystis sp genome gb D90911. EST gb W43807 comes from this gene. [Arabidopsis thaliana]	0	EC_2.7.6.5	pyro- phospho- kinase
20030_at (AL078637.51_AT)	emb CAB45058.1 (AL078637) putative protein [Arabidopsis thaliana]	1E-168		
20051_at (AC000106.38_AT)	gb AAB70412.1 (AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb Z49209). ESTs gb T44436,gb 42252 come from this gene. [Arabidopsis thaliana]	1E-166		
20053_at (AC002292.27_AT)	gb AAB71973.1 (AC002292) Unknown protein [Arabidopsis thaliana]	0		
20096_at (AC004238.31_AT)	gb AAC12821.1 (AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]	0		
20098_at (AC004697.123_AT)	gb AAC28986.1 (AC004697) similar to latex allergen from Hevea brasiliensis [Arabidopsis thaliana]	0		
20133_i_at (AC007178.71_I_AT)	gb AAD28682.1 AC007178_2 (AC007178) hypothetical protein [Arabidopsis thaliana]	0		
20134_s_at (AC007178.71_S_AT)	gb AAD28682.1 AC007178_2 (AC007178) hypothetical protein [Arabidopsis thaliana]	0		
20142_at (AL035521.155_AT)	emb CAB36716.1 (AL035521) extra-large G- protein-like [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
20144_at (AL079350.68_AT)	emb CAB45516.1 (AL079350) receptor kinase- like protein [Arabidopsis thaliana]	0		kinase
20165_at (AC002311.16_AT)	gb AAC00605.1 (AC002311) Unknown protein [Arabidopsis thaliana]	6E-75		
20179_at (AL035538.229_AT)	emb CAB37546.1 (AL035538) putative protei [Arabidopsis thaliana]	2E-63		
20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]	2E-57		
20194_at (AC007584.48_AT)	gb AAD32907.1 AC007584_5 (AC007584) unknown protein [Arabidopsis thaliana]	0		
20200_at (AL050400.67_AT)	emb CAB43700.1 (AL050400) hypothetical protein [Arabidopsis thaliana]	4E-95		
20215_s_at (AF117125.2_S_AT)	gb AAD29957.1 (AF117125) endoplasmic reticulum-type calcium-transporting ATPase 4 [Arabidopsis thaliana]	0		
20223_at (AL022347.145_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]	0		kinase
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]	0	EC_3.2.1.26	hydrolase
20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]	0		
20245_s_at (AC005309.97_S_AT)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]	0		
20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
20247_at (AC004392.4_AT)	gb AAC28501.1 (AC004392) Similar to beta-glucosidase BGQ60 precursor gb L41869 from <i>Hordeum vulgare</i> . [<i>Arabidopsis thaliana</i>]	0	EC_3.2.1.21	glucosidase
20258_at (AF130252.1_AT)	gb AAD28759.1 AF130252_1 (AF130252) calcium dependent protein kinase CP4 [<i>Arabidopsis thaliana</i>]	0		kinase
20262_at (AC002294.26_AT)	gb AAB71480.1 (AC002294) Similar to transcription factor gb Z46606 1658307 and others [<i>Arabidopsis thaliana</i>]	0		
20263_at (AB004798.1_AT)	dbj BAA20519.1 (AB004798) ascorbate oxidase [<i>Arabidopsis thaliana</i>]	0		oxidase
20269_at (AC002387.237_AT)	gb AAB82640.1 (AC002387) putative pectinesterase [<i>Arabidopsis thaliana</i>]	0		pectin- esterase
20271_at (Z99707.27_AT)	emb CAB16771.1 (Z99707) cytochrome P450-like protein [<i>Arabidopsis thaliana</i>]	0		
20285_s_at (AC003674.18_S_AT)	gb AAB97121.1 (AC003674) putative protein kinase [<i>Arabidopsis thaliana</i>]	0		
20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [<i>Arabidopsis thaliana</i>]	1E-166		chitinase
20288_g_at (Y14590.5_G_AT)	emb CAA74930.1 (Y14590) class IV chitinase [<i>Arabidopsis thaliana</i>]	1E-166		
20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [<i>Arabidopsis thaliana</i>]	0		
20297_at (AC007153.27_AT)	gb AAD30627.1 AC007153_1 9 (AC007153) Similar to indole-3-acetate beta- glucosyltransferase [<i>Arabidopsis thaliana</i>]	0		glucosyl- transferase
20323_at (AC004561.62_AT)	gb AAC95188.1 (AC004561) putative small heat shock protein [<i>Arabidopsis thaliana</i>]	1E-67		

ProbeSet	Description	Blast Score	EC #	Family
20346_at (AL031135.156_AT)	emb CAA20030.1 (AL031135) protein kinase - like protein [Arabidopsis thaliana]	0		
20348_at (AC005967.35_AT)	gb AAD03382.1 (AC005967) putative limonene cyclase [Arabidopsis thaliana]	0		cyclase
20356_at (AC004561.74_AT)	gb AAC95191.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	1E-128		transferase
20365_s_at (AC005850.19_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana]	0		
20370_at (AC004561.263_AT)	gb AAC95219.1 (AC004561) putative tropinone reductase [Arabidopsis thaliana]	1E-151		reductase
20382_s_at (AC002338.35_S_AT)	gb AAC16930.1 (AC002338) putative WRKY-type DNA binding protein [Arabidopsis thaliana]	0		
20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]	0		chitinase
20421_at (U81294.2_AT)	emb CAB10242.1 (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]	8E-98		
20422_g_at (U81294.2_G_AT)	emb CAB10242.1 (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]	8E-98		
20432_at (U43486.2_AT)	gb AAB18365.1 (U43486) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]	1E-174		trans- glycosylase
20433_at (AC006232.147_AT)	gb AAD15611.1 (AC006232) putative beta-1,3-glucanase [Arabidopsis thaliana]	0		glucanase
20450_at (AJ005930.2_AT)	emb CAA06772.1 (AJ005930) squalene epoxidase homologue [Arabidopsis thaliana]	0		epoxidase

ProbeSet	Description	Blast Score	EC #	Family
20461_at (AL049480.157_AT)	emb CAB39609.1 (AL049480) pumilio-like protein [Arabidopsis thaliana]	0		
20462_at (U82399.2_AT)	gb AAB40725.1 (U82399) putative protein kinase PK1 [Arabidopsis thaliana]	3E-38		kinase
20479_i_at (AF069495.2_I_AT)	emb CAB38908.1 (AL035708) cytochrome P450-like protein [Arabidopsis thaliana]	0		
20480_s_at (AF069495.2_S_AT)	emb CAB38908.1 (AL035708) cytochrome P450-like protein [Arabidopsis thaliana]	0		
20485_at (AC007660.131_AT)	gb AAD32811.1 AC007660_1 2 (AC007660) putative two- component response regulator protein [Arabidopsis thaliana]	1E-80		
20491_at (AC004561.146_AT)	gb AAC95203.1 (AC004561) putative tropinone reductase [Arabidopsis thaliana]	1E-153	EC_1.1.1.10 0	reductase
20511_at (AC007290.24_AT)	gb AAD26884.1 AC007290_3 (AC007290) putative nucleotide-binding protein [Arabidopsis thaliana]	0		
20517_at (Y17722.7_AT)	emb CAB50690.1 (Y17722) telomere repeat-binding protein TRP1 [Arabidopsis thaliana]	0		
20529_at (Z97341.125_AT)	emb CAB10426.1 (Z97341) cysteine proteinase inhibitor like protein [Arabidopsis thaliana]	7E-35		
20551_at (AC006081.211_AT)	gb AAD24395.1 AC006081_7 (AC006081) unknown protein [Arabidopsis thaliana]	0		
20572_s_at (AC005560.229_S_A T)	gb AAD12710.1 (AC006069) unknown protein [Arabidopsis thaliana]	1E-114		
20577_at (AL078464.72_AT)	emb CAB43841.1 (AL078464) putative protein [Arabidopsis thaliana]	0		

ProbeSet	Description	Blast Score	EC #	Family
20584_at (AC004450.75_AT)	gb AAC64305.1 (AC004450) putative clathrin binding protein (epsin) [Arabidopsis thaliana]	2E-92		
20586_i_at (AC005824.195_I_A T)	gb AAC73042.1 (AC005824) unknown protein [Arabidopsis thaliana]	2E-67		
20587_s_at (AC005824.195_S_A T)	gb AAC73042.1 (AC005824) unknown protein [Arabidopsis thaliana]	2E-67		
20589_at (AF081066.3_AT)	gb AAC31939.1 (AF081066) IAA-amino acid hydrolase homolog ILL3 [Arabidopsis thaliana]	0		hydrolase
20591_at (AL080252.115_AT)	emb CAB45800.1 (AL080252) nodulin-like protein [Arabidopsis thaliana]	0		
20646_at (AC002291.20_AT)	gb AAC00619.1 (AC002291) Unknown protein [Arabidopsis thaliana]	0		
20656_at (AL035396.46_AT)	emb CAA23064.1 (AL035396) putative protein [Arabidopsis thaliana]	0		
20658_s_at (AL050400.70_S_AT)	emb CAB43701.1 (AL050400) beta-carotene hydroxylase [Arabidopsis thaliana]	1E-165		
20669_s_at (AC002388.6_S_AT)	gb AAD32838.1 AC007659_2 0 (AC007659) unknown protein [Arabidopsis thaliana]	0		
20685_at (AL049751.46_AT)	emb CAB41928.1 (AL049751) short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana]	1E-139	EC_1.1.1.-	dehydro- genase
20686_at (Y14424.2_AT)	emb CAA74766.1 (Y14424) hypothetical protein [Arabidopsis thaliana]	0		
20689_s_at (AC002335.19_S_AT)	gb AAB64310.1 (AC002335) putative calcium binding protein [Arabidopsis thaliana]	6E-95		
20715_at (AF079183.1_AT)	gb AAC69857.1 (AF079183) RING-H2 finger protein RHG1a [Arabidopsis thaliana]	4E-99		

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Table 4a Probe Sets in addition to those in Table 4b corresponding to genes, the expression of which is induced by *Pseudomonas* infection in wild-type *Arabidopsis* plants and perturbed in at least one mutant plant

ProbeSet	Description	Blast Score
13716_at (NOVARTIS103_RC_AT)	emb CAA62665.1 (X91259) lectin like protein [<i>Arabidopsis thaliana</i>]	6E-70
13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [<i>Arabidopsis thaliana</i>]	2E-27
13755_at (NOVARTIS15_AT)	emb CAA16797.1 (AL021713) receptor serine/threonine kinase-like protein [<i>Arabidopsis thaliana</i>]	1E-114
13763_at (NOVARTIS21_AT)	gb AAF24849.1 AC012679_20 (AC012679) putative calmodulin-binding protein [<i>Arabidopsis thaliana</i>]	1E-105
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [<i>Arabidopsis thaliana</i>]	2E-30
14139_at (NOVARTIS30_AT)	gb AAD09343.1 (AF026538) ABA-responsive protein [<i>Hordeum vulgare</i>]	7E-36
14148_at (NOVARTIS38_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [<i>Arabidopsis thaliana</i>]	4E-53
14170_at (NOVARTIS51_AT)	gb AAF29406.1 AC022354_5 (AC022354) unknown protein [<i>Arabidopsis thaliana</i>]	9E-26
14197_at (NOVARTIS71_AT)	No hits found.	
14214_at (NOVARTIS83_AT)	gb AAF24849.1 AC012679_20 (AC012679) putative calmodulin-binding protein [<i>Arabidopsis thaliana</i>]	2E-92
14223_at (NOVARTIS9_AT)	emb CAA19683.1 (AL024486) putative protein [<i>Arabidopsis thaliana</i>]	0

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Table 4b Probe Sets as referred to in Table 3 corresponding to genes, the expression of which is induced by *Pseudomonas* infection in wild-type *Arabidopsis* plants and perturbed in at least one mutant plant

10

11997_at (AC005967.4_AT)	12004_at (AL022023.132_AT)
12007_at (Z99708.249_AT)	12037_at (AC004005.174_AT)
12072_at (AL035396.4_AT)	12079_s_at (A71597.1_S_AT)
12081_at (AC001645.140_AT)	12115_at (AL033545.26_AT)
12136_at (AC007591.60_AT)	12150_at (AC004005.151_AT)
12198_at (AC006954.90_AT)	12216_at (AC007119.56_AT)

12233_at (AJ001807.1_AT)	12307_at (AC002392.162_AT)
12314_at (AC001229.28_AT)	12317_at (AC004138.27_AT)
12323_at (AC002333.18_AT)	12332_s_at (AB023448.2_S_AT)
12341_s_at (AL021637.176_S_AT)	12349_s_at (X84728.6_S_AT)
12369_at (AC002535.59_AT)	12400_at (X98453.1_AT)
12438_at (AL021710.83_AT)	12449_s_at (AC002343.179_S_AT)
12454_at (AC006232.164_AT)	12475_at (Y11794.1_AT)
12487_at (AC004411.126_AT)	12497_at (AC006533.51_AT)
12500_s_at (AF081067.3_S_AT)	12525_at (AC006587.85_AT)
12530_at (Z99707.184_AT)	12535_at (AL035538.156_AT)
12538_at (AF033205.2_AT)	12574_at (X82624.2_AT)
12584_at (AC004521.233_AT)	12626_at (AC006234.95_AT)
12645_at (AL021712.56_AT)	12712_f_at (Z95774_F_AT)
12736_f_at (Z97048_F_AT)	12744_at (AC001645.15_AT)
12760_g_at (AC005278.32_G_AT)	12764_f_at (AC004138.69_F_AT)
12772_at (AC005278.34_AT)	12797_s_at (AC007138.25_S_AT)
12851_s_at (ACCSYN1_S_AT)	12879_s_at (AIG1_S_AT)
12880_s_at (AIG2_S_AT)	12883_s_at (APX_S_AT)
12889_s_at (ASA1_S_AT)	12891_at (ATACS6_AT)
12892_g_at (ATACS6_G_AT)	12904_s_at (ATERF1_S_AT)
12905_s_at (ATERF2_S_AT)	12911_s_at (ATG6PDHE5_S_AT)
12921_s_at (ATHHMGCOAR_S_AT)	12951_at (AC005489.5_AT)
12958_at (AC002332.249_AT)	12965_at (AL021711.118_AT)
12966_s_at (AL023094.197_S_AT)	12989_s_at (AC004077.149_S_AT)
13003_s_at (AB021936.1_S_AT)	13014_at (U93215.87_AT)
13040_at (AC002392.134_AT)	13070_at (AC006919.171_AT)
13094_at (AL035523.163_AT)	13134_s_at (AC002337.9_S_AT)
13152_s_at (AC005322.24_S_AT)	13154_s_at (AC002333.210_S_AT)
13157_at (AC002409.35_AT)	13176_at (AL031394.56_AT)
13177_at (AL049640.42_AT)	13190_s_at (ATTHIREDA_S_AT)
13211_s_at (BCHI_S_AT)	13212_s_at (BGL2_S_AT)
13215_s_at (cafferoylcoamethyltrans_S_AT)	13219_s_at (CHI4_S_AT)
13243_r_at (ELI32_R_AT)	13244_s_at (ELI32_S_AT)
13255_i_at (gammaglutamyltranspepti_I_AT)	13266_s_at (GST4_S_AT)
13273_s_at (HSF4_S_AT)	13275_f_at (HSP174_F_AT)
13277_i_at (HSP176A_I_AT)	13285_s_at (HSP83_S_AT)

13312_at (AC006223.75_AT)	13370_at (AC005322.4_AT)
13381_at (AC006580.8_AT)	13395_at (AL035528.202_AT)
13435_at (AF003102.3_AT)	13437_at (AF096371.8_AT)
13467_at (AL096860.198_AT)	13536_at (AL021636.47_AT)
13538_at (AL080254.75_AT)	13565_at (AL035601.21_AT)
13588_at (AL021961.24_AT)	13589_at (AC000132.24_AT)
13617_at (AC006592.64_AT)	13627_at (AL035394.196_AT)
13645_at (AC000098.8_AT)	13656_at (AC007138.31_AT)
13659_at (AL022347.46_AT)	13666_s_at (INDOLE3GPS_S_AT)
13680_s_at (LOX1_S_AT)	13685_s_at (MLOLIKE2_S_AT)
13688_s_at (MONOPTEROS_S_AT)	13697_at (NI16_AT)
13705_s_at (AC003671X_S_AT)	13789_at (AJ132436.2_AT)
13803_at (Z97341.376_AT)	13818_s_at (AC006218.175_S_AT)
13842_at (AC002396.12_AT)	13848_at (AC003981.31_AT)
13880_s_at (AL049480.183_S_AT)	13908_s_at (A71590.1_S_AT)
13918_at (AC005388.29_AT)	13920_at (AC005990.53_AT)
13949_s_at (Z97343.352_S_AT)	13963_at (AL021711.26_AT)
13999_at (AF071527.56_AT)	14015_s_at (A71588.1_S_AT)
14016_s_at (A71596.1_S_AT)	14025_s_at (AC007293.3_S_AT)
14030_at (AC005970.225_AT)	14032_at (AL035601.11_AT)
14041_at (AC003970.28_AT)	14052_at (AC004122.24_AT)
14068_s_at (AC006922.197_S_AT)	14070_at (AL049658.217_AT)
14089_at (AC006223.65_AT)	14100_at (AF002109.108_AT)
14110_i_at (AL035528.279_I_AT)	14240_s_at (NR1_S_AT)
14242_s_at (NRA_S_AT)	14248_at (PAD3_AT)
14249_i_at (PAD4_I_AT)	14254_s_at (PAL1-MRNA_S_AT)
14256_f_at (PAL1-INTRON_F_AT)	14320_at (AC005956.54_AT)
14408_at (AC002291.14_AT)	14448_at (AC002387.243_AT)
14450_at (AC002986.49_AT)	14461_at (AC006202.73_AT)
14468_at (AC007576.62_AT)	14475_at (AL021811.121_AT)
14487_at (Z97341.343_AT)	14584_at (AC007658.25_AT)
14609_at (AC002340.147_AT)	14620_s_at (PAT1_S_AT)
14635_s_at (PR.1_S_AT)	14638_s_at (PRXCB_S_AT)
14640_s_at (putativemloHI_S_AT)	14643_s_at (RAR047_S_AT)
14663_s_at (trehalaseprecursor_RC_S_AT)	14667_s_at (TRPB_S_AT)
14672_s_at (TSA1_S_AT)	14673_s_at (TSB2_S_AT)

15839_at (AC005662.203_AT)	15859_at (AC006587.164_AT)
15866_s_at (AC007133.59_S_AT)	15874_at (AL022223.106_AT)
15886_at (AL078637.204_AT)	15919_at (AC007060.42_AT)
15921_s_at (AC007067.1_S_AT)	15924_at (AC007138.61_AT)
15970_s_at (X71794.2_S_AT)	15978_at (X68592.6_AT)
15982_s_at (AC006260.78_S_AT)	16001_at (AF035385.2_AT)
16003_s_at (AL021749.64_S_AT)	16021_s_at (AL022224.182_S_AT)
16031_at (X94248.1_AT)	16043_at (AC005489.17_AT)
16053_i_at (Y14251.4_I_AT)	16063_s_at (AB008103_S_AT)
16073_f_at (AF062908_F_AT)	16083_s_at (AF153283_S_AT)
16091_s_at (ATHHSP83_S_AT)	16103_s_at (ATU60445_S_AT)
16105_s_at (ATU68017_S_AT)	16108_s_at (D78604_S_AT)
16130_s_at (AF078683_S_AT)	16173_s_at (D78607_S_AT)
16203_at (AC007519.53_AT)	16232_s_at (AL080252.77_S_AT)
16233_at (AL080254.83_AT)	16272_at (AC006304.136_AT)
16298_at (AL021890.71_AT)	16299_at (AL024486.185_AT)
16301_s_at (AL031018.105_S_AT)	16306_at (AL049751.112_AT)
16335_at (AL079347.105_AT)	16340_at (AC004255.15_AT)
16357_at (AF149413.38_AT)	16363_at (AC004255.14_AT)
16383_at (AC006300.64_AT)	16398_s_at (AL022603.3_S_AT)
16405_at (AC005850.9_AT)	16409_at (AC004393.2_AT)
16440_s_at (AF002109.137_S_AT)	16461_i_at (AC004683.79_I_AT)
16462_s_at (AC004683.79_S_AT)	16465_at (Y08892.1_AT)
16470_s_at (AF068299.4_S_AT)	16510_at (AL034567.198_AT)
16522_at (X77500.2_AT)	16526_at (Z49227.1_AT)
16541_s_at (AB023423_S_AT)	16545_s_at (AF037229_S_AT)
16553_f_at (AF078821_F_AT)	16570_s_at (ATHCDPKA_S_AT)
16578_s_at (ATHRPRP1B_S_AT)	16589_s_at (ATU26937_S_AT)
16594_s_at (ATU39783_S_AT)	16603_s_at (ATU81293_S_AT)
16609_s_at (AB008104_S_AT)	16611_s_at (AB008782_S_AT)
16638_s_at (AF139098_S_AT)	16646_s_at (ATHDHS1_S_AT)
16649_s_at (ATHORF_S_AT)	16701_at (AC005312.61_AT)
16721_at (AC006533.58_AT)	16747_at (AL021713.3_AT)
16781_at (AC002392.100_AT)	16810_at (AC002339.46_AT)
16859_at (AL035523.135_AT)	16864_i_at (AF037367.4_I_AT)
16865_s_at (AF037367.4_S_AT)	16888_s_at (AC004684.174_S_AT)

16914_s_at (AL049500.57_S_AT)	16916_s_at (X77199.8_S_AT)
16968_at (AL021961.93_AT)	16989_at (AL030978.46_AT)
16995_at (AC002391.188_AT)	17007_at (AC005896.26_AT)
17008_at (AC006585.212_AT)	17039_s_at (D78602_S_AT)
17041_s_at (D89631_S_AT)	17051_s_at (AF098947_S_AT)
17066_s_at (ATHLIPOXY_S_AT)	17073_s_at (ATTS4391_S_AT)
17075_s_at (ATU09961_S_AT)	17104_s_at (D88541_S_AT)
17111_s_at (ATHACSC_S_AT)	17119_s_at (AF132212_S_AT)
17128_s_at (ATHRPRP1A_S_AT)	17180_at (AF007270.30_AT)
17187_at (AF128396.2_AT)	17300_at (X66017.2_AT)
17303_s_at (AC004683.25_S_AT)	17323_at (U95973.69_AT)
17338_at (AC002535.97_AT)	17341_at (AL021713.89_AT)
17356_s_at (Z97338.190_S_AT)	17371_at (AF076243.44_AT)
17379_at (AF085279.9_AT)	17413_s_at (AJ006961.4_S_AT)
17451_at (AC002343.47_AT)	17452_g_at (AC002343.47_G_AT)
17484_at (X79052.2_AT)	17485_s_at (Z97340.345_S_AT)
17487_s_at (U18993.2_S_AT)	17511_s_at (AF067605_S_AT)
17514_s_at (AF076277_S_AT)	17522_s_at (D78606_S_AT)
17533_s_at (ATU43488_S_AT)	17544_s_at (ATU40856_S_AT)
17548_s_at (AF118823_S_AT)	17585_s_at (AF134487_S_AT)
17595_s_at (AF166352_S_AT)	17648_at (AL021684.43_AT)
17653_at (AL035679.144_AT)	17702_at (AC005700.212_AT)
17719_at (AC006592.17_AT)	17752_at (AC003974.37_AT)
17758_at (AF076243.41_AT)	17775_at (AC004392.2_AT)
17781_at (AL049746.177_AT)	17840_s_at (AC002333.223_S_AT)
17860_at (AL078467.4_AT)	17876_at (AJ007587.2_AT)
17877_g_at (AJ007587.2_G_AT)	17893_at (AC004401.135_AT)
17899_at (Z97339.197_AT)	17930_s_at (AJ006960.4_S_AT)
17945_at (Z97341.411_AT)	17963_at (AL049730.88_AT)
18012_s_at (AJ002295_S_AT)	18054_at (AJ238846_AT)
18109_s_at (AC002391.206_S_AT)	18121_s_at (AC002337.21_S_AT)
18122_at (AC002338.110_AT)	18148_at (AC004669.25_AT)
18176_at (AL035540.31_AT)	18194_i_at (AL096859.227_I_AT)
18213_at (AL022140.126_AT)	18224_s_at (AL021890.57_S_AT)
18228_at (X91259.1_AT)	18236_s_at (AC004683.69_S_AT)
18242_g_at (AC006580.71_G_AT)	18255_at (AC005770.25_AT)

18258_s_at (AC006439.222_S_AT)
 18266_at (AC004684.33_AT)
 18299_s_at (M23872.2_S_AT)
 18508_s_at (AC006532.89_S_AT)
 18582_s_at (AC003671.36_S_AT)
 18590_at (AJ222713.4_AT)
 18596_at (AC005698.13_AT)
 18604_at (AF069298.31_AT)
 18625_at (AC005278.22_AT)
 18636_at (AC006577.22_AT)
 18686_s_at (U18126_S_AT)
 18735_s_at (Z29490_S_AT)
 18782_at (AC003040.90_AT)
 18885_at (AC006921.147_AT)
 18899_s_at (X13434.1_S_AT)
 18909_s_at (AF055848.2_S_AT)
 18930_at (AC005990.57_AT)
 18949_at (Z54136.1_AT)
 18963_at (AC004561.99_AT)
 19019_i_at (X82623.2_I_AT)
 19092_at (AL078606.188_AT)
 19137_at (X74755.2_AT)
 19181_s_at (AF053065.2_S_AT)
 19247_at (AF071527.44_AT)
 19284_at (AC003028.196_AT)
 19325_at (AL022604.42_AT)
 19383_at (AC006200.203_AT)
 19405_at (AJ223803.1_AT)
 19409_at (AC007357.56_AT)
 19421_at (X70990.4_AT)
 19451_at (AC004392.6_AT)
 19465_at (AL021768.96_AT)
 19555_at (AF058919.48_AT)
 19614_at (AC003970.32_AT)
 19625_s_at (AC002311.26_S_AT)
 19640_at (AC004561.78_AT)

18263_at (AC005724.36_AT)
 18267_at (AC006223.23_AT)
 18456_s_at (AC004697.159_S_AT)
 18544_at (AC007060.14_AT)
 18587_s_at (AC007166.53_S_AT)
 18591_at (X74756.2_AT)
 18597_at (AL080282.74_AT)
 18622_g_at (AJ005902.2_G_AT)
 18631_at (AC002510.112_AT)
 18668_at (AJ249794_AT)
 18698_s_at (X17528_S_AT)
 18753_s_at (AF118222.28_S_AT)
 18803_at (AC005315.94_AT)
 18888_at (AC007591.68_AT)
 18908_i_at (AF055848.2_I_AT)
 18928_at (AC002333.181_AT)
 18933_at (AC007020.48_AT)
 18953_at (AF077955.1_AT)
 18966_at (AC004561.106_AT)
 19060_at (AC003671.34_AT)
 19110_s_at (X86947.2_S_AT)
 19140_at (AC005170.24_AT)
 19207_at (AC006069.117_AT)
 19257_s_at (AC000104.57_S_AT)
 19288_at (AC005824.130_AT)
 19364_at (AL022023.142_AT)
 19395_at (AF007270.32_AT)
 19407_at (AC004697.81_AT)
 19411_at (AC007661.104_AT)
 19432_s_at (AL035680.11_S_AT)
 19460_s_at (AC000132.66_S_AT)
 19546_at (AC005398.172_AT)
 19591_at (AJ010735.4_AT)
 19624_at (AL049481.196_AT)
 19635_at (AL049746.38_AT)
 19641_at (AC004561.66_AT)

20685_at (AL049751.46_AT)
20689_s_at (AC002335.19_S_AT)

20686_at (Y14424.2_AT)

0968727.06201

Table 5 Probe Sets as referred to in Tables 4a and 4b corresponding to genes encoding regulatory proteins, the expression of which is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis*, with *Pseudomonas syringae*

ProbeSet	Regulatory factor
12497_at (AC006533.51_AT)	putative receptor-like protein kinase
16409_at (AC004393.2_AT)	putative receptor-like kinase
12307_at (AC002392.162_AT)	putative receptor-like protein kinase
13659_at (AL022347.46_AT)	serine/threonine kinase-like protein
17341_at (AL021713.89_AT)	receptor serine/threonine kinase-like protein
12958_at (AC002332.249_AT)	putative protein kinase
17758_at (AF076243.41_AT)	putative receptor-like protein kinase
16570_s_at (ATHCDPKA_S_AT)	CDPK1 calcium dependent protein kinase 1
19092_at (AL078606.188_AT)	protein kinase-like protein
17371_at (AF076243.44_AT)	putative receptor-like protein kinase
20223_at (AL022347.145_AT)	putative ser/thr protein kinase
19655_at (Y14199.1_AT)	MAP3K delta-1 protein kinase
14030_at (AC005970.225_AT)	putative protein kinase
20462_at (U82399.2_AT)	putative protein kinase PK1
16781_at (AC002392.100_AT)	putative receptor-like protein kinase
14763_at (X86958.1_AT)	protein kinase catalytic domain (fragment)
17752_at (AC003974.37_AT)	putative protein kinase
13755_at (NOVARTIS15_AT)	putative ser/thr kinase
13370_at (AC005322.4_AT)	similar to Dsor1 protein kinase
20144_at (AL079350.68_AT)	receptor kinase-like protein
16357_at (AF149413.38_AT)	putative protein kinase
18176_at (AL035540.31_AT)	putative protein kinase
15798_at (AC002521.173_AT)	putative receptor-like protein kinase
12965_at (AL021711.118_AT)	protein kinase-like protein
16398_s_at (AL022603.3_S_AT)	putative ser/thr protein kinase
18122_at (AC002338.110_AT)	putative protein kinase
17323_at (U95973.69_AT)	putative ser/thr protein kinase
18782_at (AC003040.90_AT)	putative protein kinase
16405_at (AC005850.9_AT)	putative serine/threonine protein kinase

ProbeSet	Regulatory factor
14110_i_at (AL035528.279_I_AT)	putative R protein. Like Hcr9-9A, Lycopersicon pimpinellifolium F18A5_290 chr.4
14214_at (NOVARTIS83_AT)	putative calmodulin-binding protein (duplicate)
13763_at (NOVARTIS21_AT)	putative calmodulin-binding protein (duplicate)
12438_at (AL021710.83_AT)	membrane-bound small GTP-binding - like protein
19848_s_at (AC004261.94_S_AT)	calmodulin-related protein
16103_s_at (ATU60445_S_AT)	GRF7 general regulatory factor encoding 14-3-3 protein
14249_i_at (PAD4_I_AT)	PAD4 phytoalexin deficient 4
19465_at (AL021768.96_AT)	RPP5-like NBS-LRR resistance protein
14640_s_at (putativemloHI_S_AT)	Mlo-like (duplicate)
18456_s_at (AC004697.159_S_AT)	Mlo-like (duplicate)
14320_at (AC005956.54_AT)	putative RING zinc finger protein
18054_at (AJ238846_AT)	SGP1 monomeric G-protein
16130_s_at (AF078683_S_AT)	RHA1a RING-H2 finger protein
20485_at (AC007660.131_AT)	putative two-component response regulator protein
15052_at (AC002332.103_AT)	putative calcium-binding EF-hand protein
15632_s_at (AB012570_S_AT)	ATHP3 two-compoent phosphorelay mediator with a single HPt domain
16553_f_at (AF078821_F_AT)	RHA1b RING-H2 finger protein
13685_s_at (MLOLIKE2_S_AT)	Mlo-like 2 (duplicate)
20365_s_at (AC005850.19_S_AT)	Mlo-like 2 (duplicate)
13312_at (AC006223.75_AT)	putative disease resistance protein
17180_at (AF007270.30_AT)	similar to GATA-type zinc fingers
15779_g_at (X98676.2_G_AT)	zinc finger protein (duplicate)
15778_at (X98676.2_AT)	zinc finger protein (duplicate)
14711_s_at (ZFPL_S_AT)	hypothetical Cys-3-His zinc finger protein
17379_at (AF085279.9_AT)	putative CCCH-type zinc finger protein
12525_at (AC006587.85_AT)	putative DOF zinc finger protein
16589_s_at (ATU26937_S_AT)	AtMYB7 transcription factor
12712_f_at (Z95774_F_AT)	AtMYB51 R2R3 myb transcription factor
13273_s_at (HSF4_S_AT)	HSF4 heat shock transcription factor 4 (duplicate)
16105_s_at (ATU68017_S_AT)	HSF4 heat shock transcription factor 4 (duplicate)
18803_at (AC005315.94_AT)	putative SCARECROW homeobox gene regulator

ProbeSet	Regulatory factor
12905_s_at (ATERF2_S_AT)	EREBP2 ethylene responsive element binding factor 2 (duplicate)
16609_s_at (AB008104_S_AT)	EREBP2 ethylene responsive element binding factor 2 (duplicate)
19755_at (AC006593.64_AT)	ethylene reponse factor-like AP2 domain transcription factor
17514_s_at (AF076277_S_AT)	ERF1 ethylene response factor 1 transcription factor
18121_s_at (AC002337.21_S_AT)	AtMYB2 MYB transcription factor
13688_s_at (monopteros_S_AT)	transcription factor
12904_s_at (ATERF1_S_AT)	EREBP1 ethylene responsive element binding factor 1 (duplicate)
16063_s_at (AB008103_S_AT)	EREBP1 ethylene responsive element binding factor 1 (duplicate)
16638_s_at (AF139098_S_AT)	putative zinc finger protein
16545_s_at (AF037229_S_AT)	transcription factor
13435_at (AF003102.3_AT)	RAP2.9 AP2 domain containing putative transcription factor
15665_s_at (AF022658_S_AT)	putative c2h2 zinc finger transcription factor
19673_g_at (AC005687.19_G_AT)	RAP2.6 AP2 domain containing putative transcription factor (duplicate)
19672_at (AC005687.19_AT)	RAP2.6 AP2 domain containing putative transcription factor (duplicate)
14780_at (AC004683.103_AT)	DREB-like AP2 domain transcription factor
17303_s_at (AC004683.25_S_AT)	WRKY33 transcription factor
18949_at (Z54136.1_AT)	MYB-related protein
19707_s_at (Z95768.3_S_AT)	AtMYB44 transcription factor
16073_f_at (AF062908_F_AT)	putative transcription factor
12966_s_at (AL023094.197_S_AT)	ATB2 bZIP transcription factor
12736_f_at (Z97048_F_AT)	AtMYB13 transcription factor

Table 6 Probe Sets as referred to in Tables 4a and 4b corresponding to genes, the expression of which is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis* having a mutation that results in enhanced susceptibility to *Pseudomonas*

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12079_s_at (A71597.1_S_AT)	12081_at (AC001645.140_AT)
12115_at (AL033545.26_AT)	12150_at (AC004005.151_AT)
12233_at (AJ001807.1_AT)	12307_at (AC002392.162_AT)
12314_at (AC001229.28_AT)	12332_s_at (AB023448.2_S_AT)
12341_s_at (AL021637.176_S_AT)	12400_at (X98453.1_AT)
12438_at (AL021710.83_AT)	12475_at (Y11794.1_AT)
12487_at (AC004411.126_AT)	12497_at (AC006533.51_AT)
12500_s_at (AF081067.3_S_AT)	12530_at (Z99707.184_AT)
12574_at (X82624.2_AT)	12584_at (AC004521.233_AT)
12712_f_at (Z95774_F_AT)	12760_g_at (AC005278.32_G_AT)
12764_f_at (AC004138.69_F_AT)	12772_at (AC005278.34_AT)
12851_s_at (ACCSYN1_S_AT)	12879_s_at (AIG1_S_AT)
12883_s_at (APX_S_AT)	12889_s_at (ASA1_S_AT)
12891_at (ATACS6_AT)	12892_g_at (ATACS6_G_AT)
12905_s_at (ATERF2_S_AT)	12911_s_at (ATG6PDHE5_S_AT)
12921_s_at (ATHHMGCOAR_S_AT)	12958_at (AC002332.249_AT)
12989_s_at (AC004077.149_S_AT)	13003_s_at (AB021936.1_S_AT)
13014_at (U93215.87_AT)	13040_at (AC002392.134_AT)
13070_at (AC006919.171_AT)	13094_at (AL035523.163_AT)
13157_at (AC002409.35_AT)	13177_at (AL049640.42_AT)
13190_s_at (ATTHIREDA_S_AT)	13211_s_at (BCHI_S_AT)
13212_s_at (BGL2_S_AT)	13219_s_at (CHI4_S_AT)
13266_s_at (GST4_S_AT)	13273_s_at (HSF4_S_AT)
13275_f_at (HSP174_F_AT)	13370_at (AC005322.4_AT)
13381_at (AC006580.8_AT)	13435_at (AF003102.3_AT)
13467_at (AL096860.198_AT)	13538_at (AL080254.75_AT)
13565_at (AL035601.21_AT)	13588_at (AL021961.24_AT)
13589_at (AC000132.24_AT)	13617_at (AC006592.64_AT)
13627_at (AL035394.196_AT)	13656_at (AC007138.31_AT)
13659_at (AL022347.46_AT)	13666_s_at (INDOLE3GPS_S_AT)
13680_s_at (LOX1_S_AT)	13688_s_at (MONOPTEROS_S_AT)

13697_at (NI16_AT)
 13751_at (NOVARTIS127_AT)
 13763_at (NOVARTIS21_AT)
 13818_s_at (AC006218.175_S_AT)
 13880_s_at (AL049480.183_S_AT)
 14015_s_at (A71588.1_S_AT)
 14025_s_at (AC007293.3_S_AT)
 14032_at (AL035601.11_AT)
 14052_at (AC004122.24_AT)
 14110_i_at (AL035528.279_I_AT)
 14148_at (NOVARTIS38_AT)
 14214_at (NOVARTIS83_AT)
 14248_at (PAD3_AT)
 14408_at (AC002291.14_AT)
 14461_at (AC006202.73_AT)
 14584_at (AC007658.25_AT)
 14620_s_at (PAT1_S_AT)
 14638_s_at (PRXCB_S_AT)
 14667_s_at (TRPB_S_AT)
 14673_s_at (TSB2_S_AT)
 14706_r_at (WT77_RC_R_AT)
 14763_at (X86958.1_AT)
 14882_at (AL022605.63_AT)
 14959_at (AC007202.26_AT)
 15073_at (AC007069.93_AT)
 15098_s_at (ATU26945_S_AT)
 15124_s_at (ATU59508_S_AT)
 15137_s_at (ATU57320_S_AT)
 15162_s_at (U01880_S_AT)
 15199_s_at (AB005804_S_AT)
 15406_at (AC006931.179_AT)
 15483_s_at (AC005819.20_S_AT)
 15518_at (AC005322.28_AT)
 15526_at (AC004122.16_AT)
 15540_at (AC006585.205_AT)
 15544_at (AL021633.110_AT)

13716_at (NOVARTIS103_RC_AT)
 13755_at (NOVARTIS15_AT)
 13764_at (NOVARTIS22_AT)
 13842_at (AC002396.12_AT)
 13920_at (AC005990.53_AT)
 14016_s_at (A71596.1_S_AT)
 14030_at (AC005970.225_AT)
 14041_at (AC003970.28_AT)
 14068_s_at (AC006922.197_S_AT)
 14139_at (NOVARTIS30_AT)
 14170_at (NOVARTIS51_AT)
 14242_s_at (NRA_S_AT)
 14249_i_at (PAD4_I_AT)
 14450_at (AC002986.49_AT)
 14487_at (Z97341.343_AT)
 14609_at (AC002340.147_AT)
 14635_s_at (PR.1_S_AT)
 14663_s_at (trehalaseprecursor_RC_S_AT)
 14672_s_at (TSA1_S_AT)
 14705_i_at (WT77_RC_I_AT)
 14735_s_at (AF008124_S_AT)
 14786_at (AC005397.115_AT)
 14924_at (AC006283.46_AT)
 14978_at (AC002333.49_AT)
 15091_at (AC004683.97_AT)
 15116_f_at (AF121356_F_AT)
 15125_f_at (D85190_F_AT)
 15154_s_at (ATHMTGDAS_S_AT)
 15196_s_at (ATU43412_S_AT)
 15216_s_at (ATU75191_S_AT)
 15431_at (AL030978.64_AT)
 15496_at (AC006282.167_AT)
 15522_i_at (AL078637.213_I_AT)
 15531_i_at (AL078637.191_I_AT)
 15543_at (AF096371.10_AT)
 15551_at (AL035440.289_AT)

15594_s_at (ATU56635_S_AT)
 15632_s_at (AB012570_S_AT)
 15672_s_at (AF082299_S_AT)
 15779_g_at (X98676.2_G_AT)
 15839_at (AC005662.203_AT)
 15866_s_at (AC007133.59_S_AT)
 15886_at (AL078637.204_AT)
 15970_s_at (X71794.2_S_AT)
 15982_s_at (AC006260.78_S_AT)
 16003_s_at (AL021749.64_S_AT)
 16031_at (X94248.1_AT)
 16053_i_at (Y14251.4_I_AT)
 16091_s_at (ATHHSP83_S_AT)
 16105_s_at (ATU68017_S_AT)
 16130_s_at (AF078683_S_AT)
 16272_at (AC006304.136_AT)
 16299_at (AL024486.185_AT)
 16340_at (AC004255.15_AT)
 16363_at (AC004255.14_AT)
 16409_at (AC004393.2_AT)
 16462_s_at (AC004683.79_S_AT)
 16545_s_at (AF037229_S_AT)
 16578_s_at (ATHRPRP1B_S_AT)
 16594_s_at (ATU39783_S_AT)
 16609_s_at (AB008104_S_AT)
 16721_at (AC006533.58_AT)
 16810_at (AC002339.46_AT)
 16864_i_at (AF037367.4_I_AT)
 16914_s_at (AL049500.57_S_AT)
 16989_at (AL030978.46_AT)
 17007_at (AC005896.26_AT)
 17066_s_at (ATHLIPOXY_S_AT)
 17128_s_at (ATHRPRP1A_S_AT)
 17338_at (AC002535.97_AT)
 17356_s_at (Z97338.190_S_AT)
 17413_s_at (AJ006961.4_S_AT)

15622_s_at (ATU43945_S_AT)
 15665_s_at (AF022658_S_AT)
 15778_at (X98676.2_AT)
 15815_s_at (Z97342.366_S_AT)
 15859_at (AC006587.164_AT)
 15874_at (AL022223.106_AT)
 15924_at (AC007138.61_AT)
 15978_at (X68592.6_AT)
 16001_at (AF035385.2_AT)
 16021_s_at (AL022224.182_S_AT)
 16043_at (AC005489.17_AT)
 16083_s_at (AF153283_S_AT)
 16103_s_at (ATU60445_S_AT)
 16108_s_at (D78604_S_AT)
 16233_at (AL080254.83_AT)
 16298_at (AL021890.71_AT)
 16306_at (AL049751.112_AT)
 16357_at (AF149413.38_AT)
 16383_at (AC006300.64_AT)
 16461_i_at (AC004683.79_I_AT)
 16470_s_at (AF068299.4_S_AT)
 16570_s_at (ATHCDPKA_S_AT)
 16589_s_at (ATU26937_S_AT)
 16603_s_at (ATU81293_S_AT)
 16701_at (AC005312.61_AT)
 16781_at (AC002392.100_AT)
 16859_at (AL035523.135_AT)
 16865_s_at (AF037367.4_S_AT)
 16968_at (AL021961.93_AT)
 16995_at (AC002391.188_AT)
 17051_s_at (AF098947_S_AT)
 17075_s_at (ATU09961_S_AT)
 17180_at (AF007270.30_AT)
 17341_at (AL021713.89_AT)
 17371_at (AF076243.44_AT)
 17451_at (AC002343.47_AT)

Table 7 Probe Sets as referred to in Tables 4a and 4b corresponding to genes, the expression of which is increased after infection of wild-type *Arabidopsis*, and altered after infection of at least one mutant *Arabidopsis* having a mutation in a gene whose expression is important for resistance to necrotrophic fungi

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11997_at (AC005967.4_AT)	12004_at (AL022023.132_AT)
12037_at (AC004005.174_AT)	12072_at (AL035396.4_AT)
12079_s_at (A71597.1_S_AT)	12081_at (AC001645.140_AT)
12115_at (AL033545.26_AT)	12136_at (AC007591.60_AT)
12150_at (AC004005.151_AT)	12216_at (AC007119.56_AT)
12317_at (AC004138.27_AT)	12323_at (AC002333.18_AT)
12332_s_at (AB023448.2_S_AT)	12369_at (AC002535.59_AT)
12400_at (X98453.1_AT)	12449_s_at (AC002343.179_S_AT)
12475_at (Y11794.1_AT)	12487_at (AC004411.126_AT)
12500_s_at (AF081067.3_S_AT)	12530_at (Z99707.184_AT)
12535_at (AL035538.156_AT)	12538_at (AF033205.2_AT)
12574_at (X82624.2_AT)	12584_at (AC004521.233_AT)
12626_at (AC006234.95_AT)	12645_at (AL021712.56_AT)
12744_at (AC001645.15_AT)	12760_g_at (AC005278.32_G_AT)
12772_at (AC005278.34_AT)	12797_s_at (AC007138.25_S_AT)
12851_s_at (ACCSYN1_S_AT)	12880_s_at (AIG2_S_AT)
12889_s_at (ASA1_S_AT)	12904_s_at (ATERF1_S_AT)
12905_s_at (ATERF2_S_AT)	12921_s_at (ATHHMGCOAR_S_AT)
12951_at (AC005489.5_AT)	12965_at (AL021711.118_AT)
12966_s_at (AL023094.197_S_AT)	12989_s_at (AC004077.149_S_AT)
13040_at (AC002392.134_AT)	13094_at (AL035523.163_AT)
13134_s_at (AC002337.9_S_AT)	13152_s_at (AC005322.24_S_AT)
13176_at (AL031394.56_AT)	13211_s_at (BCHI_S_AT)
13215_s_at (cafferoylcoAmethyltrans_S_AT)	13243_r_at (ELI32_R_AT)
13244_s_at (ELI32_S_AT)	13266_s_at (GST4_S_AT)
13275_f_at (HSP174_F_AT)	13277_i_at (HSP176A_I_AT)
13312_at (AC006223.75_AT)	13370_at (AC005322.4_AT)
13381_at (AC006580.8_AT)	13395_at (AL035528.202_AT)
13435_at (AF003102.3_AT)	13437_at (AF096371.8_AT)
13536_at (AL021636.47_AT)	13538_at (AL080254.75_AT)
13565_at (AL035601.21_AT)	13588_at (AL021961.24_AT)

13680_s_at (LOX1_S_AT)
 13751_at (NOVARTIS127_AT)
 13764_at (NOVARTIS22_AT)
 13848_at (AC003981.31_AT)
 13949_s_at (Z97343.352_S_AT)
 14015_s_at (A71588.1_S_AT)
 14041_at (AC003970.28_AT)
 14068_s_at (AC006922.197_S_AT)
 14089_at (AC006223.65_AT)
 14197_at (NOVARTIS71_AT)
 14450_at (AC002986.49_AT)
 14475_at (AL021811.121_AT)
 14609_at (AC002340.147_AT)
 14667_s_at (TRPB_S_AT)
 14675_s_at (VSP_S_AT)
 14706_r_at (WT77_RC_R_AT)
 14750_s_at (AF096370.12_S_AT)
 14786_at (AC005397.115_AT)
 15052_at (AC002332.103_AT)
 15088_s_at (AC002311.37_S_AT)
 15098_s_at (ATU26945_S_AT)
 15125_f_at (D85190_F_AT)
 15141_s_at (D85191_S_AT)
 15161_s_at (ATU90522_S_AT)
 15188_s_at (AF081202_S_AT)
 15211_s_at (ATH243813_S_AT)
 15406_at (AC006931.179_AT)
 15483_s_at (AC005819.20_S_AT)
 15496_at (AC006282.167_AT)
 15523_s_at (AL078637.213_S_AT)
 15526_at (AC004122.16_AT)
 15532_r_at (AL078637.191_R_AT)
 15594_s_at (ATU56635_S_AT)
 15625_s_at (ATU74610_S_AT)
 15665_s_at (AF022658_S_AT)
 15792_at (AC002341.106_AT)

13688_s_at (monopteros_S_AT)
 13755_at (NOVARTIS15_AT)
 13803_at (Z97341.376_AT)
 13918_at (AC005388.29_AT)
 13999_at (AF071527.56_AT)
 14016_s_at (A71596.1_S_AT)
 14052_at (AC004122.24_AT)
 14070_at (AL049658.217_AT)
 14100_at (AF002109.108_AT)
 14240_s_at (NR1_S_AT)
 14461_at (AC006202.73_AT)
 14584_at (AC007658.25_AT)
 14663_s_at (trehalaseprecursor_RC_S_AT)
 14673_s_at (TSB2_S_AT)
 14705_i_at (WT77_RC_I_AT)
 14735_s_at (AF008124_S_AT)
 14779_at (AC004680.71_AT)
 14978_at (AC002333.49_AT)
 15073_at (AC007069.93_AT)
 15091_at (AC004683.97_AT)
 15124_s_at (ATU59508_S_AT)
 15137_s_at (ATU57320_S_AT)
 15154_s_at (ATHMTGDAS_S_AT)
 15162_s_at (U01880_S_AT)
 15196_s_at (ATU43412_S_AT)
 15342_at (AC006593.101_AT)
 15479_at (AL049483.205_AT)
 15485_at (AC006233.109_AT)
 15522_i_at (AL078637.213_I_AT)
 15524_at (AC005508.25_AT)
 15531_i_at (AL078637.191_I_AT)
 15547_at (AC005970.122_AT)
 15622_s_at (ATU43945_S_AT)
 15632_s_at (AB012570_S_AT)
 15670_s_at (AF061638_S_AT)
 15798_at (AC002521.173_AT)

18109_s_at (AC002391.206_S_AT)
18122_at (AC002338.110_AT)
18176_at (AL035540.31_AT)
18224_s_at (AL021890.57_S_AT)
18236_s_at (AC004683.69_S_AT)
18266_at (AC004684.33_AT)
18587_s_at (AC007166.53_S_AT)
18596_at (AC005698.13_AT)
18668_at (AJ249794_AT)
18782_at (AC003040.90_AT)
18888_at (AC007591.68_AT)
18908_i_at (AF055848.2_I_AT)
18949_at (Z54136.1_AT)
18963_at (AC004561.99_AT)
19060_at (AC003671.34_AT)
19137_at (X74755.2_AT)
19284_at (AC003028.196_AT)
19325_at (AL022604.42_AT)
19383_at (AC006200.203_AT)
19409_at (AC007357.56_AT)
19451_at (AC004392.6_AT)
19546_at (AC005398.172_AT)
19614_at (AC003970.32_AT)
19640_at (AC004561.78_AT)
19645_at (AC004561.70_AT)
19672_at (AC005687.19_AT)
19700_s_at (AL031326.154_S_AT)
19707_s_at (Z95768.3_S_AT)
19762_at (AL035527.204_AT)
19851_at (U23794.3_AT)
19956_at (AC006282.11_AT)
20023_at (AC006577.46_AT)
20053_at (AC002292.27_AT)
20133_i_at (AC007178.71_I_AT)
20144_at (AL079350.68_AT)
20189_at (AC005489.2_AT)

18121_s_at (AC002337.21_S_AT)
18148_at (AC004669.25_AT)
18213_at (AL022140.126_AT)
18228_at (X91259.1_AT)
18258_s_at (AC006439.222_S_AT)
18299_s_at (M23872.2_S_AT)
18590_at (AJ222713.4_AT)
18636_at (AC006577.22_AT)
18735_s_at (Z29490_S_AT)
18803_at (AC005315.94_AT)
18899_s_at (X13434.1_S_AT)
18933_at (AC007020.48_AT)
18953_at (AF077955.1_AT)
19019_i_at (X82623.2_I_AT)
19110_s_at (X86947.2_S_AT)
19257_s_at (AC000104.57_S_AT)
19288_at (AC005824.130_AT)
19364_at (AL022023.142_AT)
19395_at (AF007270.32_AT)
19432_s_at (AL035680.11_S_AT)
19460_s_at (AC000132.66_S_AT)
19591_at (AJ010735.4_AT)
19635_at (AL049746.38_AT)
19641_at (AC004561.66_AT)
19667_at (AL021710.5_AT)
19673_g_at (AC005687.19_G_AT)
19704_i_at (AJ005927.2_I_AT)
19755_at (AC006593.64_AT)
19818_i_at (AL021749.33_I_AT)
19895_s_at (U77347.4_S_AT)
19960_at (AL035527.360_AT)
20051_at (AC000106.38_AT)
20096_at (AC004238.31_AT)
20134_s_at (AC007178.71_S_AT)
20179_at (AL035538.229_AT)
20194_at (AC007584.48_AT)

20247_at (AC004392.4_AT)	20263_at (AB004798.1_AT)
20291_s_at (M92353.4_S_AT)	20297_at (AC007153.27_AT)
20323_at (AC004561.62_AT)	20348_at (AC005967.35_AT)
20356_at (AC004561.74_AT)	20370_at (AC004561.263_AT)
20433_at (AC006232.147_AT)	20450_at (AJ005930.2_AT)
20479_i_at (AF069495.2_I_AT)	20485_at (AC007660.131_AT)
20572_s_at (AC005560.229_S_AT)	20646_at (AC002291.20_AT)
20656_at (AL035396.46_AT)	20658_s_at (AL050400.70_S_AT)
20669_s_at (AC002388.6_S_AT)	20686_at (Y14424.2_AT)

Table 8 Probe Sets as referred to in Table 6 corresponding to genes, the expression of which is increased after infection of wild-type *Arabidopsis* and altered after infection of at least one mutant *Arabidopsis* having a mutation in a gene that interferes with salicylic acid dependent signaling

5

12079_s_at (A71597.1_S_AT)	12081_at (AC001645.140_AT)
12115_at (AL033545.26_AT)	12150_at (AC004005.151_AT)
12233_at (AJ001807.1_AT)	12307_at (AC002392.162_AT)
12314_at (AC001229.28_AT)	12332_s_at (AB023448.2_S_AT)
12341_s_at (AL021637.176_S_AT)	12400_at (X98453.1_AT)
12438_at (AL021710.83_AT)	12475_at (Y11794.1_AT)
12487_at (AC004411.126_AT)	12497_at (AC006533.51_AT)
12500_s_at (AF081067.3_S_AT)	12530_at (Z99707.184_AT)
12574_at (X82624.2_AT)	12584_at (AC004521.233_AT)
12712_f_at (Z95774_F_AT)	12760_g_at (AC005278.32_G_AT)
12764_f_at (AC004138.69_F_AT)	12879_s_at (AIG1_S_AT)
12883_s_at (APX_S_AT)	12889_s_at (ASA1_S_AT)
12891_at (ATACS6_AT)	12892_g_at (ATACS6_G_AT)
12905_s_at (ATERF2_S_AT)	12911_s_at (ATG6PDHE5_S_AT)
12921_s_at (ATHHMGCOAR_S_AT)	12958_at (AC002332.249_AT)
12989_s_at (AC004077.149_S_AT)	13003_s_at (AB021936.1_S_AT)
13014_at (U93215.87_AT)	13040_at (AC002392.134_AT)
13070_at (AC006919.171_AT)	13094_at (AL035523.163_AT)
13157_at (AC002409.35_AT)	13190_s_at (ATTHIREDA_S_AT)
13211_s_at (BCHI_S_AT)	13212_s_at (BGL2_S_AT)
13219_s_at (CHI4_S_AT)	13273_s_at (HSF4_S_AT)
13275_f_at (HSP174_F_AT)	13370_at (AC005322.4_AT)

13381_at (AC006580.8_AT)
 13565_at (AL035601.21_AT)
 13589_at (AC000132.24_AT)
 13627_at (AL035394.196_AT)
 13659_at (AL022347.46_AT)
 13680_s_at (LOX1_S_AT)
 13751_at (NOVARTIS127_AT)
 13763_at (NOVARTIS21_AT)
 13818_s_at (AC006218.175_S_AT)
 13920_at (AC005990.53_AT)
 14016_s_at (A71596.1_S_AT)
 14030_at (AC005970.225_AT)
 14041_at (AC003970.28_AT)
 14068_s_at (AC006922.197_S_AT)
 14139_at (NOVARTIS30_AT)
 14170_at (NOVARTIS51_AT)
 14242_s_at (NRA_S_AT)
 14249_i_at (PAD4_I_AT)
 14450_at (AC002986.49_AT)
 14487_at (Z97341.343_AT)
 14609_at (AC002340.147_AT)
 14635_s_at (PR.1_S_AT)
 14663_s_at (trehalaseprecursor_RC_S_AT)
 14672_s_at (TSA1_S_AT)
 14735_s_at (AF008124_S_AT)
 14786_at (AC005397.115_AT)
 14959_at (AC007202.26_AT)
 15073_at (AC007069.93_AT)
 15116_f_at (AF121356_F_AT)
 15162_s_at (U01880_S_AT)
 15199_s_at (AB005804_S_AT)
 15431_at (AL030978.64_AT)
 15496_at (AC006282.167_AT)
 15526_at (AC004122.16_AT)
 15543_at (AF096371.10_AT)
 15551_at (AL035440.289_AT)

13538_at (AL080254.75_AT)
 13588_at (AL021961.24_AT)
 13617_at (AC006592.64_AT)
 13656_at (AC007138.31_AT)
 13666_s_at (INDOLE3GPS_S_AT)
 13697_at (NI16_AT)
 13755_at (NOVARTIS15_AT)
 13764_at (NOVARTIS22_AT)
 13880_s_at (AL049480.183_S_AT)
 14015_s_at (A71588.1_S_AT)
 14025_s_at (AC007293.3_S_AT)
 14032_at (AL035601.11_AT)
 14052_at (AC004122.24_AT)
 14110_i_at (AL035528.279_I_AT)
 14148_at (NOVARTIS38_AT)
 14214_at (NOVARTIS83_AT)
 14248_at (PAD3_AT)
 14408_at (AC002291.14_AT)
 14461_at (AC006202.73_AT)
 14584_at (AC007658.25_AT)
 14620_s_at (PAT1_S_AT)
 14638_s_at (PRXCB_S_AT)
 14667_s_at (TRPB_S_AT)
 14673_s_at (TSB2_S_AT)
 14763_at (X86958.1_AT)
 14882_at (AL022605.63_AT)
 14978_at (AC002333.49_AT)
 15091_at (AC004683.97_AT)
 15137_s_at (ATU57320_S_AT)
 15196_s_at (ATU43412_S_AT)
 15216_s_at (ATU75191_S_AT)
 15483_s_at (AC005819.20_S_AT)
 15518_at (AC005322.28_AT)
 15540_at (AC006585.205_AT)
 15544_at (AL021633.110_AT)
 15594_s_at (ATU56635_S_AT)

15622_s_at (ATU43945_S_AT)
 15672_s_at (AF082299_S_AT)
 15779_g_at (X98676.2_G_AT)
 15839_at (AC005662.203_AT)
 15866_s_at (AC007133.59_S_AT)
 15924_at (AC007138.61_AT)
 15978_at (X68592.6_AT)
 16003_s_at (AL021749.64_S_AT)
 16031_at (X94248.1_AT)
 16053_i_at (Y14251.4_I_AT)
 16091_s_at (ATHHSP83_S_AT)
 16105_s_at (ATU68017_S_AT)
 16130_s_at (AF078683_S_AT)
 16272_at (AC006304.136_AT)
 16306_at (AL049751.112_AT)
 16357_at (AF149413.38_AT)
 16383_at (AC006300.64_AT)
 16461_i_at (AC004683.79_I_AT)
 16470_s_at (AF068299.4_S_AT)
 16578_s_at (ATHRPRP1B_S_AT)
 16594_s_at (ATU39783_S_AT)
 16609_s_at (AB008104_S_AT)
 16721_at (AC006533.58_AT)
 16810_at (AC002339.46_AT)
 16865_s_at (AF037367.4_S_AT)
 16968_at (AL021961.93_AT)
 17007_at (AC005896.26_AT)
 17066_s_at (ATHLIPOXY_S_AT)
 17128_s_at (ATHRPRP1A_S_AT)
 17338_at (AC002535.97_AT)
 17356_s_at (Z97338.190_S_AT)
 17451_at (AC002343.47_AT)
 17484_at (X79052.2_AT)
 17487_s_at (U18993.2_S_AT)
 17544_s_at (ATU40856_S_AT)
 17653_at (AL035679.144_AT)

15632_s_at (AB012570_S_AT)
 15778_at (X98676.2_AT)
 15815_s_at (Z97342.366_S_AT)
 15859_at (AC006587.164_AT)
 15874_at (AL022223.106_AT)
 15970_s_at (X71794.2_S_AT)
 15982_s_at (AC006260.78_S_AT)
 16021_s_at (AL022224.182_S_AT)
 16043_at (AC005489.17_AT)
 16083_s_at (AF153283_S_AT)
 16103_s_at (ATU60445_S_AT)
 16108_s_at (D78604_S_AT)
 16233_at (AL080254.83_AT)
 16299_at (AL024486.185_AT)
 16340_at (AC004255.15_AT)
 16363_at (AC004255.14_AT)
 16409_at (AC004393.2_AT)
 16462_s_at (AC004683.79_S_AT)
 16570_s_at (ATHCDPKA_S_AT)
 16589_s_at (ATU26937_S_AT)
 16603_s_at (ATU81293_S_AT)
 16701_at (AC005312.61_AT)
 16781_at (AC002392.100_AT)
 16864_i_at (AF037367.4_I_AT)
 16914_s_at (AL049500.57_S_AT)
 16995_at (AC002391.188_AT)
 17051_s_at (AF098947_S_AT)
 17075_s_at (ATU09961_S_AT)
 17180_at (AF007270.30_AT)
 17341_at (AL021713.89_AT)
 17413_s_at (AJ006961.4_S_AT)
 17452_g_at (AC002343.47_G_AT)
 17485_s_at (Z97340.345_S_AT)
 17533_s_at (ATU43488_S_AT)
 17585_s_at (AF134487_S_AT)
 17752_at (AC003974.37_AT)

17758_at (AF076243.41_AT)
 17781_at (AL049746.177_AT)
 17893_at (AC004401.135_AT)
 17930_s_at (AJ006960.4_S_AT)
 18054_at (AJ238846_AT)
 18194_i_at (AL096859.227_I_AT)
 18242_g_at (AC006580.71_G_AT)
 18258_s_at (AC006439.222_S_AT)
 18544_at (AC007060.14_AT)
 18591_at (X74756.2_AT)
 18604_at (AF069298.31_AT)
 18625_at (AC005278.22_AT)
 18698_s_at (X17528_S_AT)
 18753_s_at (AF118222.28_S_AT)
 18885_at (AC006921.147_AT)
 18909_s_at (AF055848.2_S_AT)
 18930_at (AC005990.57_AT)
 18953_at (AF077955.1_AT)
 19019_i_at (X82623.2_I_AT)
 19140_at (AC005170.24_AT)
 19207_at (AC006069.117_AT)
 19257_s_at (AC000104.57_S_AT)
 19364_at (AL022023.142_AT)
 19409_at (AC007357.56_AT)
 19421_at (X70990.4_AT)
 19451_at (AC004392.6_AT)
 19465_at (AL021768.96_AT)
 19555_at (AF058919.48_AT)
 19641_at (AC004561.66_AT)
 19741_at (AL049171.72_AT)
 19818_i_at (AL021749.33_I_AT)
 19892_at (AC005770.30_AT)
 19956_at (AC006282.11_AT)
 19982_at (AC002986.28_AT)
 20017_at (AC004521.66_AT)
 20051_at (AC000106.38_AT)

17775_at (AC004392.2_AT)
 17840_s_at (AC002333.223_S_AT)
 17899_at (Z97339.197_AT)
 17963_at (AL049730.88_AT)
 18148_at (AC004669.25_AT)
 18213_at (AL022140.126_AT)
 18255_at (AC005770.25_AT)
 18508_s_at (AC006532.89_S_AT)
 18590_at (AJ222713.4_AT)
 18596_at (AC005698.13_AT)
 18622_g_at (AJ005902.2_G_AT)
 18686_s_at (U18126_S_AT)
 18735_s_at (Z29490_S_AT)
 18803_at (AC005315.94_AT)
 18888_at (AC007591.68_AT)
 18928_at (AC002333.181_AT)
 18933_at (AC007020.48_AT)
 18966_at (AC004561.106_AT)
 19137_at (X74755.2_AT)
 19181_s_at (AF053065.2_S_AT)
 19247_at (AF071527.44_AT)
 19325_at (AL022604.42_AT)
 19407_at (AC004697.81_AT)
 19411_at (AC007661.104_AT)
 19432_s_at (AL035680.11_S_AT)
 19460_s_at (AC000132.66_S_AT)
 19546_at (AC005398.172_AT)
 19624_at (AL049481.196_AT)
 19667_at (AL021710.5_AT)
 19755_at (AC006593.64_AT)
 19881_at (AC004077.49_AT)
 19944_at (AC002130.4_AT)
 19970_s_at (AC003674.10_S_AT)
 19991_at (AC007017.124_AT)
 20030_at (AL078637.51_AT)
 20098_at (AC004697.123_AT)

20133_i_at (AC007178.71_I_AT)
 20144_at (AL079350.68_AT)
 20247_at (AC004392.4_AT)
 20271_at (Z99707.27_AT)
 20288_g_at (Y14590.5_G_AT)
 20323_at (AC004561.62_AT)
 20370_at (AC004561.263_AT)
 20421_at (U81294.2_AT)
 20432_at (U43486.2_AT)
 20461_at (AL049480.157_AT)
 20479_i_at (AF069495.2_I_AT)
 20529_at (Z97341.125_AT)
 20589_at (AF081066.3_AT)
 20685_at (AL049751.46_AT)

20134_s_at (AC007178.71_S_AT)
 20245_s_at (AC005309.97_S_AT)
 20269_at (AC002387.237_AT)
 20287_at (Y14590.5_AT)
 20291_s_at (M92353.4_S_AT)
 20356_at (AC004561.74_AT)
 20420_at (AL024486.131_AT)
 20422_g_at (U81294.2_G_AT)
 20450_at (AJ005930.2_AT)
 20462_at (U82399.2_AT)
 20480_s_at (AF069495.2_S_AT)
 20572_s_at (AC005560.229_S_AT)
 20669_s_at (AC002388.6_S_AT)
 20689_s_at (AC002335.19_S_AT)

Table 9 Probe Sets corresponding to genes, the expression of which is downregulated (repressed) in an avrRpt-2-dependent manner in *Arabidopsis*

ProbeSet	Description
11991_g_at (AC002387.210_G_AT)	11991_g_at (AC002387.210_G_AT)gb AAB82645.1 (AC002387) unknown protein [Arabidopsis thaliana]
12091_at (AC004450.116_AT)	12091_at (AC004450.116_AT)gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
12124_s_at (Z97337.149_S_AT)	12124_s_at (Z97337.149_S_AT)emb CAB10270.1 (Z97337) imidazoleglycerol-phosphate dehydratase [Arabidopsis thaliana]
12125_at (Z97341.99_AT)	12125_at (Z97341.99_AT)emb CAB10421.1 (Z97341) hypothetical protein [Arabidopsis thaliana]
12160_at (AC006284.117_AT)	12160_at (AC006284.117_AT)gb AAD17436.1 (AC006284) unknown protein [Arabidopsis thaliana]
12191_at (AC006068.35_AT)	12191_at (AC006068.35_AT)gb AAD15440.1 (AC006068) unknown protein [Arabidopsis thaliana]
12193_at (AC006072.132_AT)	12193_at (AC006072.132_AT)gb AAD13708.1 (AC006072) unknown protein [Arabidopsis thaliana]
12223_s_at (AC007168.178_S_AT)	12223_s_at (AC007168.178_S_AT)gb AAF18668.1 AC007168_1 (AC007168) unknown protein [Arabidopsis thaliana]
12290_at (Y09418.2_AT)	12290_at (Y09418.2_AT)emb CAA70572.1 (Y09418) CDPK-related protein kinase [Arabidopsis thaliana]
12421_at (AJ002414.1_AT)	12421_at (AJ002414.1_AT)emb CAA05398.1 (AJ002414) hnRNP-like protein [Arabidopsis thaliana]
12460_s_at (AC006920.129_S_AT)	12460_s_at (AC006920.129_S_AT)gb AAD22284.1 AC006920_8 (AC006920) DNA-directed RNA polymerase II, third largest subunit [Arabidopsis thaliana]
12493_g_at (Y09095.1_G_AT)	12493_g_at (Y09095.1_G_AT)emb CAA70310.1 (Y09095) chloride channel [Arabidopsis thaliana]
12559_at (AC005727.83_AT)	12559_at (AC005727.83_AT)gb AAC79586.1 (AC005727) putative DOF zinc finger protein [Arabidopsis thaliana]

ProbeSet	Description
12560_at (AC005825.57_AT)	12560_at (AC005825.57_AT)gb AAD24598.1 AC005825_5 (AC005825) putative chloroplast outer membrane protein [Arabidopsis thaliana]
12561_at (AL021687.107_AT)	12561_at (AL021687.107_AT)emb CAA16701.1 (AL021687) putative protein [Arabidopsis thaliana]
12855_f_at (ADH_F_AT)	12855_f_at (ADH_F_AT)gb AAC00625.1 (AC002291) Alcohol Dehydrogenase [Arabidopsis thaliana]
12962_at (AC004697.165_AT)	12962_at (AC004697.165_AT)gb AAC28988.1 (AC004697) putative ABC transporter [Arabidopsis thaliana]
13221_at (CHS-WHOLE-SEQ_AT)	13221_at (CHS-WHOLE- SEQ_AT)gb AAF23561.1 AF112086_1 (AF112086) chalcone synthase [Arabidopsis thaliana]
13253_f_at (FPS1_F_AT)	13253_f_at (FPS1_F_AT)gb AAB49290.1 (U80605) farnesyl diphosphate synthase precursor [Arabidopsis thaliana]
13459_at (AF013294.21_AT)	13459_at (AF013294.21_AT)gb AAB62852.1 (AF013294) similar to auxin-induced protein [Arabidopsis thaliana]
13708_s_at (AC007259X_S_AT)	13708_s_at (AC007259X_S_AT)gb AAD50000.1 AC007259_1 3 (AC007259) Similar to protein kinases [Arabidopsis thaliana]
14428_s_at (AL023094.342_S_AT)	14428_s_at (AL023094.342_S_AT)emb CAA18852.1 (AL023094) putative protein [Arabidopsis thaliana]
15175_s_at (ATU28215_S_AT)	15175_s_at (ATU28215_S_AT)gb AAC62130.1 (AC005169) hexokinase (ATHXK2) [Arabidopsis thaliana]
15943_at (AC007202.16_AT)	15943_at (AC007202.16_AT)gb AAD30227.1 AC007202_9 (AC007202) Strong similarity to gb Y14272 3- deoxy-D-manno-2-octulosonate-8-phosphate synthase from Pisum sativum. ESTs gb AA067485 and gb AI100551 come from this gene. [Arabidopsis thaliana]

ProbeSet	Description
19219_at (AC007019.185_AT)	19219_at (AC007019.185_AT)gb AAD20413.1 (AC007019) unknown protein [Arabidopsis thaliana]

19219_at (AC007019.185_AT)

Table 10A: Expression data for 9 probe sets corresponding to genes that are specifically induced during incompatible interaction within 3 hours

ProbeSet	Col					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12094_at	ud	303	ud	19	28	ud
12128_at	84	255	ud	0	181	ud
12712_f_at	10	278	ud	ud	90	20
13763_at	18	176	16	64	274	40
14882_at	24	385	11	62	457	46
16398_s_at	16	104	5	17	65	18
16536_s_at	24	346	19	ud	19	30
17180_at	50	361	26	93	367	76
19970_s_at	18	175	8	14	65	11
ProbeSet	Ws					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12094_at	ud	104	ud	ud	29	ud
12128_at	ud	77	ud	ud	29	ud
12712_f_at	ud	146	ud	ud	46	ud
13763_at	ud	90	ud	15	378	25
14882_at	19	255	7	23	291	32
16398_s_at	9	93	7	4	49	ud
16536_s_at	ud	409	ud	ud	4	8
17180_at	ud	200	ud	ud	259	ud
19970_s_at	11	146	5	4	46	6
ProbeSet	Ler					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12094_at	ud	121	ud	24	41	ud
12128_at	71	160	ud	33	145	ud
12712_f_at	19	113	11	24	46	14
13763_at	22	85	19	139	248	43
14882_at	50	227	25	121	321	41

16398_s_at	20	85	20	23	57	10
16536_s_at	13	110	29	ud	ud	78
17180_at	46	181	18	123	214	37
19970_s_at	23	140	13	32	55	22
ProbeSet	Cvi					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12094_at	18	166	ud	32	54	ud
12128_at	75	204	37	52	168	28
12712_f_at	11	92	ud	14	39	13
13763_at	42	166	21	133	344	25
14882_at	45	213	34	86	417	26
16398_s_at	12	52	16	25	67	14
16536_s_at	15	164	30	ud	8	23
17180_at	45	203	ud	152	263	ud
19970_s_at	25	142	11	19	68	13

5 **Table 10B:** Expression data for 18 probe sets corresponding to genes that are specifically induced during incompatible interaction in 6 hours (but not within 3 hours)

ProbeSet	Col					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12711_f_at	ud	ud	ud	ud	100	ud
13312_at	ud	118	ud	36	176	11
13370_at	ud	ud	ud	ud	144	ud
13818_s_at	ud	9	ud	65	476	21
14609_at	ud	11	4	23	233	21
14635_s_at	ud	ud	ud	42	360	13
14931_at	ud	ud	ud	10	284	16
15120_s_at	ud	ud	ud	ud	214	12
16357_at	8	70	6	14	102	26
16968_at	19	28	7	33	257	19

17134_at	ud	ud	ud	ud	199	ud
17371_at	ud	16	ud	31	191	19
17485_s_at	ud	ud	ud	ud	86	7
18631_at	10	105	ud	32	92	17
19451_at	ud	ud	ud	ud	116	ud
20323_at	20	51	19	12	280	14
20356_at	ud	ud	ud	ud	82	ud
20421_at	ud	ud	ud	26	685	20
ProbeSet	Ws					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12711_f_at	ud	ud	ud	ud	86	ud
13312_at	ud	34	ud	11	114	2
13370_at	ud	ud	ud	20	70	ud
13818_s_at	ud	12	8	10	422	10
14609_at	ud	12	ud	ud	184	3
14635_s_at	ud	ud	ud	ud	264	ud
14931_at	ud	ud	ud	ud	36	ud
15120_s_at	ud	13	ud	ud	89	ud
16357_at	ud	31	ud	ud	80	6
16968_at	ud	5	ud	12	54	ud
17134_at	ud	ud	ud	ud	27	ud
17371_at	ud	ud	ud	ud	133	ud
17485_s_at	ud	ud	ud	8	85	ud
18631_at	10	103	ud	17	81	10
19451_at	ud	6	ud	ud	52	ud
20323_at	ud	60	11	ud	119	ud
20356_at	ud	ud	ud	ud	96	ud
20421_at	ud	5	ud	ud	67	ud
ProbeSet	Ler					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12711_f_at	ud	ud	5	15	32	ud
13312_at	ud	48	ud	133	158	12
13370_at	ud	ud	ud	36	122	ud

13818_s_at	ud	ud	4	26	211	ud
14609_at	ud	ud	5	30	359	15
14635_s_at	ud	ud	ud	22	310	17
14931_at	ud	ud	ud	ud	149	ud
15120_s_at	ud	ud	ud	17	252	ud
16357_at	14	47	10	23	117	11
16968_at	14	18	5	ud	105	5
17134_at	ud	ud	ud	ud	112	ud
17371_at	ud	ud	ud	ud	ud	ud
17485_s_at	ud	ud	ud	ud	49	ud
18631_at	16	63	27	34	68	ud
19451_at	5	7	4	14	123	ud
20323_at	11	6	8	ud	11	ud
20356_at	ud	5	ud	17	111	ud
20421_at	ud	ud	ud	7	329	ud
ProbeSet	Cvi					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
12711_f_at	ud	ud	ud	15	46	7
13312_at	10	64	5	60	116	ud
13370_at	ud	ud	18	40	88	ud
13818_s_at	4	ud	7	47	274	10
14609_at	8	23	6	127	778	ud
14635_s_at	6	ud	ud	179	519	44
14931_at	ud	ud	ud	23	182	ud
15120_s_at	ud	17	ud	31	150	ud
16357_at	17	52	16	32	132	16
16968_at	16	20	18	ud	56	3
17134_at	ud	ud	ud	ud	121	ud
17371_at	ud	ud	ud	ud	ud	ud
17485_s_at	ud	ud	ud	ud	55	ud
18631_at	11	41	10	24	85	ud
19451_at	4	6	ud	19	413	ud
20323_at	7	ud	ud	ud	11	ud
20356_at	ud	ud	ud	13	107	ud

20421_at	ud	20	ud	ud	293	ud
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5 **Table 10C:** Expression data for 6 probe sets corresponding to genes that are activated by *P. syringae* in 6 hours. Most of them are compatible interaction-specific/preferential

ProbeSet	Col					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
13243_r_at	44	ud	24	123	91	14
14573_at	ud	ud	ud	234	32	23
14613_at	ud	ud	9	138	ud	10
18122_at	34	38	25	169	96	28
19150_at	ud	ud	3	97	4	6
19673_g_at	69	34	27	596	290	ud
ProbeSet	Ws					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
13243_r_at	27	38	16	132	96	17
14573_at	ud	ud	ud	377	63	12
14613_at	ud	10	ud	136	ud	ud
18122_at	33	56	30	235	76	24
19150_at	ud	ud	ud	218	9	ud
19673_g_at	21	6	ud	496	312	ud
ProbeSet	Ler					
	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
13243_r_at	66	52	45	149	59	7
14573_at	ud	ud	ud	22	17	9
14613_at	ud	ud	14	102	13	13
18122_at	42	58	42	136	60	20
19150_at	ud	ud	ud	24	7	ud
19673_g_at	30	2	10	426	181	ud
ProbeSet	Cvi					

	3 hr			6 hr		
	Pst	Pst/aR2	cont	Pst	Pst/aR2	cont
13243_r_at	62	42	55	142	116	ud
14573_at	ud	ud	ud	25	22	ud
14613_at	13	ud	13	63	ud	ud
18122_at	36	43	41	151	81	28
19150_at	ud	6	ud	11	3	ud
19673_g_at	ud	ud	26	416	184	ud

Pst/aR2 ... represents the incompatible interaction

5 Pst ... *P. syringae* pv. tomato

aR2 ... avrRpt2

ud ... undetectable

1022290"272/13960

Table 11 Probe Sets corresponding to genes induced early after infection of different *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121 (at 3 or 6 hours) or by estradiol inducible

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ProbeSet	Description
12737_f_at (Z97049_F_AT)	12737_f_at (Z97049_F_AT)emb CAA74603.1 (Y14207) R2R3-MYB transcription factor [Arabidopsis thaliana]
12908_s_at (ATERF5_S_AT)	12908_s_at (ATERF5_S_AT)dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
16398_s_at (AL022603.3_S_AT)	16398_s_at (AL022603.3_S_AT)emb CAA20204.1 (AL031187) serine/threonine kinase-like protein [Arabidopsis thaliana]
17105_s_at (AF055357_S_AT)	17105_s_at (AF055357_S_AT)gb AAC39479.1 (AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]
19970_s_at (AC003674.10_S_AT)	19970_s_at (AC003674.10_S_AT)gb AAB97120.1 (AC003674) unknown protein [Arabidopsis thaliana]
20620_g_at (AC005896.161_G_AT)	20620_g_at (AC005896.161_G_AT)gb AAC98070.1 (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
12094_at (AC006223.143_AT)	12094_at (AC006223.143_AT)gb AAD15401.1 (AC006223) putative alanine acetyl transferase [Arabidopsis thaliana]
13255_i_at (gammaglutamyltranspepti_I_AT)	13255_i_at (GAMMAGLUTAMYLTRANSPEPTI_I_AT)emb CAA89206.1 (Z49240) gamma-glutamyl transpeptidase [Arabidopsis thaliana]
12712_f_at (Z95774_F_AT)	12712_f_at (Z95774_F_AT)emb CAB09206.1 (Z95774) R2R3-MYB transcription factor [Arabidopsis thaliana]
13015_s_at (X98673.2_S_AT)	13015_s_at (X98673.2_S_AT)emb CAA67232.1 (X98674) zinc finger protein [Arabidopsis thaliana]

ProbeSet	Description
13842_at (AC002396.12_AT)	13842_at (AC002396.12_AT)gb AAC00572.1 (AC002396) similar to zinc metalloproteinases [Arabidopsis thaliana]
14235_at (NOVARTIS97_AT)	14235_at (NOVARTIS97_AT)gb AAF14671.1 AC011713_19 (AC011713) Similar to gb Z48431 DNA-binding protein from Avena fatua. [Arabidopsis thaliana]
15779_g_at (X98676.2_G_AT)	15779_g_at (X98676.2_G_AT)emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
16059_s_at (D88206_S_AT)	16059_s_at (D88206_S_AT)dbj BAA24694.1 (D88206) protein kinase [Arabidopsis thaliana]
17180_at (AF007270.30_AT)	17180_at (AF007270.30_AT)gb AAB61058.1 (AF007270) contains similarity to GATA-type zinc fingers (PS:PS00344) [Arabidopsis thaliana]
17303_s_at (AC004683.25_S_AT)	17303_s_at (AC004683.25_S_AT)gb AAC67339.2 (AC005499) putative WRKY-type DNA binding protein [Arabidopsis thaliana]
12571_s_at (AF149413.18_S_AT)	12571_s_at (AF149413.18_S_AT)gb AAD40138.1 AF149413_19 (AF149413) Arabidopsis thaliana ferrochelatase-I (SW:P42043); Pfam
12642_at (AC006920.138_AT)	12642_at (AC006920.138_AT)gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]
13177_at (AL049640.42_AT)	13177_at (AL049640.42_AT)emb CAB40989.1 (AL049640) growth factor like protein [Arabidopsis thaliana]
14162_at (NOVARTIS46_AT)	14162_at (NOVARTIS46_AT)No hits found less than or equal to 1e-15.
14214_at (NOVARTIS83_AT)	14214_at (NOVARTIS83_AT)gb AAF24849.1 AC012679_20 (AC012679) putative calmodulin-binding protein [Arabidopsis thaliana]
14217_at (NOVARTIS85_RC_AT)	14217_at (NOVARTIS85_RC_AT)gb AAF07816.1 AC011020_16 (AC011020) putative receptor protein kinase [Arabidopsis thaliana] thaliana. [Arabidopsis thaliana]

ProbeSet	Description
14711_s_at (ZFPL_S_AT)	14711_s_at (ZFPL_S_AT)gb AAD25930.1 AF085279_3 (AF085279) hypothetical Cys-3-His zinc finger protein [Arabidopsis thaliana]
14882_at (AL022605.63_AT)	14882_at (AL022605.63_AT)emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]
15431_at (AL030978.64_AT)	15431_at (AL030978.64_AT)emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
15680_s_at (ATHATPK19B_S_AT)	15680_s_at (ATHATPK19B_S_AT)dbj BAA07661.1 (D42061) ribosomal-protein S6 kinase homolog [Arabidopsis thaliana]
17379_at (AF085279.9_AT)	17379_at (AF085279.9_AT)gb AAF18728.1 AC018721_3 (AC018721) putative CCCH-type zinc finger protein [Arabidopsis thaliana]
18267_at (AC006223.23_AT)	18267_at (AC006223.23_AT)gb AAD15384.1 (AC006223) unknown protein [Arabidopsis thaliana]
18604_at (AF069298.31_AT)	18604_at (AF069298.31_AT)gb AAC19273.1 (AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]
19460_s_at (AC000132.66_S_AT)	19460_s_at (AC000132.66_S_AT)gb AAB60749.1 (AC000132) Identical to A. thaliana HEMA2 (gb U27118). [Arabidopsis thaliana]
15775_at (AL079344.196_AT)	15775_at (AL079344.196_AT)emb CAB45334.1 (AL079344) cytokinin oxidase-like protein [Arabidopsis thaliana]
16939_at (AC002334.110_AT)	16939_at (AC002334.110_AT)gb AAC04922.1 (AC002334) putative synaptobrevin [Arabidopsis thaliana]
18672_s_at (D13983_S_AT)	18672_s_at (D13983_S_AT)dbj BAA03090.1 (D13983) chloroplast envelope Ca ²⁺ -ATPase precursor [Arabidopsis

Table 12 Probe Sets corresponding to genes repressed early after infection of *Arabidopsis* with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121

ProbeSet	Description
12212_at (AL049711.168_AT)	12212_at (AL049711.168_AT)emb CAB41327.1 (AL049711) putative protein [Arabidopsis thaliana]
17555_s_at (ATU89296_S_AT)	17555_s_at (ATU89296_S_AT)gb AAB62404.1 (U89296) auxin response transcription factor 3; ARF3 [Arabidopsis thaliana]
17975_at (AF175998_AT)	17975_at (AF175998_AT)gb AAD53103.1 AF175998_1 (AF175998) putative transcription factor [Arabidopsis thaliana]
14386_at (AC005309.177_AT)	14386_at (AC005309.177_AT)gb AAC63645.1 (AC005309) unknown protein [Arabidopsis thaliana]
16613_s_at (AF012657_S_AT)	16613_s_at (AF012657_S_AT)gb AAC49845.1 (AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]
18916_s_at (X92393.1_S_AT)	18916_s_at (X92393.1_S_AT)emb CAA63131.1 (X92393) KNAT4 homeobox protein [Arabidopsis thaliana]
20443_s_at (AC006341.42_S_AT)	20443_s_at (AC006341.42_S_AT)gb AAD34693.1 AC006341_21 (AC006341) Similar to gb AF069494 cytochrome P450 from Sinapis alba and is a member of the PF 00067 Cytochrome P450 family. EST gb F14190 comes from this gene. [Arabidopsis thaliana]
20524_at (AC005698.12_AT)	20524_at (AC005698.12_AT)gb AAD43613.1 AC005698_12 (AC005698) T3P18.12 [Arabidopsis thaliana]
12609_at (X92975.2_AT)	12609_at (X92975.2_AT)emb CAA63553.1 (X92975) xyloglucan endo-transglycosylase [Arabidopsis thaliana]
20061_at (AC005508.23_AT)	20061_at (AC005508.23_AT)gb AAD14498.1 (AC005508) 37496 [Arabidopsis thaliana]

Table 13a Probe Sets corresponding to genes, the expression of which is induced in an incompatible interaction at 3 and/or 6 hours after infection of four *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121

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ProbeSet	Description
12128_at (AC004261.157_AT)	12128_at (AC004261.157_AT)gb AAD12010.1 (AC004261) unknown protein [Arabidopsis thaliana]
12335_at (AC004411.73_AT)	12335_at (AC004411.73_AT)gb AAC34243.1 (AC004411) putative protein kinase [Arabidopsis thaliana]
12347_at (AC007258.28_AT)	12347_at (AC007258.28_AT)gb AAD39325.1 AC007258_14 (AC007258) Putative ATPase [Arabidopsis thaliana]
12497_at (AC006533.51_AT)	12497_at (AC006533.51_AT)gb AAD32284.1 AC006533_8 (AC006533) putative receptor-like protein kinase [Arabidopsis thaliana]
12759_at (AC005278.32_AT)	12759_at (AC005278.32_AT)gb AAC72120.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from <i>Daucus carota</i> . ESTs gb 84105 and gb A1100071 come from this gene. [Arabidopsis thaliana]
12790_s_at (AL021635.58_S_AT)	12790_s_at (AL021635.58_S_AT)emb CAA16554.1 (AL021635) cytochrome P450 like protein [Arabidopsis thaliana]
12801_at (AC005223.34_AT)	12801_at (AC005223.34_AT)gb AAD10652.1 (AC005223) Unknown protein [Arabidopsis thaliana]
12904_s_at (ATERF1_S_AT)	12904_s_at (ATERF1_S_AT)dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]
12909_s_at (ATERF6_S_AT)	12909_s_at (ATERF6_S_AT)emb CAB10530.1 (Z97343) EREBP-4 like protein [Arabidopsis thaliana]
12989_s_at (AC004077.149_S_AT)	12989_s_at (AC004077.149_S_AT)gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
13014_at (U93215.87_AT)	13014_at (U93215.87_AT)gb AAB63082.1 (U93215) putative lipase [Arabidopsis thaliana]

ProbeSet	Description
13110_at (AF074021.34_AT)	13110_at (AF074021.34_AT)gb AAD29776.1 AF074021_8 (AF074021) putative symbiosis-related protein [Arabidopsis thaliana]
13115_at (AC000375.44_AT)	13115_at (AC000375.44_AT)gb AAB60774.1 (AC000375) ESTs gb U75592,gb T13956,gb T43869 come from from this gene. [Arabidopsis thaliana]
13256_s_at (gammaglutamyltranspepti_S_AT)	13256_s_at (gammaglutamyltranspepti_S_AT)emb CAA89206.1 (Z49240) gamma-glutamyl transpeptidase [Arabidopsis thaliana]
13270_at (HSF21_AT)	13270_at (HSF21_AT)gb AAC31792.1 (U68561) heat shock transcription factor 21 [Arabidopsis thaliana]
13271_g_at (HSF21_G_AT)	13271_g_at (HSF21_G_AT)gb AAC31792.1 (U68561) heat shock transcription factor 21 [Arabidopsis thaliana]
13273_s_at (HSF4_S_AT)	13273_s_at (HSF4_S_AT)gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
13279_s_at (HSP176II_S_AT)	13279_s_at (HSP176II_S_AT)emb CAA45039.1 (X63443) heat shock protein 17.6-II [Arabidopsis thaliana]
13370_at (AC005322.4_AT)	13370_at (AC005322.4_AT)gb AAC97990.1 (AC005322) Strong similarity to Dsor1 protein kinase gb D13782 from Drosophila melanogaster. [Arabidopsis thaliana]
13645_at (AC000098.8_AT)	13645_at (AC000098.8_AT)gb AAB71443.1 (AC000098) EST gb ATTS0295 comes from this gene. [Arabidopsis thaliana]
13656_at (AC007138.31_AT)	13656_at (AC007138.31_AT)gb AAD22649.1 AC007138_13 (AC007138) predicted protein of unknown function [Arabidopsis thaliana]
13714_at (NOVARTIS101_RC_AT)	13714_at gb AAF18728.1 AC018721_3 (AC018721) putative CCCH-type zinc finger protein [Arabidopsis thaliana]
13806_at (AC002354.15_AT)	13806_at (AC002354.15_AT)gb AAB81668.1 (AC002354) NAM (no apical meristem)-like protein [Arabidopsis thaliana]

ProbeSet	Description
13818_s_at (AC006218.175_S_AT)	13818_s_at (AC006218.175_S_AT)gb AAD15433.1 (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]
14030_at (AC005970.225_AT)	14030_at (AC005970.225_AT)gb AAC95171.1 (AC005970) putative protein kinase [Arabidopsis thaliana]
14139_at (NOVARTIS30_AT)	14139_at gb AAD09343.1 (AF026538) ABA-responsive protein [Hordeum vulgare]
14141_at (NOVARTIS31_AT)	14141_at No hits found less than or equal to 1e-15.
14170_at (NOVARTIS51_AT)	14170_at gb AAF29406.1 AC022354_5 (AC022354) unknown protein [Arabidopsis thaliana]
14248_at (PAD3_AT)	14248_at (PAD3_AT)gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
14431_at (AL035394.279_AT)	14431_at (AL035394.279_AT)emb CAA23047.1 (AL035394) putative protein [Arabidopsis thaliana]
14605_at (AC006193.6_AT)	14605_at (AC006193.6_AT)gb AAD38247.1 AC006193_3 (AC006193) very similar to alcohol dehydrogenase [Arabidopsis thaliana]
14608_at (AC007357.49_AT)	14608_at (AC007357.49_AT)gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana]
14609_at (AC002340.147_AT)	14609_at (AC002340.147_AT)gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
14697_g_at (WT740_RC_G_AT)	14697_g_at (WT740_RC_G_AT)gb AAD23643.1 AC007119_9 (AC007119) unknown protein [Arabidopsis thaliana]
14763_at (X86958.1_AT)	14763_at (X86958.1_AT)emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]

ProbeSet	Description
14959_at (AC007202.26_AT)	14959_at (AC007202.26_AT)gb AAD30230.1 AC007202_12 (AC007202) T8K14.13 [Arabidopsis thaliana]
14978_at (AC002333.49_AT)	14978_at (AC002333.49_AT)gb AAB64024.1 (AC002333) putative glucosyltransferase [Arabidopsis thaliana]
15039_at (AF001308.67_AT)	15039_at (AF001308.67_AT)gb AAC78710.1 (AF001308) drought-induced-19-like 1 [Arabidopsis thaliana]
15040_g_at (AF001308.67_G_AT)	15040_g_at (AF001308.67_G_AT)gb AAC78710.1 (AF001308) drought-induced-19-like 1 [Arabidopsis thaliana]
15120_s_at (ATU10034_S_AT)	15120_s_at (ATU10034_S_AT)gb AAA93132.1 (U10034) glutamate decarboxylase [Arabidopsis thaliana]
15137_s_at (ATU57320_S_AT)	15137_s_at (ATU57320_S_AT)gb AAB47973.1 (U57320) blue copper-binding protein II [Arabidopsis thaliana]
15203_s_at (AB013887_S_AT)	15203_s_at (AB013887_S_AT)dbj BAA34251.1 (AB013887) RAV2 [Arabidopsis thaliana]
17376_at (AL021890.218_AT)	17376_at (AL021890.218_AT)emb CAA17164.1 (AL021890) putative protein [Arabidopsis thaliana]
17381_at (Z99708.402_AT)	17381_at (Z99708.402_AT)emb CAB16811.1 (Z99708) putative protein [Arabidopsis thaliana]
15551_at (AL035440.289_AT)	15551_at (AL035440.289_AT)emb CAB36537.1 (AL035440) putative dihydrolipoamide succinyltransferase [Arabidopsis thaliana]
15582_s_at (ATH131392_S_AT)	15582_s_at (ATH131392_S_AT)emb CAA10364.1 (AJ131392) alternative oxidase [Arabidopsis thaliana]
15665_s_at (AF022658_S_AT)	15665_s_at (AF022658_S_AT)gb AAB80922.1 (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]
15672_s_at (AF082299_S_AT)	15672_s_at (AF082299_S_AT)No hits found less than or equal to 1e-15.
15919_at (AC007060.42_AT)	15919_at (AC007060.42_AT)gb AAD25764.1 AC007060_22 (AC007060) EST gb AA721821 comes from this gene. [Arabidopsis thaliana]

ProbeSet	Description
15924_at (AC007138.61_AT)	15924_at (AC007138.61_AT)gb AAD22658.1 AC007138_22 (AC007138) predicted protein of unknown function [Arabidopsis thaliana]
15978_at (X68592.6_AT)	15978_at (X68592.6_AT)emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
16003_s_at (AL021749.64_S_AT)	16003_s_at (AL021749.64_S_AT)emb CAA16877.1 (AL021749) ADP, ATP carrier-like protein [Arabidopsis thaliana]
16053_i_at (Y14251.4_I_AT)	16053_i_at (Y14251.4_I_AT)emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]
16077_s_at (AF085230_S_AT)	16077_s_at (AF085230_S_AT)gb AAD16046.1 (AF085230) phytochelatinsynthase 1 [Arabidopsis thaliana]
16134_s_at (AF132016_S_AT)	16134_s_at (AF132016_S_AT)gb AAD33584.1 AF132016_1 (AF132016) RING-H2 zinc finger protein ATL6 [Arabidopsis thaliana]
16151_s_at (ATHPRKINA_S_AT)	16151_s_at (ATHPRKINA_S_AT)gb AAA18853.1 (L07248) protein kinase [Arabidopsis thaliana]
16232_s_at (AL080252.77_S_AT)	16232_s_at (AL080252.77_S_AT)emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana]
16357_at (AF149413.38_AT)	16357_at (AF149413.38_AT)gb AAD40144.1 AF149413_25 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]
16442_s_at (AJ002551.2_S_AT)	16442_s_at (AJ002551.2_S_AT)emb CAA05547.1 (AJ002551) heat shock protein 70 [Arabidopsis thaliana]
16457_s_at (AC005397.17_S_AT)	16457_s_at (AC005397.17_S_AT)gb AAD23036.1 AC006526_2 (AC006526) unknown protein [Arabidopsis thaliana]
16539_s_at (AB013301_S_AT)	16539_s_at (AB013301_S_AT)emb CAB10530.1 (Z97343) EREBP-4 like protein [Arabidopsis thaliana]

ProbeSet	Description
16570_s_at (ATHCDPKA_S_AT)	16570_s_at (ATHCDPKA_S_AT)gb AAF27092.1 AC011809_1 (AC011809) calcium-dependent protein kinase 1 [Arabidopsis thaliana]
16620_s_at (AF051338_S_AT)	16620_s_at (AF051338_S_AT)gb AAC05572.1 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]
16638_s_at (AF139098_S_AT)	16638_s_at (AF139098_S_AT)gb AAD37511.1 AF139098_1 (AF139098) putative zinc finger protein [Arabidopsis thaliana]
16712_at (AC006068.67_AT)	16712_at (AC006068.67_AT)gb AAD15444.1 (AC006068) putative glycogenin [Arabidopsis thaliana]
16721_at (AC006533.58_AT)	16721_at (AC006533.58_AT)gb AAD32285.1 AC006533_9 (AC006533) putative poly(ADP-ribose) glycohydrolase [Arabidopsis thaliana]
16753_at (AL031032.110_AT)	16753_at (AL031032.110_AT)emb CAA19874.1 (AL031032) putative protein [Arabidopsis thaliana]
16916_s_at (X77199.8_S_AT)	16916_s_at (X77199.8_S_AT)emb CAA54420.1 (X77199) heat shock cognate 70-2 [Arabidopsis thaliana]
16968_at (AL021961.93_AT)	16968_at (AL021961.93_AT)emb CAA17559.1 (AL021961) glucosyltransferase-like protein [Arabidopsis thaliana]
17051_s_at (AF098947_S_AT)	17051_s_at (AF098947_S_AT)gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]
17323_at (U95973.69_AT)	17323_at (U95973.69_AT)gb AAB65477.1 (U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
17352_at (AC007127.33_AT)	17352_at (AC007127.33_AT)gb AAD25140.1 AC007127_6 (AC007127) putative protein kinase [Arabidopsis thaliana]
17477_s_at (X63443.2_S_AT)	17477_s_at (X63443.2_S_AT)emb CAA45039.1 (X63443) heat shock protein 17.6-II [Arabidopsis thaliana]

ProbeSet	Description
17579_s_at (AF093753_S_AT)	17579_s_at (AF093753_S_AT)gb AAD50593.1 AF093753_1 (AF093753) phytochelatase synthase [Arabidopsis thaliana]
17775_at (AC004392.2_AT)	17775_at (AC004392.2_AT)gb AAC28500.1 (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
17840_s_at (AC002333.223_S_AT)	17840_s_at (AC002333.223_S_AT)gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
17886_at (AC004484.151_AT)	17886_at (AC004484.151_AT)gb AAC14530.1 (AC004484) unknown protein [Arabidopsis thaliana]
17894_at (AC005724.44_AT)	17894_at (AC005724.44_AT)gb AAD08938.1 (AC005724) unknown protein [Arabidopsis thaliana]
17907_s_at (AC004684.165_S_AT)	17907_s_at (AC004684.165_S_AT)gb AAC23645.1 (AC004684) unknown protein [Arabidopsis thaliana]
17990_at (AF178075_AT)	17990_at (AF178075_AT)emb CAB41312.1 (AL049711) putative calmodulin [Arabidopsis thaliana]
18167_s_at (AL021711.23_S_AT)	18167_s_at (AL021711.23_S_AT)emb CAA16745.1 (AL021711) heat shock transcription factor-like protein [Arabidopsis thaliana].
18255_at (AC005770.25_AT)	18255_at (AC005770.25_AT)gb AAC79625.1 (AC005770) unknown protein [Arabidopsis thaliana]
18263_at (AC005724.36_AT)	18263_at (AC005724.36_AT)gb AAD08937.1 (AC005724) unknown protein [Arabidopsis thaliana]
18284_at (AL021961.67_AT)	18284_at (AL021961.67_AT)emb CAA17557.1 (AL021961) putative protein [Arabidopsis thaliana]
18544_at (AC007060.14_AT)	18544_at (AC007060.14_AT)gb AAD25749.1 AC007060_7 (AC007060) Strong similarity to F19I3.8 gi 3033381 putative UDP-galactose-4-epimerase from Arabidopsis thaliana BAC gb AC004238 and is a member of PF 01370 the NAD dependent epimerase/dehydratase family. EST gb AA597338 comes from this gene.
18600_at (L76926.1_AT)	18600_at (L76926.1_AT)gb AAC77829.1 (L76926) putative zinc finger protein [Arabidopsis thaliana]

ProbeSet	Description
18662_s_at (AC002343.20_S_AT)	18662_s_at (AC002343.20_S_AT)gb AAB63608.1 (AC002343) unknown protein [Arabidopsis thaliana]
18896_at (AC002329.51_AT)	18896_at (AC002329.51_AT)gb AAA67317.1 (L19262) 3-hydroxy-3-methylglutaryl-CoA reductase [Arabidopsis thaliana]
19247_at (AF071527.44_AT)	19247_at (AF071527.44_AT)gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
19411_at (AC007661.104_AT)	19411_at (AC007661.104_AT)gb AAD32774.1 AC007661_11 (AC007661) unknown protein [Arabidopsis thaliana]
19451_at (AC004392.6_AT)	19451_at (AC004392.6_AT)gb AAC28502.1 (AC004392) Similar to F4I1.26 putative beta-glucosidase gi 3128187 from A. thaliana BAC gb AC004521. ESTs gb N97083, gb F19868 and gb F15482 come from this gene. [Arabidopsis thaliana]
19462_s_at (AF001168.2_S_AT)	19462_s_at (AF001168.2_S_AT)emb CAB75467.1 (AL138659) serine/threonine-specific kinase lecRK1 precursor, lectin
19640_at (AC004561.78_AT)	19640_at (AC004561.78_AT)gb AAC95192.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
19916_at (AC006577.34_AT)	19916_at (AC006577.34_AT)gb AAD25781.1 AC006577_17 (AC006577) EST gb R64848 comes from this gene. [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	19991_at (AC007017.124_AT)gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
20051_at (AC000106.38_AT)	20051_at (AC000106.38_AT)gb AAB70412.1 (AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb Z49209). ESTs gb T44436,gb 42252 come from this gene. [Arabidopsis thaliana]
20142_at (AL035521.155_AT)	20142_at (AL035521.155_AT)emb CAB36716.1 (AL035521) extra-large G-protein-like [Arabidopsis thaliana]
20199_at (AL050300.89_AT)	20199_at (AL050300.89_AT)emb CAB43428.1 (AL050300) putative protein [Arabidopsis thaliana]

ProbeSet	Description
20269_at (AC002387.237_AT)	20269_at (AC002387.237_AT)gb AAB82640.1 (AC002387) putative pectinesterase [<i>Arabidopsis thaliana</i>]
20335_s_at (Y14208.2_S_AT)	20335_s_at (Y14208.2_S_AT)emb CAA74604.1 (Y14208) R2R3-MYB transcription factor [<i>Arabidopsis thaliana</i>]
20356_at (AC004561.74_AT)	20356_at (AC004561.74_AT)gb AAC95191.1 (AC004561) putative glutathione S-transferase [<i>Arabidopsis thaliana</i>]
20372_at (AL021713.24_AT)	20372_at (AL021713.24_AT)emb CAA16792.1 (AL021713) putative protein [<i>Arabidopsis thaliana</i>]
20421_at (U81294.2_AT)	20421_at (U81294.2_AT)emb CAB10242.1 (Z97336) germin precursor oxalate oxidase [<i>Arabidopsis thaliana</i>]
20590_at (AL035540.159_AT)	20590_at (AL035540.159_AT)emb CAB37511.1 (AL035540) Phospholipase like protein [<i>Arabidopsis thaliana</i>]
20619_at (AC005896.161_AT)	20619_at (AC005896.161_AT)gb AAC98070.1 (AC005896) putative C2H2-type zinc finger protein [<i>Arabidopsis thaliana</i>]
20686_at (Y14424.2_AT)	20686_at (Y14424.2_AT)emb CAA74766.1 (Y14424) hypothetical protein [<i>Arabidopsis thaliana</i>]
20689_s_at (AC002335.19_S_AT)	20689_s_at (AC002335.19_S_AT)gb AAB64310.1 (AC002335) putative calcium binding protein [<i>Arabidopsis thaliana</i>]

- 5 **Table 13b** Probe Sets corresponding to genes, the expression of which is decreased in an incompatible interaction at 3 and/or 6 hours after infection of four *Arabidopsis* ecotypes with *Pseudomonas syringae* pv tomato DC3000, *P. maculicola* ES4326 and *P. phaseolica* NPS3121

ProbeSet	Description
12048_at (AF001308.46_AT)	12048_at (AF001308.46_AT)gb AAC78704.1 (AF001308) predicted glycosyl transferase [<i>Arabidopsis thaliana</i>]
12218_at (AJ242588.2_AT)	12218_at (AJ242588.2_AT)emb CAB43344.1 (AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase [<i>Arabidopsis thaliana</i>]

ProbeSet	Description
12727_f_at (Z95799_F_AT)	12727_f_at (Z95799_F_AT)gb AAD53097.1 AF175992_1 (AF175992) putative transcription factor [Arabidopsis thaliana]
13144_at (AC007017.246_AT)	13144_at (AC007017.246_AT)gb AAD21471.1 (AC007017) unknown protein [Arabidopsis thaliana]
13161_at (AF002109.89_AT)	13161_at (AF002109.89_AT)gb AAB95278.1 (AF002109) putative isoamylase [Arabidopsis thaliana]
13220_s_at (CHS-EXON1_S_AT)	13220_s_at (CHS-EXON1_S_AT)gb AAA32771.1 (M20308) chalcone synthase [Arabidopsis thaliana]
13482_at (AC005896.195_AT)	13482_at (AC005896.195_AT)gb AAC98071.1 (AC005896) nodulin-like protein [Arabidopsis thaliana]
13547_s_at (AC004450.15_S_AT)	13547_s_at (AC004450.15_S_AT)gb AAC64299.1 (AC004450) 3-isopropylmalate dehydratase, small subunit [Arabidopsis thaliana]
13637_at (AL049482.9_AT)	13637_at (AL049482.9_AT)emb CAB39634.1 (AL049482) AX110P-like protein [Arabidopsis thaliana]
13651_at (AL035538.320_AT)	13651_at (AL035538.320_AT)emb CAB37556.1 (AL035538) putative protein [Arabidopsis thaliana]
15832_at (AC004561.255_AT)	15832_at (AC004561.255_AT)gb AAC95217.1 (AC004561) unknown protein [Arabidopsis thaliana]
16110_s_at (AB004822_S_AT)	16110_s_at (AB004822_S_AT)dbj BAA22215.1 (AB004822) plastid RNA polymerase sigma-subunit [Arabidopsis thaliana]
16229_at (AL049638.148_AT)	16229_at (AL049638.148_AT)emb CAB40944.1 (AL049638) putative transport protein [Arabidopsis thaliana]
16351_at (AL021684.194_AT)	16351_at (AL021684.194_AT)emb CAA16688.1 (AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
16468_at (AF049870.5_AT)	16468_at (AF049870.5_AT)gb AAD02499.1 (AF049870) thaumatin-like protein [Arabidopsis thaliana]
16548_s_at (AF054617_S_AT)	16548_s_at (AF054617_S_AT)gb AAC25108.1 (AF054617) one helix protein [Arabidopsis thaliana]

ProbeSet	Description
16978_g_at (AF076641.2_G_AT)	16978_g_at (AF076641.2_G_AT)gb AAD46064.1 AF076641_1 (AF076641) homeodomain leucine-zipper protein ATHB16 [Arabidopsis thaliana]
17018_s_at (ATU18929_S_AT)	17018_s_at (ATU18929_S_AT)gb AAA79982.1 (U18929) cytochrome p450 dependent monooxygenase [Arabidopsis thaliana]
17494_s_at (ATU30478_S_AT)	17494_s_at (ATU30478_S_AT)gb AAB38071.1 (U30478) expansin At-EXP5 [Arabidopsis thaliana]
17823_s_at (AC006555.10_S_AT)	17823_s_at (AC006555.10_S_AT)gb AAD26909.1 AC007233_1 (AC007233) putative beta-1,3-glucanase [Arabidopsis thaliana]
18215_at (Z97335.114_AT)	18215_at (Z97335.114_AT)emb CAB46000.1 (Z97335) selenium-binding protein like [Arabidopsis thaliana]
18301_s_at (AL022223.48_S_AT)	18301_s_at (AL022223.48_S_AT)emb CAA18218.1 (AL022223) fructose-bisphosphate aldolase [Arabidopsis thaliana]
18471_at (AC006533.103_AT)	18471_at (AC006533.103_AT)gb AAD32293.1 AC006533_17 (AC006533) putative glucosyltransferase [Arabidopsis thaliana]
18634_s_at (Z97343.468_S_AT)	18634_s_at (Z97343.468_S_AT)emb CAB10536.1 (Z97343) hypothetical protein [Arabidopsis thaliana]
18976_at (AC000106.31_AT)	18976_at (AC000106.31_AT)gb AAB70409.1 (AC000106) Contains similarity to Rhodococcus amidase (gb D16207). ESTs gb T20504,gb H36650,gb N97423,gb H36595 come from this gene. [Arabidopsis thaliana]
18984_at (AC003096.100_AT)	18984_at (AC003096.100_AT)gb AAC16266.1 (AC003096) unknown protein [Arabidopsis thaliana]
19494_at (AC007296.26_AT)	19494_at (AC007296.26_AT)gb AAD30251.1 AC007296_12 (AC007296) Strong similarity to gb X95759 soluble- starch-synthase precursor (SSIII) from Solanum tuberosum. [Arabidopsis thaliana]

ProbeSet	Description
20442_i_at (AC006341.42_I_AT)	20442_i_at (AC006341.42_I_AT)gb AAD34693.1 AC006341_2 1 (AC006341) Similar to gb AF069494 cytochrome P450 from Sinapis alba and is a member of the PF 00067 Cytochrome P450 family. EST gb F14190 comes from this gene. [Arabidopsis thaliana]

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Table 14 Probe Sets as referred to in Table 3 corresponding to genes with promoters conferring low basal expression in all ecotypes (Col, Ler, Ws, and Cvi) and high inducibility in Col

ProbeSet	Description
20421_at (U81294.2_AT)	see Table 3
20142_at (AL035521.155_AT)	see Table 3
14635_s_at (PR.1_S_AT)	see Table 3
12908_s_at (ATERF5_S_AT)	see Table 11
20620_g_at (AC005896.161_G_AT)	see Table 11

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102290 "2/2/8860

Table 15 Probe Sets as referred to in Table 3 corresponding to genes with promoters inducing expression in *Pseudomonas syringae* pv. *maculiola*-infected *Arabidopsis*

12891_at (ATACS6_AT)	13015_s_at (X98673.2_S_AT)
13100_at (AC003680.50_AT)	13115_at (AC000375.44_AT)
13217_s_at (CALMODULINLIKE_S_AT)	13467_at (AL096860.198_AT)
13645_at (AC000098.8_AT)	13818_s_at (AC006218.175_S_AT)
14032_at (AL035601.11_AT)	14248_at (PAD3_AT)
14609_at (AC002340.147_AT)	15116_f_at (AF121356_F_AT)
15622_s_at (ATU43945_S_AT)	16173_s_at (D78607_S_AT)
17485_s_at (Z97340.345_S_AT)	17511_s_at (AF067605_S_AT)
17548_s_at (AF118823_S_AT)	17775_at (AC004392.2_AT)
17930_s_at (AJ006960.4_S_AT)	19284_at (AC003028.196_AT)
19546_at (AC005398.172_AT)	19640_at (AC004561.78_AT)
20134_s_at (AC007178.71_S_AT)	20194_at (AC007584.48_AT)
20348_at (AC005967.35_AT)	12892_g_at (ATACS6_G_AT)
12904_s_at (ATERF1_S_AT)	12989_s_at (AC004077.149_S_AT)
13215_s_at (cafferoylcoAmethyltrans_S_AT)	13565_at (AL035601.21_AT)
13627_at (AL035394.196_AT)	16649_s_at (ATHORF_S_AT)
16914_s_at (AL049500.57_S_AT)	16995_at (AC002391.188_AT)
19991_at (AC007017.124_AT)	20356_at (AC004561.74_AT)

Table 16 Probe Sets corresponding to genes with promoters inducing expression in *Botrytis cinerea*-infected *Arabidopsis*

Probe Set	Description
12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]
12574_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]
12989_s_at (AC004077.149_S_AT)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
13015_s_at (X98673.2_S_AT)	emb CAA67232.1 (X98674) zinc finger protein [Arabidopsis thaliana]
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
13215_s_at (cafferoylCoAmethyltrans_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
13565_at (AL035601.21_AT)	emb CAB38206.1 (AL035601) auxin-responsive GH3-like protein [Arabidopsis thaliana]
14015_s_at (A71588.1_S_AT)	emb CAB42612.1 (A71639) unnamed protein product [Arabidopsis thaliana]
14016_s_at (A71596.1_S_AT)	emb CAB42592.1 (A71596) unnamed protein product [Arabidopsis thaliana]
14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
16638_s_at (AF139098_S_AT)	gb AAD37511.1 AF139098_1 (AF139098) putative zinc finger protein [Arabidopsis thaliana]
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
16892_at (U37336.3_AT)	gb AAC49135.1 (U37336) senescence-specific cysteine protease
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]

Probe Set	Description
17533_s_at (ATU43488_S_AT)	gb AAB18367.1 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]
17744_s_at (AC004684.168_S_AT)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
18716_at (X91916_AT)	
18888_at (AC007591.68_AT)	gb AAD39666.1 AC007591_31 (AC007591) Is a member of the PF 00903 gyloxalase family. ESTs gb T44721, gb T21844 and gb AA395404 come from this gene. [Arabidopsis thaliana]
19019_i_at (X82623.2_I_AT)	emb CAA57943.1 (X82623) SRG2At [Arabidopsis thaliana]
19284_at (AC003028.196_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
20356_at (AC004561.74_AT)	gb AAC95191.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Table 17 Probe sets which correspond to genes downregulated in response to infection by 5 different viruses

Probe Set	Description	Function	Blast
17191_i_at (AL021961.178_I_AT)	emb CAA17564.1 (AL021961) putative protein [Arabidopsis thaliana]	DNA binding protein	MyB TF
18866_at (AC005917.178_AT)	gb AAD10163.1 (AC005917) putative Ta11-like non-LTR retroelement protein [Arabidopsis thaliana]	transposon	
20678_at (AC007296.30_AT)	gb AAD30253.1 AC007296_14 (AC007296) ESTs gb R65381 and gb T44635 come from this gene. [Arabidopsis thaliana]	unknown	unknown
12356_at (X99952.1_AT)	emb CAA68212.1 (X99952) peroxidase [Arabidopsis thaliana]	metabolic protein	
12448_at (AC002337.58_AT)	gb AAB63824.1 (AC002337) putative acyl-CoA synthetase [Arabidopsis thaliana]	metabolic protein	
12854_s_at (ACS1_S_AT)	gb AAA96006.1 (U26542) 1- aminocyclopropane-1- carboxylate synthase-like protein [Arabidopsis thaliana]	hormone response	
13812_s_at (AC005275.104_S_AT)	gb AAD14468.1 (AC005275) putative GH3-like protein [Arabidopsis thaliana]	hormone response	
14530_at (AL021889.231_AT)	emb CAA17145.1 (AL021889) putative protein [Arabidopsis thaliana]	unknown	unknown
16461_i_at (AC004683.79_I_AT)	gb AAC28766.1 (AC004683) peroxidase [Arabidopsis thaliana]	metabolic protein	
16462_s_at (AC004683.79_S_AT)	gb AAC28766.1 (AC004683) peroxidase [Arabidopsis thaliana]	metabolic protein	
17305_at (U25649.3_AT)	gb AAC50023.1 (U25649) ATPME2 precursor [Arabidopsis thaliana]	cell wall polymer	

Probe Set	Description	Function	Blast
14965_at (AC002329.22_AT)	gb AAB86507.1 (AC002329) unknown protein [Arabidopsis thaliana]	unknown	unknown
15578_s_at (AF004213_S_AT)	gb AAC49746.1 (AF004213) ethylene-insensitive3-like1 [Arabidopsis thaliana]	hormone response	
16062_s_at (AB007789_S_AT)	gb AAD15976.1 (AF074601) CRT/DRE binding factor 2 [Arabidopsis thaliana]	stress response	
16111_f_at (AB007788_F_AT)	dbj BAA33435.1 (AB013816) DREB1B [Arabidopsis thaliana] [Arabidopsis thaliana]	stress response	
16434_at (AL021711.157_AT)	emb CAA16754.1 (AL021711) putative protein [Arabidopsis thaliana]	metabolic protein	similar to APG (non proline-rich region) [Arabidopsis thaliana] /putative GDSL-motif lipase/hydrolase
16891_s_at (AF080120.33_S_AT)	gb AAC35539.1 (AF080120) contains similarity to glycosyl hydrolases family 9 (Pfam: glycosyl_hydro5.hmm, score: 88.03) [Arabidopsis thaliana]	cell wall polymer	
16990_at (AC004684.91_AT)	gb AAC23634.1 (AC004684) putative expansin [Arabidopsis thaliana]	cell wall polymer	
17577_g_at (AF087820_G_AT)	gb AAD52697.1 AF087820_1 (AF087820) auxin transport protein [Arabidopsis thaliana]	hormone response	
17743_at (AC002341.99_AT)	gb AAB67624.1 (AC002341) putative peroxidase [Arabidopsis thaliana]	metabolic protein	
19017_at (AL035709.69_AT)	emb CAB38928.1 (AL035709) endo-xyloglucan transferase-like protein [Arabidopsis thaliana]	cell wall polymer	
19396_at (AJ001855.2_AT)	emb CAA05054.1 (AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]	structural protein	

Probe Set	Description	Function	Blast
19660_at (AC002336.29_AT)	gb AAB87577.1 (AC002336) putative expansin [Arabidopsis thaliana]	cell wall polymer	
20675_at (AC006234.204_AT)	gb AAD20920.1 (AC006234) beta-expansin [Arabidopsis thaliana]	cell wall polymer	
12086_s_at (AC002409.88_S_AT)	gb AAB86456.1 (AC002409) unknown protein [Arabidopsis thaliana]	unknown	
13728_at (NOVARTIS111_AT)	gb AAF27057.1 AC008262_6 (AC008262) F4N2.12 [Arabidopsis thaliana]	unknown	unknown
14770_s_at (AC002338.167_S_AT)	gb AAB63092.1 (U93215) putative MYB family transcription factor [Arabidopsis thaliana]	DNA binding protein	
15067_at (AC004683.36_AT)	gb AAC28758.1 (AC004683) unknown protein [Arabidopsis thaliana]	membrane protein	transporter or ferroportin
15154_s_at (ATHMTGDAS_S_AT)	emb CAB51206.1 (AL096860) glutamine-dependent asparagine synthetase [Arabidopsis thaliana]	metabolic protein	
15544_at (AL021633.110_AT)	emb CAA16532.1 (AL021633) predicted protein [Arabidopsis thaliana]	membrane protein	E. coli cation transporter ChaC
15631_s_at (AB005805_S_AT)	dbj BAA28625.1 (AB005805) aldehyde oxidase [Arabidopsis thaliana]	metabolic protein	
16048_at (X78586.2_AT)	emb CAA55323.1 (X78586) Dr4 [Arabidopsis thaliana]	stress response	
16090_s_at (ATHFAD8A_S_AT)	gb AAB60302.1 (U08216) chloroplast linoleate desaturase [Arabidopsis thaliana]	metabolic protein	
16164_s_at (ATU47029_S_AT)	gb AAC49302.1 (U47029) ERECTA [Arabidopsis thaliana]	receptor/kinase	
16241_at (AL022604.84_AT)	emb CAA18733.1 (AL022604) putative protein [Arabidopsis thaliana]	unknown	unknown

Probe Set	Description	Function	Blast
16327_at (AC002334.12_AT)	gb AAF18589.1 AC002332_1 (AC002332) putative myosin heavy chain [Arabidopsis thaliana]	structural protein	
16406_at (AC006921.33_AT)	gb AAD21431.1 (AC006921) putative protein kinase [Arabidopsis thaliana]	receptor/kinase	
16868_at (AL035679.123_AT)	emb CAB38821.1 (AL035679) putative endo-1, 4-beta- glucanase [Arabidopsis thaliana]	cell wall polymer	
17362_s_at (Z97338.181_S_AT)	emb CAB10305.1 (Z97338) glucosyltransferase [Arabidopsis thaliana]	metabolic protein	
17916_at (U22428.2_AT)	gb AAB03100.1 (U22428) starch branching enzyme class II [Arabidopsis thaliana]	metabolic protein	
18515_at (AC007063.215_AT)	gb AAF24822.1 AC007592_15 (AC007592) F12K11.17 [Arabidopsis thaliana]	metabolic protein	putative 1,3- beta-D-glucan synthase [Arabidopsis thaliana]
18635_at (AC004005.44_AT)	gb AAC23401.1 (AC004005) unknown protein [Arabidopsis thaliana]	metabolic protein	methyl Cl transferase
18667_at (AJ249442_AT)	emb CAB55758.1 (AJ249442) putative AUX1-like permease [Arabidopsis thaliana]	hormone response	
18683_s_at (L27158_S_AT)	gb AAB60302.1 (U08216) chloroplast linoleate desaturase [Arabidopsis thaliana]	metabolic protein	
18694_s_at (U89272_S_AT)	gb AAB61458.1 (U89272) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana]	membrane protein	
19870_s_at (AL021811.48_S_AT)	emb CAA16958.1 (AL021811) putative protein [Arabidopsis thaliana]	unknown	unknown

Table 18 Probe sets which correspond to genes upregulated in response to infection by 5 different viruses

Probeset	Description	Time	Function	Blast
12904_s_at (ATERF1_S_AT)	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]	5dpi	hormone response	
16063_s_at (AB008103_S_AT)	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]	5dpi	hormone response	
12906_s_at (ATERF3_S_AT)	dbj BAA32420.1 (AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]	1dpi	stress response	
16537_s_at (AB008111_S_AT)	dbj BAA28953.1 (AB008111) Atrboh F [Arabidopsis thaliana]	4dpi	stress response	
16610_s_at (AB008490_S_AT)	dbj BAA34729.1 (AB008490) response regulator 7 [Arabidopsis thaliana]	1dpi	signaling not kinase	
13645_at (AC000098.8_AT)	gb AAB71443.1 (AC000098) EST gb ATTS0295 comes from this gene. [Arabidopsis thaliana]	4-5dpi	unknown	unknown
19388_at (AC000104.61_AT)	gb AAB70450.1 (AC000104) ESTs gb N65789,gb T04628 come from this gene. [Arabidopsis thaliana]	4dpi	kinase/recept or	prenylated Rab receptor
19368_at (AC000348.22_AT)	gb AAB61497.1 (AC000348) T7N9.21 [Arabidopsis thaliana]	5dpi	unknown	unknown
13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592,gb T13956,gb T4386 9 come from from this gene. [Arabidopsis thaliana]	4dpi	DNA binding protein	putative WRKY DNA binding protein [Oryza sativa]
14964_at (AC001229.8_AT)	gb AAB60905.1 (AC001229) F5I14.4 gene product [Arabidopsis thaliana]	5dpi	unknown	unknown
17840_s_at (AC002333.223_S_AT)	gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]	5dpi	stress response	

Probeset	Description	Time	Function	Blast
15379_at (AC002335.182_AT)	gb AAB64323.1 (AC002335) unknown protein [Arabidopsis thaliana]	1dpi	unknown	unknown
20689_s_at (AC002335.19_S_AT)	gb AAB64310.1 (AC002335) putative calcium binding protein [Arabidopsis thaliana]	5dpi	stress response	
12449_s_at (AC002343.179_S_AT)	gb AAB63623.1 (AC002343) cellulose synthase isolog [Arabidopsis thaliana]	4-5dpi	cell wall polymer	
13842_at (AC002396.12_AT)	gb AAC00572.1 (AC002396) similar to zinc metalloproteinases [Arabidopsis thaliana]	5dpi	protein processing	
19424_at (AC002396.44_AT)	gb AAC00588.1 (AC002396) glucose-6-phosphate 1- dehydrogenase [Arabidopsis thaliana]	5dpi	metabolic protein	
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]	5dpi	metabolic protein	
16365_at (AC003974.136_AT)	gb AAC04495.1 (AC003974) putative disease resistance protein [Arabidopsis thaliana]	2-5dpi	stress response	
17752_at (AC003974.37_AT)	gb AAC04483.1 (AC003974) putative protein kinase [Arabidopsis thaliana]	4dpi	kinase/recept or	
20409_g_at (AC004077.132_G_AT)	emb CAB40383.1 (AJ131180) ribosomal protein S14 [Arabidopsis thaliana]	5dpi	protein processing	
13048_s_at (AC004138.22_S_AT)	gb AAC32906.1 (AC004138) putative basic blue protein (plantacyanin) [Arabidopsis thaliana]	4dpi	stress response	
12764_f_at (AC004138.69_F_AT)	gb AAC32912.1 (AC004138) putative glutathione S- transferase [Arabidopsis thaliana]	5dpi	stress response	
13895_at (AC004218.63_AT)	gb AAC27833.1 (AC004218) putative phospholipase [Arabidopsis thaliana]	4dpi	signaling not kinase	

Probeset	Description	Time	Function	Blast
20477_at (AC004238.154_AT)	gb AAC12841.1 (AC004238) putative UDP-N- acetylglucosamine pyrophosphorylase [Arabidopsis thaliana]	5dpi	metabolic protein	
16972_at (AC004261.89_AT)	gb AAA87347.1 (M88307) calmodulin [Brassica juncea]	5dpi	signaling not kinase	
19848_s_at (AC004261.94_S_AT)	dbj BAA08282.1 (D45848) calmodulin-related protein [Arabidopsis thaliana]	5dpi	signaling not kinase	
19044_at (AC004392.38_AT)	gb AAC28514.1 (AC004392) Strong similarity to gi 2160138 F19K23.6 gene product from A. thaliana BAC gb AC000375. [Arabidopsis thaliana]	5dpi	unknown	unknown
19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S- transferase [Arabidopsis thaliana]	5dpi	stress response	
20491_at (AC004561.146_AT)	gb AAC95203.1 (AC004561) putative tropinone reductase [Arabidopsis thaliana]	5dpi	metabolic protein	
16888_s_at (AC004684.174_S_AT)	gb AAC23647.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]	4dpi	stress response	
15389_at (AC004786.100_AT)	gb AAC32433.1 (AC004786) unknown protein [Arabidopsis thaliana]	4dpi	unknown	unknown
18844_at (AC005315.131_AT)	gb AAC33239.1 (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]	4dpi	signaling not kinase	
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis]	5dpi	stress response	
17894_at (AC005724.44_AT)	gb AAD08938.1 (AC005724) unknown protein [Arabidopsis thaliana]	5dpi	unknown	unknown
18263_at (AC005724.36_AT)	gb AAD08937.1 (AC005724) unknown protein [Arabidopsis thaliana]	5dpi	unknown	unknown

Probeset	Description	Time	Function	Blast
15539_at (AC005770.21_AT)	gb AAC79601.1 (AC005770) unknown protein [Arabidopsis thaliana]	2dpi 4dpi	unknown	unknown
13920_at (AC005990.53_AT)	gb AAC98026.1 (AC005990) EST gb AA597511 comes from this gene. [Arabidopsis thaliana]	5dpi	unknown	unknown
18267_at (AC006223.23_AT)	gb AAD15384.1 (AC006223) unknown protein [Arabidopsis thaliana]	4dpi	unknown	unknown
12627_at (AC006533.99_AT)	gb AAD32292.1 AC006533_16 (AC006533) putative protein kinase [Arabidopsis thaliana]	1dpi	kinase/recept or	
12497_at (AC006533.51_AT)	gb AAD32284.1 AC006533_8 (AC006533) putative receptor- like protein kinase [Arabidopsis thaliana]	5dpi	kinase/recept or	
12656_at (AC006569.43_AT)	gb AAD21751.1 (AC006569) unknown protein [Arabidopsis thaliana]	5dpi	unknown	unknown
17008_at (AC006585.212_AT)	gb AAD23027.1 AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]	4-5dpi	metabolic protein	
19386_at (AC006592.51_AT)	No hits found less than or equal to 1e-15.	2dpi	metabolic protein	
13617_at (AC006592.64_AT)	gb AAD22351.1 AC006592_8 (AC006592) putative mitochondrial dicarboxylate carrier protein [Arabidopsis thaliana]	5dpi	unknown	unknown
15473_at (AC006836.125_AT)	gb AAD20072.1 (AC006836) putative ubiquinone biosynthesis protein [Arabidopsis thaliana]	5dpi	metabolic protein	
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]	5dpi	metabolic protein	putative xyloglucan fucosyltransf erase [Arabidopsis thaliana]

Probeset	Description	Time	Function	Blast
15921_s_at (AC007067.1_S_AT)	gb AAD39561.1 AC007067_1 (AC007067) T10O24.1 [Arabidopsis thaliana]	4dpi	unknown	unknown
14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.	5dpi	metabolic protein	
19903_at (AC007660.40_AT)	gb AAD32803.1 AC007660_4 (AC007660) unknown protein [Arabidopsis thaliana]	4dpi	unknown	unknown
15487_at (AC007661.87_AT)	gb AAD32771.1 AC007661_8 (AC007661) unknown protein [Arabidopsis thaliana]	5dpi	unknown	unknown
13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]	4dpi	unknown	unknown
13246_at (ERECTAL_AT)	gb AAF26067.1 AC012562_22 (AC012562) putative protein kinase [Arabidopsis thaliana]	4dpi	kinase/recept or	
14636_s_at (PR5_S_AT)	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [Arabidopsis thaliana]	2-5dpi	stress response	
16153_s_at (ATHRPRP1C_S_AT)	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [Arabidopsis thaliana]	2-5dpi	stress response	
16617_s_at (AF029980_S_AT)	gb AAD01897.1 (AF029980) A37 [Arabidopsis thaliana]	5dpi	unknown	unknown
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]	4dpi	cell wall polymer	
18681_at (L23573_AT)	gb AAD02548.1 (AF049922) PGP169-12 [Petunia x hybrida]	4dpi	membrane protein	

Probeset	Description	Time	Function	Blast
19181_s_at (AF053065.2_S_AT)	gb AAC39464.1 (AF053065) late embryogenesis abundant protein homolog [Arabidopsis thaliana]	5dpi	stress response	
19555_at (AF058919.48_AT)	gb AAC13630.1 (AF058919) F6N23.8 gene product [Arabidopsis thaliana]	4dpi	metabolic protein	probable methylene- tetrahydrofol ate dehydrogenas e (NADP+)
15515_r_at (AF058919.32_R_AT)	gb AAC13627.1 (AF058919) F6N23.26 gene product [Arabidopsis thaliana]	5dpi	metabolic protein	putative phosphoribos ylanthranilate transferase [Arabidopsis thaliana]
15606_s_at (AF061517_S_AT)	gb AAC15807.1 (AF061517) putative copper/zinc superoxide dismutase copper chaperone [Arabidopsis thaliana]	5dpi	stress response	
18604_at (AF069298.31_AT)	gb AAC19273.1 (AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]	5dpi	stress response	
12002_at (AF069442.47_AT)	gb AAC79112.1 (AF069442) hypothetical protein [Arabidopsis thaliana]	4-5dpi	protein processing	ubiquitin-like
20480_s_at (AF069495.2_S_AT)	emb CAB38908.1 (AL035708) cytochrome P450-like protein [Arabidopsis thaliana]	4-5dpi	metabolic protein	
20479_i_at (AF069495.2_I_AT)	emb CAB38908.1 (AL035708) cytochrome P450-like protein [Arabidopsis thaliana]	5dpi	metabolic protein	
19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]	4-5dpi	unknown	Ankyrin repeats

Probeset	Description	Time	Function	Blast
12500_s_at (AF081067.3_S_AT)	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]	4-5dpi	hormone response	
14711_s_at (ZFPL_S_AT)	gb AAD25930.1 AF085279_3 (AF085279) hypothetical Cys-3- His zinc finger protein [Arabidopsis thaliana]	5dpi	DNA binding protein	
20345_at (AF104919.16_AT)	gb AAC72865.1 (AF104919) similar to class I chitinases (Pfam: PF00182, E=1.2e-142, N=1) [Arabidopsis thaliana]	4dpi	stress response	
17589_at (AF156783_AT)	gb AAF00612.1 AF156783_1 (AF156783) apyrase [Arabidopsis thaliana]	5dpi	membrane protein	
18010_s_at (AJ001264_S_AT)	emb CAA77109.1 (Y18291) uncoupling protein [Arabidopsis thaliana]	5dpi	stress response	
12421_at (AJ002414.1_AT)	emb CAA05398.1 (AJ002414) hnRNP-like protein [Arabidopsis thaliana]	2dpi	RNA processing	
13284_s_at (HSP70_S_AT)	emb CAA05547.1 (AJ002551) heat shock protein 70 [Arabidopsis thaliana]	2dpi 5dpi	heat shock	
16442_s_at (AJ002551.2_S_AT)	emb CAA05547.1 (AJ002551) heat shock protein 70 [Arabidopsis thaliana]	2dpi	heat shock	
19591_at (AJ010735.4_AT)	emb CAA09330.1 (AJ010735) gr1-protein [Arabidopsis thaliana]	4dpi	stress response	
20507_at (AL021635.67_AT)	emb CAA16557.1 (AL021635) glycoprotein endopeptidase - like protein [Arabidopsis thaliana]	5dpi	metabolic protein	
19531_at (AL021960.91_AT)	emb CAA17531.1 (AL021960) amino acid transport protein AAT1 [Arabidopsis thaliana]	5dpi	membrane protein	
14595_at (AL022580.163_AT)	emb CAA18626.1 (AL022580) putative protein [Arabidopsis thaliana]	4dpi	membrane protein	putative integral membrane protein

Probeset	Description	Time	Function	Blast
13212_s_at (BGL2_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]	2-5dpi	stress response	
16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]	2-5dpi	stress response	
15622_s_at (ATU43945_S_AT)	gb AAB40594.1 (U43945) strictosidine synthase [Arabidopsis thaliana]	4dpi	stress response	
14145_at (NOVARTIS35_AT)	dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]	4dpi	DNA binding protein	
15680_s_at (ATHATPK19B_S_AT)	dbj BAA07661.1 (D42061) ribosomal-protein S6 kinase homolog [Arabidopsis thaliana]	5dpi	signaling not kinase	
16173_s_at (D78607_S_AT)	dbj BAA28539.1 (D78607) cytochrome P450 monooxygenase [Arabidopsis thaliana]	4dpi	metabolic protein	
12832_f_at (U33014.2_M_F_AT)	gb AAD03342.1 (L81140) ubiquitin [Pisum sativum]	1dpi	protein degradation	
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]	5dpi	heat shock	
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]	5dpi	heat shock	
13722_at (NOVARTIS108_AT)	No hits found less than or equal to 1e-15.	5dpi	DNA binding protein	transcription factor
13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	5dpi	stress response	
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	5dpi	stress response	
13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	5dpi	stress response	

Probeset	Description	Time	Function	Blast
16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]	5dpi	stress response	
17544_s_at (ATU40856_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]	5dpi	stress response	
12880_s_at (AIG2_S_AT)	gb AAC49283.1 (U40857) AIG2 [Arabidopsis thaliana]	1dpi	stress response	
17097_s_at (ATU66345_S_AT)	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana]	5dpi	protein processing	
17027_s_at (ATU72958_S_AT)	gb AAB38795.1 (U72958) AtHSP23.6-mito [Arabidopsis thaliana] protein (AtHSP23.6- mito) [Arabidopsis thaliana]	5dpi	heat shock	
14998_at (U93215.42_AT)	gb AAB63078.1 (U93215) unknown protein [Arabidopsis thaliana]	5dpi	DNA binding protein	Petroselinum crispum transcription factor (WRKY3) WRKY3 DNA-binding protein, TMV response- related gene product
13275_f_at (HSP174_F_AT)	emb CAA35182.1 (X17293) heat shock protein (AA 1 - 156) [Arabidopsis thaliana]	4-5dpi	heat shock	
12831_f_at (U33014.2_5_F_AT)	emb CAA40323.1 (X57003) polyubiquitin protein [Helianthus annuus]	1dpi	protein degradation	
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]	4dpi	metabolic protein	
15118_s_at (ATHGLUGRFS_S_AT)	emb CAA53051.1 (X75303) glutathione S-transferase [Arabidopsis thaliana]	5dpi	stress response	
17484_at (X79052.2_AT)	emb CAA55654.1 (X79052) SRG1 [Arabidopsis thaliana]	5dpi	stress response	

Probeset	Description	Time	Function	Blast
16236_g_at (X92657.3_G_AT)	emb CAA63346.1 (X92657) cationic amino acid transporter [Arabidopsis thaliana]	5dpi	membrane protein	
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]	5dpi	DNA binding protein	salt-tolerance zinc finger protein
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]	5dpi	DNA binding protein	A.thaliana mRNA for salt-tolerance zinc finger protein
20660_s_at (X97488.2_S_AT)	emb CAA66120.1 (X97488) beta-transducin like protein [Arabidopsis thaliana]	4dpi	signaling not kinase	
13015_s_at (X98673.2_S_AT)	emb CAA67232.1 (X98674) zinc finger protein [Arabidopsis thaliana]	5dpi	DNA binding protein	
16465_at (Y08892.1_AT)	emb CAA70105.1 (Y08892) Hsc70-G8 protein [Arabidopsis thaliana]	4-5dpi	heat shock	
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]	2-5dpi	heat shock	
16054_s_at (Y14251.4_S_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]	5dpi	stress response	
20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]	4-5dpi	stress response	
19178_at (Y18227.2_AT)	dbj BAA86999.1 (AB035137) blue copper binding protein [Arabidopsis thaliana]	5dpi	metabolic protein	
16943_s_at (Z97339.466_S_AT)	emb CAB10370.1 (Z97339) drought-induced protein like [Arabidopsis thaliana]	5dpi	stress response	
13803_at (Z97341.376_AT)	emb CAB10444.1 (Z97341) cyanohydrin lyase like protein [Arabidopsis thaliana]	4dpi	metabolic protein	
18140_at (Z97341.319_AT)	emb CAB10440.1 (Z97341) growth regulator like protein [Arabidopsis thaliana]	5dpi	hormone response	

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Table 19 Probe sets corresponding to genes, the expression of which is altered after infection of *Arabidopsis* with a pathogen

- 5 Preferred gene and promoter families that regulate at least two or more pathways, conditions or phenotypes can be identified by determining the activity of each gene or promoter by reading each of the relevant tables herein and then selecting those having the desired activit(ies).

11991_g_at (AC002387.210_G_AT)	11997_at (AC005967.4_AT)
12002_at (AF069442.47_AT)	12004_at (AL022023.132_AT)
12007_at (Z99708.249_AT)	12037_at (AC004005.174_AT)
12048_at (AF001308.46_AT)	12051_at (AL021889.94_AT)
12062_at (AC006069.147_AT)	12068_at (AF118223.24_AT)
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13215_s_at (cafferoylcoAmethyltrans_S_AT)	13217_s_at (calmodulinlike_S_AT)
13219_s_at (CHI4_S_AT)	13220_s_at (CHS-EXON1_S_AT)
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13261_s_at (glutathionereductase1_S_AT)	13263_s_at (GST1_RC_S_AT)
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Table 20a: cDNA-AFLP gene fragments with similarity to other known proteins

cDNA***	Known protein	Organism	Related accession number**	Blast score*
DESCA1	no significant similarity	-	-	-
DESCA2	ser/thr kinase	bean	AF078082	2e-12
DESCA3	endo-1,4-betaglucanase	rape	AJ242807	4e-19
DESCA4	pdr 5-abc transporter	duckweed	Z70524	1e-27
DESCA5	transcriptional regulator	yeast	NP 014933	9e-1
DESCA6	kinase	Arabidopsis	T00502	7e-1
DESCA7	salicylate-induced glucosyltransferase IS5a	tobacco	T03747	2e-21
DESCA8	nbs-LRR	rice	AAF82158	5e-2
DESCA9	cytochrome p450 monooxygenase	tobacco	X96784	7e-31
DESCA10	MRP-like ABC transporter	Arabidopsis	U96399	8e-7
DESCA11	phosphoribosylanthranilate transferase	Arabidopsis	AAF18518	8e-17
DESCA12	hypersensitivity-related 201	tobacco	X95343	3e-23
DESCA13	integral membrane glycoprotein	puffer fish	AF013613	9e-1
7a tgaa	no significant similarity	-	-	-
10d tcg	hypothetical protein F3F9.18	Arabidopsis	AC013430	7e-15
11a tgca	no significant similarity	-	-	-
c.r. actin	actin	C. rubrum	X92353	7e-45

* NCBI BLASTX translated search (Altschul et al., 1997)

5 ** Accession numbers are listed in SEQ ID Nos 1967-1980

*** (DESCA sequences are listed in SEQ ID Nos 1954-1966)

Table 20b: Relative gene expression fold changes of cDNA-AFLP gene fragments with similarity to other known proteins at different time points during viral infections as determined by quantitative RT-PCR

cDNA	Gene expression fold changes				
	<i>C. amaranticolor</i>			TRV ²	<i>C. quinoa</i>
	TMV ¹		TMV ³		
	4dai	7dai	11dai	4dai	4dai
DESCA1	200	180	6.1	278	not detectable
DESCA2	36	25	27	10	700
DESCA3	23	15	2.7	19	46
DESCA4	21	9.2	4.5	6.8	52
DESCA5	19	8.0	9.1	15	1100
DESCA6	8.4	9.6	12	2.1	not detectable
DESCA7	8.9	2.8	5.6	53	150
DESCA8	5.9	3.2	2.0	5.8	120
DESCA9	5.1	5.9	4.2	3.1	not detectable
DESCA10	5.6	1.9	0.95	4.1	not detectable
DESCA11	5.5	3.6	3.0	3.9	230
DESCA12	5.0	2.4	1.7	5.6	7.9
DESCA13	2.9	1.8	1.9	3.3	34
7a tgaa	1.5	1.4	1.7	not tested	not tested
10d tcg	2.2	0.75	0.25	not tested	not tested
11a tgca	1.6	0.54	0.18	not tested	not tested
c.r. actin	1.0	1.0	1.0	1.0	1.0

¹ Values are the fold increases in gene expression of TMV-MGfus infected compared to mock-inoculated plants.

² Values are the fold increases in gene expression of TRV infected compared to mock-inoculated plants.

³ Values are the fold increases in gene expression of TMV infected compared to mock-inoculated plants.

Table 22:

Correlation of Seq ID NOs to Reference Numbers

SEQ ID NO:	ProbeSet	Reference Number
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2	11997_at	AC005967.4_AT
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4	12004_at	AL022023.132_AT
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6	12037_at	AC004005.174_AT
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23	12150_at	AC004005.151_AT
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86	12759_at	AC005278.32_AT
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98	12854_s_at	ACS1_S_AT
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101	12880_s_at	AIG2_S_AT
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103	12889_s_at	ASA1_S_AT
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105	12892_g_at	ATACS6_G_AT
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107	12905_s_at	ATERF2_S_AT
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157	13244_s_at	ELI32_S_AT
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159	13253_f_at	FPS1_F_AT
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161	13256_s_at	GAMMAGLUTAMYLTRANSPEPTI_S_AT
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163	13261_s_at	GLUTATHIONEREDUCTASE1_S_AT
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165	13266_s_at	GST4_S_AT
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271	14235_at	NOVARTIS97_AT
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273	14242_s_at	NRA_S_AT
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275	14249_i_at	PAD4_I_AT
276	14250_r_at	PAD4_R_AT

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1074	14609_at
1075	14613_at
1076	12094_at
1077	13312_at
1078	19970_s_at
1079	12128_at
1080	18631_at
1081	14573_at
1082	17371_at
1083	20421_at
1084	20422_g_at
1085	17485_s_at
1086	16398_s_at
1087	16968_at
1088	13243_r_at
1089	13244_s_at
1090	14882_at
1091	15120_s_at
1092	16357_at
1093	17180_at
1094	12908_s_at
1095	16536_s_at

Table 23

Correlation of Seq ID NOs to the Rice Orthologs and their Promoters

3		
5		
	rice homolog:	promoter:
	2808	4884
	3066	5142
	3820	5896
10	4655	6731
6		
	rice homolog:	promoter:
15	2757	4833
	3013	5089
	3393	5469
	3899	5975
20	7	
	rice homolog:	promoter:
	3227	5303
	3579	5655
25	3851	5927
	3890	5966
	4516	6592
8		
30		
	rice homolog:	promoter:
	3086	5162
	3341	5417
	3762	5838
35	3767	5843
	4285	6361
	4487	6563
	4488	6564
	4489	6565
40	10	
	rice homolog:	promoter:
	3629	5705
45	3914	5990

[illegible]

5

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[illegible]

rice homolog: promoter:
3718 5794
4345 6421

rice homolog: 4493 promoter: 6569

rice homolog:	promoter:
3479	5555
4208	6284
4236	6312

rice homolog: 3891 promoter: 5967

rice homolog: promoter:
4645 6721

rice homolog: promoter:
4210 6286

rice homolog:	promoter:
2864	4940
2964	5040
4218	6294
4307	6383
4458	6534

	rice homolog:	promoter:
	3035	5111
	3157	5233
	3379	5455
5	3626	5702
	3990	6066

55

10	rice homolog:	promoter:
	2687	4763
	2869	4945
	2984	5060
	3054	5130
15	3180	5256
	3561	5637
	4306	6382
	4326	6402
	4460	6536
20	4476	6552
	4521	6597
	4603	6679

57

25	rice homolog:	promoter:
	4005	6081

59

30	rice homolog:	promoter:
	2922	4998
	3833	5909
	3967	6043
35	4202	6278

60

40	rice homolog:	promoter:
	2706	4782
	4125	6201
	4720	6796

65

45	rice homolog:	promoter:
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2815	4891
4112	6188
4288	6364

5 67

rice homolog:	promoter:
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	2716	4792
	2928	5004
10	2940	5016
	3182	5258
	3333	5409
	3351	5427
	3386	5462
15	3387	5463
	3445	5521
	3530	5606
	3581	5657
	3727	5803
20	3825	5901
	3915	5991
	4120	6196
	4170	6246
	4267	6343
25	4280	6356
	4350	6426
	4479	6555
	4713	6789

30 68

rice homolog:	promoter:
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	2764	4840
	3072	5148
35	3192	5268
	3290	5366
	3546	5622
	3553	5629
	3658	5734
40	3747	5823
	3972	6048
	4543	6619

70

45

rice homolog:	promoter:
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[illegible]

rice homolog:	promoter:
3245	5321
4329	6405
4412	6488

rice homolog:	promoter:
2862	4938
3012	5088
3506	5582

	rice homolog:	promoter:
20	2920	4996
	3417	5493
	3742	5818
	3927	6003
	4061	6137

rice homolog:	promoter:
2705	4781
2737	4813
2738	4814
4654	6730
4681	6757

rice homolog:	promoter:
3163	5239
3525	5601
3965	6041
4114	6190

45 rice homolog: promoter:
 3138 5214

93

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2903	4979
3230	5306
3676	5752
4480	6556
4631	6707

20

97

25

2959	5035
3105	5181
3222	5298
3838	5914
4026	6102
4224	6300
4523	6599
4646	6722

30

100

35

2667	4743
2751	4827
2948	5024
3167	5243
3198	5274
3319	5395
3797	5873
4048	6124
4184	6260
4259	6335

45

102

115

rice homolog: promoter:

2707 4783
5 2871 4947
3261 5337
3452 5528
4513 6589

10 116

rice homolog: promoter:

2833 4909
2939 5015
15 3200 5276
3571 5647
4031 6107

118

20

rice homolog: promoter:

2944 5020
3186 5262
3631 5707
25 3633 5709
3697 5773
3726 5802
4009 6085
4597 6673

30

119

rice homolog: promoter:

3169 5245
35 3637 5713
3638 5714
3639 5715
3656 5732

40 121

rice homolog: promoter:

4692 6768

45 122

	rice homolog:	promoter:
	3041	5117
	3179	5255
	3291	5367
5	4269	6345
	4633	6709

124

	rice homolog:	promoter:
10	3388	5464
	3410	5486
	3469	5545
	4316	6392
15	4449	6525

126

	rice homolog:	promoter:
20	3215	5291
	3557	5633
	3575	5651
	3847	5923
	4044	6120
25	4400	6476
	4444	6520
	4496	6572
	4593	6669
	4629	6705

30

127

	rice homolog:	promoter:
	2981	5057
35	3199	5275
	3467	5543
	3963	6039
	4053	6129

40 128

	rice homolog:	promoter:
	3267	5343
	4182	6258
45	4530	6606

130

	rice homolog:	promoter:
	2890	4966
5	3293	5369
	3312	5388
	3326	5402
	3812	5888
	3889	5965
10	4134	6210
	4254	6330

133

	rice homolog:	promoter:
15	2799	4875
	3008	5084
	3208	5284
	3706	5782
20	3765	5841

134

	rice homolog:	promoter:
25	3005	5081
	3145	5221
	3146	5222
	3328	5404
	3511	5587
30	4572	6648
	4584	6660

135

	rice homolog:	promoter:
35	2832	4908
	3073	5149
	3257	5333
	3352	5428
40	3378	5454
	3555	5631
	3761	5837
	3869	5945
	4609	6685

45

137

	rice homolog:	promoter:
	2723	4799
	3220	5296
5	4173	6249
	138	

	rice homolog:	promoter:
10	3024	5100
	3487	5563
	3583	5659
	4503	6579
	4591	6667
15	139	

	rice homolog:	promoter:
	2699	4775
20	3463	5539
	3584	5660
	4451	6527
	4595	6671
25	140	

	rice homolog:	promoter:
	3042	5118
	3175	5251
30	4337	6413
	148	

	rice homolog:	promoter:
35	3558	5634
	3655	5731
	4084	6160
	150	
40		

	rice homolog:	promoter:
	3107	5183
	3560	5636
45	151	

	rice homolog:	promoter:
	4146	6222
	4398	6474
	4399	6475
5	152	

	rice homolog:	promoter:
	4368	6444
10	4483	6559
	4550	6627
	4551	6628
	4616	6692
15	158	

	rice homolog:	promoter:
	3023	5099
	3880	5956
20	4237	6313
	4492	6568
	159	

25	rice homolog:	promoter:
	2720	4796
	3115	5191
	3383	5459
	3844	5920
30	3989	6065
	4157	6233
	4627	6703
	162	
35		

	rice homolog:	promoter:
	2813	4889
	2927	5003
	3346	5422
40	3423	5499
	3682	5758
	3781	5857
	3830	5906
	4225	6301
45	4475	6551
	4622	6698

164

rice homolog: promoter:
5 3232 5308
3491 5567
4590 6666
4625 6701

10 165

rice homolog: promoter:
3271 5347
3322 5398
15 3406 5482
3681 5757
3973 6049
4231 6307
4324 6400

20

166

rice homolog: promoter:
2767 4843
25 2781 4857
3347 5423
4093 6169
4130 6206

30 171

rice homolog: promoter:
2733 4809
2761 4837
35 3049 5125
3402 5478
3945 6021

172

40

rice homolog: promoter:
3389 5465
3509 5585
3603 5679
45 3664 5740
3665 5741

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[illegible]

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4680 6756

202

5	rice homolog:	promoter:
	2711	4787
	3015	5091
	3774	5850
	3906	5982
10	3943	6019

203

	rice homolog:	promoter:
15	3135	5211
	3318	5394
	3443	5519
	3523	5599
	3911	5987
20	3924	6000
	4596	6672

204

25	rice homolog:	promoter:
	2851	4927
	2852	4928
	3151	5227
	3152	5228
30	4186	6262

205

	rice homolog:	promoter:
35	3078	5154
	3984	6060
	4085	6161

206

40	rice homolog:	promoter:
	3051	5127
	3075	5151
	3117	5193
45	3527	5603
	3756	5832

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[illegible]

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	3634	5710
	3673	5749
	3920	5996
	4440	6516
5	4668	6744

229

	rice homolog:	promoter:
10	2731	4807
	3466	5542
	3897	5973
	4395	6471
	4664	6740

15

237

	rice homolog:	promoter:
	2847	4923
20	3126	5202
	3237	5313
	3508	5584
	3704	5780
	3930	6006
25	4006	6082

239

	rice homolog:	promoter:
30	2924	5000
	4707	6783

240

	rice homolog:	promoter:
35	3211	5287
	3751	5827

247

	rice homolog:	promoter:
40	3971	6047

250

	rice homolog:	promoter:
45		

	2971	5047
	3696	5772
	3719	5795
	4035	6111
5	4273	6349
	4675	6751

252

10	rice homolog:	promoter:
	2909	4985
	3738	5814
	3831	5907
	3904	5980
15	4039	6115
	4219	6295
	4246	6322
	4467	6543
	4495	6571

20

254

	rice homolog:	promoter:
	2771	4847
25	2874	4950
	3413	5489
	3510	5586
	4143	6219

30 255

	rice homolog:	promoter:
	2664	4740
	2740	4816
35	2792	4868
	3171	5247
	3368	5444
	3425	5501
	3788	5864
40	4183	6259
	4206	6282
	4439	6515

256

45

	rice homolog:	promoter:
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[illegible]

	rice homolog:	promoter:
	2952	5028
	3283	5359
15	4001	6077
	4040	6116
	4397	6473

	263	
30	rice homolog:	promoter:
	2752	4828
	3098	5174
	3276	5352
	3625	5701
35	4309	6385

45
267

	rice homolog:	promoter:
	2866	4942
	2941	5017
5	3002	5078
	4330	6406

270

	rice homolog:	promoter:
10	2875	4951
	3001	5077
	3061	5137
	3282	5358
15	3590	5666
	3608	5684
	3618	5694
	3817	5893
	3969	6045
20	4211	6287
	4265	6341
	4333	6409
	4377	6453

25 271

	rice homolog:	promoter:
	3979	6055
	4570	6646
30	4571	6647

274

	rice homolog:	promoter:
35	3426	5502
	3534	5610

275

	rice homolog:	promoter:
40	2951	5027
	3268	5344
	3909	5985
	4277	6353
45	4490	6566

285

	rice homolog:	promoter:
	3336	5412
5	3987	6063
	4431	6507

286

	rice homolog:	promoter:
10	3430	5506

287

	rice homolog:	promoter:
15	2703	4779
	3028	5104
	3329	5405
	3595	5671
20	3667	5743
	3895	5971
	4598	6674
	4602	6678
	4688	6764

25

288

	rice homolog:	promoter:
	2820	4896
30	2977	5053
	2991	5067
	3007	5083
	3057	5133
	3097	5173
35	3155	5231
	3170	5246
	3464	5540
	3528	5604
	3532	5608
40	3872	5948
	3953	6029
	3966	6042
	4025	6101
	4161	6237
45	4544	6620

289

	rice homolog:	promoter:
	2668	4744
5	2746	4822
	3147	5223
	3284	5360
	3285	5361
	3878	5954
10	4373	6449
	4457	6533

290

	rice homolog:	promoter:
15	2780	4856
	2896	4972
	3569	5645
	4486	6562
20	4731	6807

295

	rice homolog:	promoter:
25	2785	4861
	2807	4883
	2921	4997
	2957	5033
	3281	5357
30	3303	5379
	3477	5553
	3792	5868
	3925	6001
	3946	6022
35	4175	6251

296

	rice homolog:	promoter:
40	2689	4765
	2995	5071
	2996	5072
	3133	5209
	4058	6134
45	4185	6261
	4695	6771

298

	rice homolog:	promoter:
5	2685	4761
	2769	4845
	2777	4853
	3122	5198
	3153	5229
10	3187	5263
	3323	5399
	4542	6618

299

15	rice homolog:	promoter:
	2915	4991
	3705	5781
	4313	6389
20	4353	6429
	4415	6491
	4600	6676
	4721	6797

25 300

	rice homolog:	promoter:
	3380	5456
	3381	5457
30	3456	5532
	3755	5831
	4027	6103

301

35	rice homolog:	promoter:
	2679	4755
	2865	4941
	3565	5641
40	4029	6105
	4272	6348

302

45	rice homolog:	promoter:
	2836	4912

3236 5312

304

5 rice homolog: promoter:
2960 5036
3111 5187
3252 5328
3884 5960
10 3885 5961

305

rice homolog: promoter:
15 2899 4975
3074 5150
3431 5507
3713 5789
4008 6084

20

312

rice homolog: promoter:
25 2721 4797
3256 5332
3385 5461
3539 5615
3541 5617
4145 6221

30

314

rice homolog: promoter:
35 2839 4915
3240 5316
3485 5561
3643 5719
3848 5924
3957 6033
40 4406 6482
4514 6590

316

45 rice homolog: promoter:
3119 5195

	3142	5218
	3251	5327
	3274	5350
	3619	5695

5

318

 rice homolog: promoter:

	2972	5048
10	3875	5951
	4152	6228
	4375	6451
	4461	6537

15 319

 rice homolog: promoter:

	4197	6273
	4334	6410

20

324

 rice homolog: promoter:

	3033	5109
25	3771	5847
	3910	5986

326

 30 rice homolog: promoter:

	2934	5010
	3114	5190
	3806	5882
	4359	6435
35	4520	6596

330

 rice homolog: promoter:

40	3401	5477
	3804	5880
	4098	6174
	4331	6407
	4381	6457
45	4430	6506
	4533	6609

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15 333

339

341

346

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348

	rice homolog:	promoter:
5	3000	5076
	3137	5213
	3866	5942
	4038	6114
	4327	6403
10	4425	6501

360

	rice homolog:	promoter:
15	2989	5065
	2990	5066
	3090	5166
	3100	5176
	3436	5512
20	3515	5591
	3522	5598
	3636	5712
	3883	5959
	3977	6053
25	4028	6104
	4199	6275
	4201	6277
	4223	6299
	4317	6393
30	4354	6430
	4408	6484
	4450	6526
	4509	6585

35 365

	rice homolog:	promoter:
	3678	5754
	3941	6017
40	4547	6623
	4577	6653
	4684	6760
	4714	6790

45 366

	rice homolog:	promoter:
	2691	4767
	3614	5690
	3711	5787
5	3763	5839
	3975	6051

369

10	rice homolog:	promoter:
	2708	4784
	3125	5201
	3144	5220
	3190	5266
15	3370	5446
	3432	5508
	4067	6143
	4355	6431
	4410	6486
20	4546	6622
	4587	6663

370

25	rice homolog:	promoter:
	4056	6132

372

30	rice homolog:	promoter:
	3414	5490
	3471	5547
	4247	6323
	4482	6558
35	4650	6726

374

40	rice homolog:	promoter:
	2776	4852
	3497	5573
	3645	5721
	3728	5804
	3837	5913

45

378

<hr/>		
	rice homolog:	promoter:
	3808	5884
	4045	6121
5	4308	6384
	4525	6601
<hr/>		
	380	
<hr/>		
10	rice homolog:	promoter:
	3207	5283
	3773	5849
	4701	6777
	4715	6791
15	4716	6792
<hr/>		
	381	
<hr/>		
20	rice homolog:	promoter:
	4034	6110
<hr/>		
	382	
<hr/>		
25	rice homolog:	promoter:
	4405	6481
	4537	6613
<hr/>		
	385	
<hr/>		
30	rice homolog:	promoter:
	3490	5566
	4065	6141
	4104	6180
	4454	6530
35	4456	6532
	4730	6806
<hr/>		
	389	
<hr/>		
40	rice homolog:	promoter:
	2750	4826
	3529	5605
	3620	5696
	4575	6651
45	4694	6770
	4723	6799

391

	rice homolog:	promoter:
5	2671	4747
	3862	5938
	3863	5939
	3955	6031
	3956	6032
10	4133	6209

393

	rice homolog:	promoter:
15	3010	5086
	3802	5878
	3839	5915
	3923	5999
	4421	6497
20	4556	6632
	4614	6690

394

	rice homolog:	promoter:
25	3069	5145
	3159	5235
	3870	5946
	4147	6223
30	4512	6588

398

	rice homolog:	promoter:
35	2976	5052
	3680	5756

404

	rice homolog:	promoter:
40	4217	6293

405

	rice homolog:	promoter:
45	4116	6192

410

	rice homolog:	promoter:
5	2754	4830
	3260	5336

411

10	rice homolog:	promoter:
	3824	5900
	4004	6080

412

15	rice homolog:	promoter:
	2967	5043
	2988	5064
	3887	5963
20	3935	6011
	4462	6538

418

25	rice homolog:	promoter:
	3223	5299
	4376	6452
	4504	6580
	4505	6581
30	4663	6739

419

	rice homolog:	promoter:
35	2854	4930
	3085	5161
	3442	5518
	3537	5613
	3552	5628
40	4200	6276
	4378	6454

420

45	rice homolog:	promoter:
	3321	5397

	3517	5593
	3544	5620
	3689	5765
	4243	6319
5	422	

	rice homolog:	promoter:
	3228	5304
10	3249	5325
	3250	5326
	3709	5785
	4589	6665
15	426	

	rice homolog:	promoter:
	2919	4995
	2943	5019
20	3022	5098
	3273	5349
	3739	5815
	4409	6485
25	428	

	rice homolog:	promoter:
	2753	4829
	2897	4973
30	3096	5172
	3500	5576
	4438	6514
	431	
35	-----	
	rice homolog:	promoter:
	3193	5269
	432	
40	-----	
	rice homolog:	promoter:
	3029	5105
	3219	5295
	3375	5451
45	3376	5452
	3623	5699

[illegible]

rice homolog:	promoter:
2855	4931
2937	5013
4341	6417
4640	6716

rice homolog:	promoter:
2818	4894
2863	4939
3344	5420
3454	5530
3613	5689
4683	6759
439	

441

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[illegible]

450

451

457

460

463

- 396 -

Figure 1: Schematic representation of the experimental design. The diagram shows a sequence of events: 'Pretest' (with 'Pretest' and 'Posttest' labels), 'Training' (with 'Training' and 'Posttest' labels), 'Transfer' (with 'Transfer' and 'Posttest' labels), and 'Retention' (with 'Retention' and 'Posttest' labels). Each stage includes a 'Pretest' and a 'Posttest' measurement. The 'Training' stage is divided into 'Pretest' and 'Posttest' sub-stages. The 'Transfer' stage is divided into 'Pretest' and 'Posttest' sub-stages. The 'Retention' stage is divided into 'Pretest' and 'Posttest' sub-stages. The diagram also shows a 'Control' group that receives no training and is measured at the same points as the experimental group.

rice homolog: promoter:

rice homolog: promoter:

rice homolog: promoter:

rice homolog: promoter:

475

	rice homolog:	promoter:
	2739	4815
	2772	4848
5	3168	5244
	3382	5458
	3451	5527
	3865	5941
	3974	6050
10	3982	6058
	4364	6440

476

	rice homolog:	promoter:
15	2829	4905
	3343	5419
	3593	5669
	3741	5817
20	3829	5905

482

	rice homolog:	promoter:
25	2853	4929
	4062	6138
	4106	6182
	4127	6203

30 484

	rice homolog:	promoter:
	2702	4778
	3302	5378
35	3327	5403
	3701	5777
	4502	6578

487

	rice homolog:	promoter:
40	3143	5219
	3677	5753
	4075	6151
45	4443	6519
	4710	6786

10

20

25

40

45

rice homolog:	promoter:
3857	5933
4611	6687

5 505

rice homolog:	promoter:
3165	5241
3242	5318
3749	5825
4383	6459
4718	6794

10

507

15

rice homolog:	promoter:
2763	4839
3026	5102
3409	5485
3468	5544
3983	6059

20

509

25

rice homolog:	promoter:
2759	4835
3418	5494
3912	5988
4079	6155
4470	6546

30

517

rice homolog:	promoter:
2672	4748
2690	4766
2727	4803
2846	4922
3278	5354
3337	5413
3526	5602
3730	5806
3929	6005
4052	6128
4081	6157
4089	6165

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4314 6390
4628 6704

525

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rice homolog: promoter:
4162 6238

526

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rice homolog: promoter:
2840 4916
2994 5070
3003 5079
15 4020 6096
4653 6729

528

20

rice homolog: promoter:
3004 5080
3433 5509
3674 5750
3789 5865
25 4638 6714

533

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rice homolog: promoter:
3044 5120
3241 5317
3646 5722
3961 6037
4518 6594

35

535

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rice homolog: promoter:
3859 5935
4328 6404

536

45

rice homolog: promoter:
3286 5362
3545 5621

[illegible]

549

	rice homolog:	promoter:
	3369	5445
	3420	5496
5	3421	5497
	3441	5517
	3559	5635
	4069	6145
	4300	6376
10	4301	6377
	4561	6637

550

	rice homolog:	promoter:
15	3141	5217
	3361	5437
	3377	5453
	3939	6015
20	3960	6036
	4091	6167

551

	rice homolog:	promoter:
25	3340	5416
	3363	5439
	4142	6218
	4159	6235
30	4436	6512

552

	rice homolog:	promoter:
35	3805	5881
	3993	6069
	4016	6092
	4077	6153
	4136	6212

40

553

	rice homolog:	promoter:
	2666	4742
45	2945	5021
	3101	5177

[illegible]

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2929 5005

3811 5887

10

559

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3611 5687

4179 6255

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25

3599 5675

3712 5788

2954 5030

4386 6462

3019 5095

45

3307 5383

rice homolog:	promoter:
2674	4750
4099	6175
4366	6442

rice homolog:	promoter:
2825	4901
3006	5082
3136	5212
3822	5898
4010	6086

rice homolog:	promoter:
2765	4841
3065	5141
3513	5589
4043	6119
4416	6492

30	rice homolog:	promoter:
	3212	5288
	3411	5487
	3841	5917
	4169	6245
35	4293	6369

	rice homolog:	promoter:
40	2712	4788
	2713	4789
	2725	4801
	2812	4888
	3031	5107
45	3794	5870
	4274	6350

4699 6775

586

5 rice homolog: promoter:
3746 5822
4672 6748

595

10 rice homolog: promoter:
2821 4897
3275 5351
3473 5549
15 3877 5953
4097 6173
4312 6388
4362 6438
4554 6626

20 599

rice homolog: promoter:
3055 5131
25 3213 5289
4166 6242
4167 6243
4562 6638

30 601

rice homolog: promoter:
3079 5155
3424 5500
35 4241 6317
4321 6397

602

40 rice homolog: promoter:
4083 6159

603

45 rice homolog: promoter:
2775 4851

	3685	5761
	3934	6010
	4235	6311
	4351	6427
5	4657	6733

605

	rice homolog:	promoter:
10	2724	4800
	2784	4860
	3052	5128
	3288	5364
	3422	5498
15	3731	5807
	3944	6020
	4007	6083
	4346	6422
	4389	6465

20

609

	rice homolog:	promoter:
	3311	5387
25	3791	5867

610

	rice homolog:	promoter:
30	4011	6087
	4522	6598

612

	rice homolog:	promoter:
35	2795	4871
	3130	5206
	3574	5650
	4315	6391
40	4529	6605

613

	rice homolog:	promoter:
45	3162	5238

Fig. 2 8 hr.	Fig. 3 12 hr.	Fig. 4 16 hr.

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45

rice homolog: promoter:

2756 4832

3470	5546
------	------

4078 6154

4365	6441
------	------

1151 5155

rice homolog: promoter:

3258	5334
------	------

640

rice homolog: promoter:

3790	5866
------	------

4511	6587
------	------

641

rice homolog: promoter:

2793 4869

3714 5790

rice homolog: promoter:

4082 6158

4437 6513

4563 6639

647

5 rice homolog: promoter:
 2758 4834
 2879 4955
 3214 5290
 3476 5552
10 3564 5640
 3661 5737
 3772 5848

651

15 -----
 rice homolog: promoter:
 2867 4943
 3244 5320
 4017 6093
20 4191 6267
 4242 6318

653

25 rice homolog: promoter:
 3077 5153

654

30 rice homolog: promoter:
 2663 4739
 2835 4911
 3459 5535
 3908 5984
35 4582 6658

656

 rice homolog: promoter:
40 3660 5736
 3893 5969
 4012 6088
 4021 6097
 4508 6584

45

657

rice homolog: 4139 promoter: 6215

5 658

rice homolog:	promoter:
2878	4954
3437	5513
3486	5562
4002	6078
4160	6236

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660

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rice homolog:	promoter:
3132	5208
3292	5368
4426	6502
4632	6708
4687	6763

20

662

25	rice homolog:	promoter:
	2969	5045
	3535	5611
	4260	6336
	4261	6337
30	4262	6338

30

664

	rice homolog:	promoter:
35	2704	4780
	3766	5842
	4094	6170
	4689	6765
	4732	6808

40

665

rice homolog:	promoter:
2741	4817
2827	4903
3056	5132

45

	3181	5257
	3448	5524
	3520	5596
	3882	5958
5	4080	6156
	4101	6177
	4171	6247
	4176	6252
	4205	6281
10	4264	6340
	4278	6354
	4507	6583
	4676	6752
	4691	6767
15	4734	6810

672

	rice homolog:	promoter:
20	3104	5180
	3907	5983
	4141	6217
	4612	6688
	4669	6745

25 675

	rice homolog:	promoter:
	2717	4793
30	3149	5225
	3622	5698
	3940	6016
	4367	6443

35 676

	rice homolog:	promoter:
	2963	5039
	3084	5160
40	3112	5188
	3221	5297
	3332	5408
	3507	5583
	3570	5646
45	3699	5775
	4138	6214

4390 6466

677

	rice homolog:	promoter:
5	3439	5515
	3440	5516
	3952	6028
	4072	6148
10	4073	6149

678

	rice homolog:	promoter:
15	2810	4886
	2883	4959
	3195	5271
	3266	5342
	3427	5503

20

680

	rice homolog:	promoter:
	2797	4873
25	3750	5826
	4588	6664

683

	rice homolog:	promoter:
30	2735	4811
	2970	5046
	3760	5836
	3778	5854
35	4560	6636

684

	rice homolog:	promoter:
40	4320	6396

685

	rice homolog:	promoter:
45	3140	5216
	3587	5663

3876	5952
4119	6195
4727	6803

5 686

rice homolog:	promoter:
2907	4983
2917	4993
3540	5616
3892	5968
3937	6013

15 687

rice homolog:	promoter:
3779	5855
3902	5978
4569	6645
4615	6691
4722	6798

20 688

rice homolog:	promoter:
3297	5373
4095	6171
4282	6358
4433	6509
4446	6522

25 691

rice homolog:	promoter:
2837	4913
3238	5314
3364	5440
3542	5618
3768	5844

35 692

rice homolog:	promoter:
3585	5661
3586	5662
4658	6734

40 45

4659 6735

693

	rice homolog:	promoter:
5	2806	4882
	2923	4999
	3043	5119
	3229	5305
10	3320	5396

695

	rice homolog:	promoter:
15	4258	6334

698

	rice homolog:	promoter:
20	2842	4918
	2843	4919
	2844	4920
	2908	4984
	2949	5025
25	3554	5630
	3670	5746
	3926	6002
	4338	6414

30 700

	rice homolog:	promoter:
	2947	5023
	3246	5322
35	4180	6256
	4441	6517
	4666	6742
	4667	6743

40 702

	rice homolog:	promoter:
	3216	5292
	3549	5625
45	3654	5730
	3733	5809

4132 6208

706

	rice homolog:	promoter:
5	2697	4773
	2770	4846
	2788	4864
	2845	4921
10	3156	5232
	3234	5310
	3744	5820
	4013	6089

15 707

	rice homolog:	promoter:
	2983	5059
	3582	5658
20	3642	5718
	4059	6135
	4076	6152
	4194	6270
	4686	6762

25 712

	rice homolog:	promoter:
	3038	5114
30	3392	5468
	3400	5476
	3512	5588
	3758	5834
	4110	6186
35	4118	6194
	4177	6253
	4422	6498
	4538	6614
	4607	6683
40	4704	6780
	4705	6781
	4706	6782

45 715

	rice homolog:	promoter:
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	3757	5833
	3936	6012
	4229	6305
	4230	6306
5	4528	6604

718

	rice homolog:	promoter:
10	3047	5123

719

	rice homolog:	promoter:
15	2817	4893
	2894	4970
	3076	5152
	3314	5390
	3759	5835
20	4092	6168
	4271	6347
	4302	6378
	4303	6379
	4304	6380
25	4305	6381
	4455	6531
	4473	6549

720

30	rice homolog:	promoter:
	2930	5006
	3062	5138
	3172	5248
35	3289	5365
	4384	6460

725

40	rice homolog:	promoter:
	4228	6304

729

45	rice homolog:	promoter:
	2787	4863

	2975	5051
	3095	5171
	3494	5570
	3495	5571
5	3496	5572
	3702	5778
	3725	5801
	4189	6265
	4402	6478

10

731

	rice homolog:	promoter:
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	2688	4764
15	2900	4976
	2962	5038
	2979	5055
	3016	5092
	3048	5124
20	3070	5146
	3092	5168
	3589	5665
	3617	5693
	3720	5796
25	3782	5858
	3962	6038
	4155	6231
	4174	6250
	4474	6550
30	4510	6586
	4545	6621
	4729	6805

732

35

	rice homolog:	promoter:
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	3027	5103
	3064	5140
	3710	5786
40	4524	6600
	4566	6642

740

45

	rice homolog:	promoter:
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	3861	5937
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741

	rice homolog:	promoter:
5	3196	5272
	3871	5947

744

	rice homolog:	promoter:
10	2732	4808
	3210	5286
	4255	6331
	4256	6332
15	4347	6423
	4374	6450
	4500	6576
	4626	6702

20 745

	rice homolog:	promoter:
	2892	4968
	4428	6504

25 752

	rice homolog:	promoter:
	2686	4762
30	2830	4906
	2831	4907
	2932	5008
	4623	6699

35 756

	rice homolog:	promoter:
	3094	5170
	3484	5560
40	3597	5673
	3652	5728
	3860	5936
	3879	5955
	3964	6040

45 757

	rice homolog:	promoter:
5	2826	4902
	2910	4986
	3017	5093
	3030	5106
	3067	5143
10	3080	5156
	3113	5189
	3178	5254
	3272	5348
	3482	5558
15	4585	6661
	4671	6747
	4711	6787

	rice homolog:	promoter:
20	2868	4944
	3124	5200
	3679	5755
	4203	6279
	4432	6508
25	4498	6574
	4712	6788

30	rice homolog:	promoter:
	3301	5377
	3715	5791
	4144	6220
	4196	6272
35	4295	6371
	4396	6472
	4724	6800

40	-----	
	rice homolog:	promoter:
	3231	5307
	3627	5703
	4268	6344
45	4361	6437
	4661	6737

DEPT OF THE ARMY
OFFICE OF THE CHIEF OF STAFF
WASHINGTON, D.C. 20315

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	2670	4746
	3209	5285
	3780	5856
	4209	6285
5	4485	6561

782

	rice homolog:	promoter:
10	3783	5859
	3834	5910
	3854	5930
	4165	6241
	4586	6662

15

788

	rice homolog:	promoter:
	2677	4753
20	3573	5649
	4192	6268
	4434	6510

790

25

	rice homolog:	promoter:
	3349	5425
	3793	5869
	4263	6339

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792

	rice homolog:	promoter:
	2877	4953
35	2901	4977
	3516	5592
	3918	5994
	3947	6023
	4019	6095
40	4279	6355
	4296	6372
	4356	6432
	4643	6719

45 793

	rice homolog:	promoter:
	2698	4774
	2794	4870
	2811	4887
5	3350	5426

794

	rice homolog:	promoter:
10	3919	5995
	3954	6030
	3986	6062
	4448	6524
	4665	6741

15

795

	rice homolog:	promoter:
	2676	4752
20	3058	5134
	3139	5215
	3690	5766
	3691	5767
	3692	5768
25	3693	5769
	3928	6004
	4214	6290

797

30

	rice homolog:	promoter:
	2700	4776
	2828	4904
	2882	4958
35	3306	5382
	3695	5771
	4135	6211

798

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	rice homolog:	promoter:
	3358	5434
	3405	5481
	3407	5483
45	3460	5536
	3596	5672

803

	rice homolog:	promoter:
5	3194	5270
	3239	5315
	3299	5375
	3588	5664
	3612	5688
10	4736	6812

804

	rice homolog:	promoter:
15	2692	4768
	3059	5135
	3399	5475
	3721	5797
	3729	5805

20

808

	rice homolog:	promoter:
	2904	4980
25	3280	5356
	3827	5903
	4429	6505
	4660	6736

30

	rice homolog:	promoter:
	2872	4948
	4717	6793

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811

	rice homolog:	promoter:
	4033	6109

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814

	rice homolog:	promoter:
	2880	4956
45	2987	5063
	3416	5492

4055	5131
4559	6635

816

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rice homolog:	promoter:
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2768	4844
------	------

3150	5226
------	------

3846	5922
------	------

10	3894	5970
----	------	------

4057	6133
------	------

820

15

rice homolog:	promoter:
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3648	5724
------	------

3855	5931
------	------

4257	6333
------	------

20

823

rice homolog:	promoter:
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3800	5876
------	------

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825

rice homolog:	promoter:
---------------	-----------

2870	4946
------	------

4096	6172
------	------

30	4283	6359
----	------	------

4284	6360
------	------

4564	6640
------	------

826

35

rice homolog:	promoter:
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2931	5007
------	------

3331	5407
------	------

3429	5505
------	------

40	3601	5677
----	------	------

4103	6179
------	------

4494	6570
------	------

4541	6617
------	------

45

827

	rice homolog:	promoter:
	2814	4890
	3707	5783
	3784	5860
5	3785	5861
	4188	6264

829

10	rice homolog:	promoter:
	3786	5862

830

15	rice homolog:	promoter:
	2673	4749
	2982	5058
	3390	5466
	4435	6511
20	4649	6725
	4690	6766

831

25	rice homolog:	promoter:
	3334	5410
	3543	5619
	3743	5819
	4369	6445

30

832

	rice homolog:	promoter:
35	2790	4866

833

	rice homolog:	promoter:
	2824	4900
40	2889	4965
	2956	5032
	3360	5436
	3397	5473
	3521	5597
45	3647	5723
	3698	5774

096787

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857

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4568 6644

4109 6185

0 **1** **2** **3** **4** **5** **6** **7** **8** **9**

	rice homolog:	promoter:
	2729	4805
	2925	5001
10	3576	5652
	4148	6224
	4195	6271

15	867	

	rice homolog:	promoter:
	2726	4802
20	4310	6386
	4332	6408
	4442	6518
	4452	6528
	4599	6675

25	868	

	rice homolog:	promoter:
	2681	4757
	2895	4971
	2980	5056
30	4193	6269
	4477	6553
	4478	6554
	4696	6772

35	871	

	rice homolog:	promoter:
	3308	5384
	3309	5385
40	3310	5386
	4567	6643
	4576	6652

876
45
rice homolog: promoter:

[illegible]

883

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30 891

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[illegible]

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911

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912

- 431 -

	2816	4892
	3185	5261
	3662	5738
	4393	6469
5	914	

	rice homolog:	promoter:
	2728	4804
10	3177	5253
	3483	5559
	3809	5885
	4339	6415
15	918	

	rice homolog:	promoter:
	2968	5044
	3577	5653
20	3787	5863
	4297	6373
	4445	6521
	919	
25	-----	
	rice homolog:	promoter:
	2985	5061
	3356	5432
	3881	5957
30	4090	6166
	4652	6728
	921	

35	rice homolog:	promoter:
	2887	4963
	926	

40	rice homolog:	promoter:
	2946	5022
	3128	5204
	3649	5725
	3858	5934
45	928	

	rice homolog:	promoter:
	4121	6197
	4392	6468
5	4552	6629

929

	rice homolog:	promoter:
10	2743	4819
	2745	4821
	3666	5742
	4276	6352
	4343	6419
15	4630	6706

930

	rice homolog:	promoter:
20	4249	6325

932

	rice homolog:	promoter:
25	2965	5041
	3014	5090
	3840	5916
	4041	6117
	4137	6213
30	4506	6582

934

	rice homolog:	promoter:
35	3616	5692
	3816	5892
	4105	6181
	4111	6187
	4172	6248

40

943

	rice homolog:	promoter:
	2881	4957
45	2998	5074
	3203	5279

[illegible]

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Table 24

Correlation of Arabidopsis promoter regions to the
Open Reading Frames listed in SEQ ID NOs: 1-953

SEQ ID NOs corresponding to Arabidopsis promoters	SEQ ID NOs corresponding to Arabidopsis ORFs
2137	97
2138	780
2139	238
2140	454
2141	89
2142	86
2143	732
2144	801
2145	792
2146	195
2147	394
2148	138
2149	176
2150	200
2151	899
2152	83
2153	423
2154	367
2155	595
2156	231
2157	601
2158	79
2159	868
2160	770
2161	670
2162	247
2163	120
2164	251
2165	639
2166	380
2167	194
2168	812
2169	318
2170	398
2171	252
2172	879
2173	114
2174	452

2175	25
2176	608
2177	212
2178	66
2179	949
2180	816
2181	411
2182	301
2183	35
2184	291
2185	457
2186	22
2187	756
2188	916
2189	627
2190	740
2191	417
2192	81
2193	533
2194	539
2195	208
2196	710
2197	767
2198	822
2199	201
2200	355
2201	528
2202	877
2203	237
2204	763
2205	230
2206	565
2207	809
2208	870
2209	397
2210	700
2211	336
2212	797
2213	695
2214	219
2215	742
2216	223
2217	324
2218	721
2219	244
2220	16

2267	858
2268	508
2269	151
2270	378
2271	217
2272	724
2273	210
2274	776
2275	216
2276	765
2277	453
2278	221
2279	415
2280	307
2281	516
2282	747
2283	283
2284	943
2285	99
2286	272
2287	164
2288	132
2289	287
2290	863
2291	341
2292	444
2293	267
2294	523
2295	271
2296	288
2297	799
2298	814
2299	142
2300	933
2301	9
2302	788
2303	353
2304	719
2305	548
2306	190
2307	432
2308	281
2309	41
2310	88
2311	24
2312	387

2313	310
2314	873
2315	246
2316	205
2317	340
2318	658
2319	405
2320	248
2321	599
2322	720
2323	227
2324	489
2325	306
2326	818
2327	76
2328	376
2329	68
2330	535
2331	225
2332	192
2333	611
2334	532
2335	343
2336	148
2337	880
2338	490
2339	798
2340	289
2341	705
2342	706
2343	668
2344	211
2345	553
2346	125
2347	39
2348	365
2349	754
2350	372
2351	932
2352	339
2353	78
2354	948
2355	74
2356	479
2357	319
2358	31

2359	789
2360	34
2361	425
2362	197
2363	800
2364	651
2365	383
2366	667
2367	685
2368	582
2369	664
2370	751
2371	859
2372	781
2373	2
2374	470
2375	676
2376	904
2377	28
2378	584
2379	402
2380	503
2381	666
2382	480
2383	407
2384	927
2385	390
2386	915
2387	55
2388	936
2389	794
2390	290
2391	337
2392	338
2393	63
2394	436
2395	67
2396	752
2397	753
2398	907
2399	434
2400	925
2401	769
2402	768
2403	827
2404	905

2405	829
2406	828
2407	900
2408	175
2409	328
2410	304
2411	909
2412	687
2413	327
2414	122
2415	346
2416	302
2417	303
2418	689
2419	440
2420	841
2421	381
2422	135
2423	162
2424	718
2425	75
2426	550
2427	60
2428	17
2429	174
2430	256
2431	708
2432	650
2433	502
2434	654
2435	569
2436	414
2437	495
2438	351
2439	115
2440	771
2441	640
2442	652
2443	431
2444	119
2445	852
2446	772
2447	871
2448	921
2449	549
2450	26

2451	136
2452	864
2453	755
2454	507
2455	127
2456	860
2457	392
2458	253
2459	277
2460	623
2461	447
2462	583
2463	941
2464	185
2465	707
2466	581
2467	671
2468	653
2469	560
2470	712
2471	807
2472	391
2473	793
2474	329
2475	356
2476	513
2477	646
2478	121
2479	352
2480	606
2481	344
2482	401
2483	704
2484	853
2485	116
2486	309
2487	872
2488	805
2489	233
2490	862
2491	895
2492	141
2493	257
2494	510
2495	297
2496	323

2543	830
2544	58
2545	44
2546	134
2547	686
2548	53
2549	619
2550	609
2551	49
2552	887
2553	282
2554	27
2555	630
2556	526
2557	468
2558	848
2559	642
2560	262
2561	371
2562	475
2563	803
2564	427
2565	464
2566	158
2567	326
2568	536
2569	149
2570	172
2571	920
2572	885
2573	448
2574	542
2575	13
2576	85
2577	214
2578	728
2579	951
2580	32
2581	419
2582	409
2583	683
2584	634
2585	84
2586	163
2587	426
2588	588

2635	496
2636	229
2637	228
2638	902
2639	92
2640	203
2641	443
2642	7
2643	348
2644	296
2645	730
2646	359
2647	3
2648	226
2649	243
2650	791
2651	647
2652	655
2653	614
2654	375
2655	130
2656	10
2657	826
2658	485
2659	850
2660	940
2661	102

Table 25
Ortholog Table

12	
5	-----
	AAD17487.1 AF049347 Berberis stolonifera
	DESCRIPTION: Catalyzes the oxidative cyclization of the N-methyl group of (S)-reticuline into the berberine bridge carbon (C-8) of (S)-scoulerine. berberine bridge enzyme. bbe1. Covalently flavinylated oxidase of isoquinoline alkaloid biosynthesis in plants.
10	
	AAB20352.1 S65550 Eschscholzia californica
15	DESCRIPTION: (S)-reticuline:oxygen oxidoreductase (methylene-bridge-forming). /gene="(S)-reticuline:oxygen oxidoreductase. This sequence comes from Fig 2; berberine bridge enzyme.
20	AAC39358.1 AF005655 Eschscholzia californica
	DESCRIPTION: oxidizes the N-methyl group of (S)-reticuline to the berberine bridge carbon C-8 of (S)-scoulerine in berberine and benzophenanthridine alkaloid biosynthesis. berberine bridge enzyme. bbe1. covalently-bound FAD-dependent oxidase; elicitor-inducible.
25	
	AAC61839.1 AF025430 Papaver somniferum
	DESCRIPTION: berberine bridge enzyme. bbe1. (S)-reticuline:oxygen oxidoreductase (methylene bridge forming).
30	
19	-----
	AAC83458.1 AF023140 Thlaspi goesingense
35	DESCRIPTION: imidazoleglycerol phosphate dehydratase. THB1.
	AAB67738.1 U49978 Pisum sativum
	DESCRIPTION: imidazoleglycerol-phosphate dehydratase. PSHIS3.
40	
	AAA93197.1 U02690 Triticum aestivum
	DESCRIPTION: imidazoleglycerolphosphate dehydratase. partial interval represents the confirmed coding region based on homology to sequence U02689, maybe a chimeric molecule.
45	

BAB16915.1 AP002863 *Oryza sativa*
 DESCRIPTION: 1-deoxy-d-xylulose-5-phosphate reductoisomerase.
 5 P0005A05.19. contains ESTs AU108198(S11168),D46469(S11168).
 37

 AAD21872.1 AF078082 *Phaseolus vulgaris*
 10 DESCRIPTION: receptor-like protein kinase homolog RK20-1.
 CAA73134.1 Y12531 *Brassica oleracea*
 DESCRIPTION: serine/threonine kinase. BRLK.
 15
 AAB93834.1 U82481 *Zea mays*
 DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
 kinase; serine/threonine protein kinase.
 20
 CAA67145.1 X98520 *Brassica oleracea*
 DESCRIPTION: receptor-like kinase. SFR2.
 25
 AAC23542.1 U20948 *Ipomoea trifida*
 DESCRIPTION: receptor protein kinase. IRK1.
 30
 CAA73133.1 Y12530 *Brassica oleracea*
 DESCRIPTION: serine /threonine kinase. ARLK.
 35
 CAB41878.1 Y18259 *Brassica oleracea*
 DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.
 CAB41879.1 Y18260 *Brassica oleracea*
 DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.
 40
 CAA74661.1 Y14285 *Brassica oleracea*
 DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain:
 1343-1411; intracellular kinase domain: 1412-2554.
 45

- CAA74662.1 Y14286 Brassica oleracea
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
- 5
AAA33000.1 M76647 Brassica oleracea
DESCRIPTION: receptor protein kinase. SKR6.
- 10
BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.
- 15
AAA33008.1 M97667 Brassica napus
DESCRIPTION: serine/threonine kinase receptor.
- 20
AAA62232.1 U00443 Brassica napus
DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like domain.
- 25
CAB89179.1 AJ245479 Brassica napus subsp. napus
DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.
- 30
BAA92836.1 AB032473 Brassica oleracea
DESCRIPTION: S18 S-locus receptor kinase. SRK18.
- 35
CAA79355.1 Z18921 Brassica oleracea
DESCRIPTION: S-receptor kinase-like protein.
- 40
BAA92837.1 AB032474 Brassica oleracea
DESCRIPTION: S60 S-locus receptor kinase. SRK60.
- 45
BAA07577.2 D38564 Brassica rapa
DESCRIPTION: receptor protein kinase SRK12.
- BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.

BAB21001.1 AB054061 Brassica rapa
DESCRIPTION: S locus receptor kinase. SRK22.

5 BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.

10 BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).

15 AAD52097.1 AF088885 Nicotiana tabacum
DESCRIPTION: receptor-like kinase CHRK1. Chrkl.

BAB18292.1 AP002860 Oryza sativa
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

20 BAB16871.1 AP002537 Oryza sativa
DESCRIPTION: putative protein kinase APK1A Arabidopsis thaliana.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

25 BAB39873.1 AP002882 Oryza sativa
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

30 BAA87853.1 AP000816 Oryza sativa
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).

35 CAA79324.1 Z18884 Brassica oleracea
DESCRIPTION: S-receptor kinase related protein.

40 AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.

45 AAK00425.1 AC069324 Oryza sativa
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

5 AAF66615.1 AF142596 *Nicotiana tabacum*
 DESCRIPTION: LRR receptor-like protein kinase.

10 BAB21240.1 AP002953 *Oryza sativa*
 DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
 C22359(C11461),C22360(C11461).

15 BAB39409.1 AP002901 *Oryza sativa*
 DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
 C23560(R0290).

20 AAG59657.1 AC084319 *Oryza sativa*
 DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.

25 AAG03090.1 AC073405 *Oryza sativa*
 DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis
 receptor-like kinase (AC007504).

30 AAG16628.1 AY007545 *Brassica napus*
 DESCRIPTION: protein serine/threonine kinase BNK1.

38 BAA94509.1 AB041503 *Populus nigra*
 DESCRIPTION: protein kinase 1. PnPK1.

35 CAA58750.1 X83869 *Daucus carota*
 DESCRIPTION: CDPK-related protein kinase. CRK (or PK421).

40 BAA12692.1 D84508 *Zea mays*
 DESCRIPTION: CDPK-related protein kinase. Does not require calcium for
 its activity.

45 AAG01179.1 AF289237 *Zea mays*
 DESCRIPTION: calcium/calmodulin dependent protein kinase MCK2. MCK2.

- 5 AAB47181.1 S82324 Zea mays
DESCRIPTION: /gene="calcium/calmodulin-dependent
protein kinase. This sequence comes from Fig. 1.
- 10 BAA12691.1 D84507 Zea mays
DESCRIPTION: CDPK-related protein kinase. Does not require calcium for
its activity (by similarity).
- 15 BAA22410.1 D38452 Zea mays
DESCRIPTION: calcium-dependent protein kinase-related kinase.
- 20 AAC24961.1 AF009337 Tradescantia virginiana
DESCRIPTION: CDPK-related protein kinase. CRK1.
- 25 AAF23901.2 AF194414 Oryza sativa
DESCRIPTION: calcium-dependent protein kinase. CDPK5. OsCDPK5.
- AAF23900.1 AF194413 Oryza sativa
DESCRIPTION: calcium-dependent protein kinase. CDPK1. OsCDPK1.
- 30 AAC78558.1 AF030879 Solanum tuberosum
DESCRIPTION: protein kinase CPK1.
- CAA57157.1 X81394 Oryza sativa
DESCRIPTION: calcium-dependent protein kinase. OSCPK2.
- 35 BAB21081.1 AP002819 Oryza sativa
DESCRIPTION: putative calcium-dependent protein kinase. P0501G01.10.
- 40 AAC25423.1 AF072908 Nicotiana tabacum
DESCRIPTION: calcium-dependent protein kinase. CDPK1.
- 45 BAA12715.1 D85039 Zea mays
DESCRIPTION: calcium-dependent protein kinase.

5 AAB49984.1 U90262 Cucurbita pepo
DESCRIPTION: calcium-dependent calmodulin-independent protein kinase
CDPK. cpCPK1. serine/threonine protein kinase that is activated by direct
binding of calcium.

10 AAA69507.1 U28376 Zea mays
DESCRIPTION: calcium-dependent protein kinase. MZECDPK2.

15 AAD17800.1 AF090835 Mesembryanthemum crystallinum
DESCRIPTION: Ca²⁺-dependent protein kinase. CPK1. serine/threonine
protein kinase.

20 AAB80693.1 U69174 Glycine max
DESCRIPTION: calmodulin-like domain protein kinase isoenzyme gamma.
CDPK
gamma.

25 BAA81751.1 AB017517 Marchantia polymorpha
DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-B;
alternative
splicing.

30 BAA81749.1 AB017515 Marchantia polymorpha
DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-B;
alternative
splicing.

35 CAA39936.1 X56599 Daucus carota
DESCRIPTION: calcium- dependent protein kinase. DcPK431.

40 BAA81748.1 AB017515 Marchantia polymorpha
DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-A;
alternative
splicing.

45 BAA81750.1 AB017516 Marchantia polymorpha

DESCRIPTION: calcium-dependent protein kinase. CDPK1. CDPK-A;
alternative
splicing.

5

AAA61682.1 L27484 Zea mays
DESCRIPTION: calcium-dependent protein kinase. CDPK.

10 BAB16888.1 AB042550 Oryza sativa
DESCRIPTION: OsCDPK7. oscdpk7.

AAB88537.1 AF035944 Fragaria x ananassa
15 DESCRIPTION: calcium-dependent protein kinase. MAX17.

AAD28192.2 AF115406 Solanum tuberosum
20 DESCRIPTION: calcium-dependent protein kinase. CDPK; catalytic domain.

CAA07481.1 AJ007366 Zea mays
DESCRIPTION: calcium-dependent protein kinase.

25 BAA12338.1 D84408 Zea mays
DESCRIPTION: calcium dependent protein kinase. ZmCDPK1.

30 BAA13440.1 D87707 Ipomoea batatas
DESCRIPTION: calcium dependent protein kinase. CDPK.

BAA13232.1 D87042 Zea mays
35 DESCRIPTION: Calcium-dependent protein kinase.

CAA65500.1 X96723 Medicago sativa
40 DESCRIPTION: protein kinase. CDPK.

AAB70706.1 U82087 Tortula ruralis
DESCRIPTION: calmodulin-like domain protein kinase. TrCPK1.

45 AAC49405.1 U08140 Vigna radiata

DESCRIPTION: calcium dependent protein kinase. CDPK.

- 5 BAA85396.1 AP000615 *Oryza sativa*
DESCRIPTION: ESTs C22369(C12239),C22370(C12239),
AU057852(S21844),AU057853(S21844) correspond to a region of the predicted
gene.; similar to calcium dependent protein kinase. (AF048691).
- 10 CAA57156.1 X81393 *Oryza sativa*
DESCRIPTION: calcium-dependent protein kinase. OSCPKII.
- 15 AAC05270.1 AF048691 *Oryza sativa*
DESCRIPTION: calcium dependent protein kinase. CDPK12.
- 20 AAF21062.1 AF216527 *Dunaliella tertiolecta*
DESCRIPTION: calcium-dependent protein kinase. CPK1; CDPK.
- 25 AAB80692.1 U69173 *Glycine max*
DESCRIPTION: calmodulin-like domain protein kinase isoenzyme beta. CDPK
beta.
- 30 AAK26164.1 AY027885 *Cucumis sativus*
DESCRIPTION: calcium-dependent calmodulin-independent protein kinase 5.
CDPK5. CsCDPK5.
- 35 AAA33443.1 L15390 *Zea mays*
DESCRIPTION: calcium-dependent protein kinase. CDPK.
- 40 CAA89202.1 Z49233 *Chlamydomonas eugametos*
DESCRIPTION: calcium-stimulated protein kinase.
- 45 AAG46110.1 AC073166 *Oryza sativa*
DESCRIPTION: calcium-dependent protein kinase. OSJNBb0064P21.2.
- BAA02698.1 D13436 *Oryza sativa*
DESCRIPTION: calcium-dependent protein kinase. spk.

BAA90814.1 AP001168 *Oryza sativa*

DESCRIPTION: ESTs AU030197(E50746),AU030196(E50746) correspond to
a

5 region of the predicted gene.; Similar to calcium-dependent
calmodulin-independent protein kinase CDPK (U90262).

CAB46228.1 Y18055 *Arachis hypogaea*

10 DESCRIPTION: calcium dependent protein kinase. CDPK.

AAC49008.1 U24188 *Lilium longiflorum*

15 DESCRIPTION: calcium/calmodulin-dependent phosphorylation activity.
calcium/calmodulin-dependent protein kinase. CCaMK. serine/threonine
kinase; binds to calcium and calmodulin.

AAF19401.1 AF203479 *Glycine max*

20 DESCRIPTION: phosphoenolpyruvate carboxylase kinase. protein kinase;
member of Ca²⁺/CaM kinase family; lacks the autoinhibitory region and EF
hands.

25 AAF06970.1 AF162662 *Kalanchoe fedtschenkoi*

DESCRIPTION: phosphoenolpyruvate carboxylase kinase. calcium-independent
protein kinase.

39

30

AAG00510.1 AF285172 *Phaseolus vulgaris*

DESCRIPTION: leaf senescence-associated receptor-like protein kinase.
SARK.

35

BAB21175.1 AP002909 *Oryza sativa*

DESCRIPTION: putative serine/threonine-specific receptor protein kinase.
P0044F08.3.

40

CAB51480.1 Y14600 *Sorghum bicolor*

DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates
in mesophyll cells.

45

AAF59905.1 AF197946 *Glycine max*

DESCRIPTION: receptor protein kinase-like protein. CLV1A.

AAF59906.1 AF197947 Glycine max

5 DESCRIPTION: receptor protein kinase-like protein. CLV1B.

AAB61708.1 U93048 Daucus carota

10 DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.

BAB39873.1 AP002882 Oryza sativa

15 DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

AAC36318.1 AF053127 Malus x domestica

20 DESCRIPTION: leucine-rich receptor-like protein kinase. LRPKml.

AAK21965.1 AY028699 Brassica napus

DESCRIPTION: receptor protein kinase PERK1.

25 AAF91324.1 AF244890 Glycine max

DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.

AAK00425.1 AC069324 Oryza sativa

30 DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

AAF91323.1 AF244889 Glycine max

35 DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.

AAG59657.1 AC084319 Oryza sativa

DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.

CAA97692.1 Z73295 Catharanthus roseus

DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation
predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.

45 BAB40094.1 AP003210 Oryza sativa

DESCRIPTION: putative receptor protein kinase. OSJNBa0010K01.7.

CAA61510.1 X89226 *Oryza sativa*

5 DESCRIPTION: leucine-rich repeat/receptor protein kinase. lrk2.

BAA87852.1 AP000816 *Oryza sativa*

10 DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).

BAA92221.1 AP001278 *Oryza sativa*

15 DESCRIPTION: Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).

AAF91322.1 AF244888 *Glycine max*

20 DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.

AAK11569.1 AF318493 *Lycopersicon hirsutum*

DESCRIPTION: Pto-like protein kinase D. LhirPtoD.

25 CAB51834.1 00069 *Oryza sativa*

DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.

BAA90808.1 AP001168 *Oryza sativa*

30 DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).

AAC48932.1 U13923 *Lycopersicon pimpinellifolium*

35 DESCRIPTION: Fen. putative serine/threonine protein kinase; similar to product encoded by *Lycopersicon pimpinellifolium* Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.

AAF76307.1 AF220602 *Lycopersicon pimpinellifolium*

40 DESCRIPTION: Fen kinase.

AAB47424.1 U59317 *Lycopersicon pimpinellifolium*

45 DESCRIPTION: serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.

- AAK11566.1 AF318490 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
- 5
- AAB47423.1 U59315 *Lycopersicon pimpinellifolium*
DESCRIPTION: serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
- 10
- AAC48914.1 U02271 *Lycopersicon pimpinellifolium*
DESCRIPTION: protein kinase.
- 15
- AAF76306.1 AF220602 *Lycopersicon pimpinellifolium*
DESCRIPTION: Pto kinase.
- 20
- BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
- 25
- AAF76313.1 AF220603 *Lycopersicon esculentum*
DESCRIPTION: Pto kinase. LescPth5.
- 30
- AAB47421.1 U59316 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
- 35
- AAG03090.1 AC073405 *Oryza sativa*
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
- 40
- AAA33915.1 L27821 *Oryza sativa*
DESCRIPTION: receptor type serine/threonine kinase. protein kinase.
- 45
- AAF76314.1 AF220603 *Lycopersicon esculentum*
DESCRIPTION: Fen kinase. Lescfen.

AAK11568.1 AF318492 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase B. LhirPtoB.

5

AAB47422.1 U59318 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase Fen. fen. allele of Fen,
fenthion sensitivity gene from tomato.

10

BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A*Arabidopsis thaliana*.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

15

BAA06538.1 D31737 *Nicotiana tabacum*
DESCRIPTION: protein-serine/threonine kinase.

20

AAK11567.1 AF318491 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase F. LhirPtoF.

25

AAF34426.1 AF172282 *Oryza sativa*
DESCRIPTION: leucine rich repeat containing protein kinase. DUPR11.16.

30

AAG25966.1 AF302082 *Nicotiana tabacum*
DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase;
transcript abundance decreases rapidly after cytokinin treatment.

35

BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

41

40

AAG12987.1 AF166498 *Lycopersicon esculentum*
DESCRIPTION: sucrose transporter-like protein. SUT2. sucrose sensor.

45

AAF08330.1 AF021809 *Vitis vinifera*
DESCRIPTION: putative sucrose transporter. VvSUC12.

BAA24071.1 D87819 *Oryza sativa*
DESCRIPTION: sucrose transporter. OsSUT1.

5 AAF90181.1 AF280050 *Oryza sativa* subsp. *indica*
DESCRIPTION: sucrose proton symporter. sucrose transporter. SUT1.

10 BAA83501.1 AB008464 *Zea mays*
DESCRIPTION: Sucrose Transporter. ZmSUT1.

15 CAB75882.1 AJ272309 *Hordeum vulgare*
DESCRIPTION: Transport sucrose through membrane. sucrose transporter 1.
sut1.

20 AAD55269.1 AF182445 *Vitis vinifera*
DESCRIPTION: sucrose transporter.

25 CAA83436.1 Z31561 *Ricinus communis*
DESCRIPTION: sucrose transport. sucrose carrier. Scr1.

CAA76368.1 Y16767 *Daucus carota*
DESCRIPTION: sucrose/H⁺ symporter. SUT1b.

30 CAA76367.1 Y16766 *Daucus carota*
DESCRIPTION: sucrose/H⁺ symporter. SUT1a.

35 CAC19688.1 AJ303198 *Daucus carota*
DESCRIPTION: essential for sucrose transport. sucrose/proton symporter.
sut1a.

40 AAG25923.1 AF237780 *Solanum tuberosum*
DESCRIPTION: sucrose transporter SUT4.

45 AAF08329.1 AF021808 *Vitis vinifera*
DESCRIPTION: putative sucrose transporter. VvSUC11.

AAG09270.1 AF176950 *Lycopersicon esculentum*
DESCRIPTION: sucrose transporter. SUT4.

5 AAF65765.1 AF242307 *Euphorbia esula*
DESCRIPTION: sucrose transport protein.

10 AAF04295.1 AF191025 *Alonsoa meridionalis*
DESCRIPTION: sucrose transporter 1. SUT1.

15 CAA57727.1 X82276 *Nicotiana tabacum*
DESCRIPTION: sucrose transporter. NtSUT1a. Var. SNN bp 1-1346, Var. SR1
bp 1172-1614.

20 BAA89458.1 AB036758 *Daucus carota*
DESCRIPTION: sucrose transporter protein. cSUT.

25 CAB75881.1 AJ272308 *Hordeum vulgare*
DESCRIPTION: transport sucrose through membrane. sucrose transporter 2.
sut2.

30 CAA76369.1 Y16768 *Daucus carota*
DESCRIPTION: sucrose/H⁺ symporter. SUT2.

CAC19689.1 AJ303199 *Daucus carota*
DESCRIPTION: essential for sucrose transport. sucrose/proton symporter.
sut2.

35 CAB07811.1 Z93774 *Vicia faba*
DESCRIPTION: sugar transport. sucrose transport protein. sut.

40 CAA47604.1 X67125 *Spinacia oleracea*
DESCRIPTION: sucrose permease. S21.

45 CAA48915.1 X69165 *Solanum tuberosum*
DESCRIPTION: sucrose transport protein. SUT1.

AAD41024.1 AF109922 Pisum sativum
DESCRIPTION: sucrose transport protein SUT1.

5

AAD53000.1 U64967 Beta vulgaris
DESCRIPTION: sucrose-proton symporter. Bv8-6.

10 AAF08331.1 AF021810 Vitis vinifera
DESCRIPTION: putative sucrose transporter. VvSUC27.

15 CAA58730.1 X83850 Beta vulgaris
DESCRIPTION: sucrose/proton-symporter. sut1.

AAC99332.1 AF063400 Apium graveolens
DESCRIPTION: sucrose transporter. SUT1.

20

AAD45391.1 AF167416 Apium graveolens
DESCRIPTION: sucrose transporter SUT2B. SUT2B.

25

AAD45390.1 AF167415 Apium graveolens
DESCRIPTION: sucrose transporter SUT2A. SUT2A.

30 AAF04294.1 AF191024 Asarina barclaiana
DESCRIPTION: sucrose transporter 1. SUT1.

35 CAA59113.1 X84379 Plantago major
DESCRIPTION: SUC1-sucrose proton symporter. SUC1.

AAD34610.1 AF149981 Nicotiana tabacum
DESCRIPTION: sucrose transporter-like protein. SUT3.

40

CAA57726.1 X82275 Lycopersicon esculentum
DESCRIPTION: sucrose transporter. LeSUT1.

45

CAA12256.1 AJ224961 Ricinus communis

DESCRIPTION: Sucrose transport. Sucrose carrier. SUT1.

CAC33492.1 AJ310643 Ricinus communis

5 DESCRIPTION: sucrose carrier. sucrose carrier. scr1.

AAD45932.1 AF168771 Betula pendula

10 DESCRIPTION: sucrose transport protein. SUC1.

CAA53390.1 X75764 Plantago major

DESCRIPTION: sucrose transporter. ptp1.

15

AAF22281.1 AF167417 Apium graveolens

DESCRIPTION: putative sucrose transporter SUT1. SUT1.

20 BAA76434.1 AB025006 Cicer arietinum

DESCRIPTION: sucrose transport protein.

42

25 AAC64184.1 AF095577 Prunus persica

DESCRIPTION: endopolygalacturonase.

30 CAA54150.1 X76735 Prunus persica

DESCRIPTION: endopolygalacturonase.

AAC28906.1 AF001003 Lycopersicon esculentum

35 DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 5. TAPG5. expressed in abscission.

AAC28947.1 AF029230 Lycopersicon esculentum

40 DESCRIPTION: polygalacturonase. TPG6.

AAC70951.1 AF072732 Lycopersicon esculentum

45 DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella. polygalacturonase 7. specifically and abundantly expressed in pistils.

AAC28905.1 AF001002 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of
plant cells. polygalacturonase 4. TAPG4. expressed in abscission.

5

AAA80489.1 U23053 *Lycopersicon esculentum*
DESCRIPTION: polygalacturonase precursor.

10 AAC28903.1 AF001000 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of
plant cells. polygalacturonase 1. TAPG1. expressed in abscission.

15 AAB09575.1 U70480 *Lycopersicon esculentum*
DESCRIPTION: abscission polygalacturonase. TAPG2.

20 AAC28904.1 AF001001 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of
plant cells. polygalacturonase 2. TAPG2. expressed in abscission.

25 AAB09576.1 U70481 *Lycopersicon esculentum*
DESCRIPTION: abscission polygalacturonase. TAPG4.

30 AAC28902.2 AF000999 *Lycopersicon esculentum*
DESCRIPTION: hydrolyzes pectin in the cell wall and middle lamella of
plant cells. polygalacturonase 3. TAPG3. expressed in abscission.

35 AAC26510.1 AF062465 *Cucumis melo*
DESCRIPTION: polygalacturonase precursor. MPG1.

AAC26511.1 AF062466 *Cucumis melo*
DESCRIPTION: polygalacturonase precursor. MPG2.

40

BAB21092.1 AP002819 *Oryza sativa*
DESCRIPTION: putative endopolygalacturonase. P0501G01.21.

45 AAA62286.1 U20431 *Medicago sativa*
DESCRIPTION: polygalacturonase.

AAA82167.1 U09717 Gossypium hirsutum
DESCRIPTION: polygalacturonase.

5

AAA58322.1 U09805 Gossypium barbadense
DESCRIPTION: polygalacturonase.

10

CAA50336.1 X71018 Nicotiana tabacum
DESCRIPTION: polygalacturonase. NPG. Protein sequence is in conflict with
the conceptual translation; G27Y.

15

CAA50334.1 X71016 Nicotiana tabacum
DESCRIPTION: polygalacturonase. NPG. Protein sequence is in conflict with
the conceptual translation; G27.X.

20

CAA50337.1 X71019 Nicotiana tabacum
DESCRIPTION: polygalacturonase. NPG. Protein sequence is in conflict with
the conceptual translation; G27W.

25

CAA65072.1 X95800 Brassica napus
DESCRIPTION: polygalacturonase.

30

BAA89478.1 AB029459 Salix gilgiana
DESCRIPTION: polygalacturonase. SgPG3.

35

CAA90272.1 Z49971 Brassica napus
DESCRIPTION: Hydrolytic enzyme. Polygalacturonase. pga.

40

CAA50335.1 X71017 Nicotiana tabacum
DESCRIPTION: polygalacturonase. Npg1. Protein sequence is in conflict
with the conceptual translation.

45

CAA50338.1 X71020 Nicotiana tabacum
DESCRIPTION: polygalacturonase. Npg1.

- BAA89479.1 AB029460 *Salix gilgiana*
DESCRIPTION: polygalacturonase. SgPG4.
- 5 AAC14453.1 L12019 *Actinidia deliciosa*
DESCRIPTION: polygalacturonase.
- 10 BAA89476.1 AB029457 *Salix gilgiana*
DESCRIPTION: polygalacturonase. SgPG1.
- 15 AAC26512.1 AF062467 *Cucumis melo*
DESCRIPTION: polygalacturonase precursor. MPG3.
- 20 CAA72003.1 Y11118 *Medicago sativa*
DESCRIPTION: polygalacturonase. PG3.
- CAB42886.1 AJ238848 *Phleum pratense*
DESCRIPTION: polygalacturonase. pg.
- 25 BAA89477.1 AB029458 *Salix gilgiana*
DESCRIPTION: polygalacturonase. SgPG2.
- 30 CAC05658.1 AJ250919 *Brassica napus*
DESCRIPTION: endopolygalacturonase. pegaz.
- 35 CAC05657.1 AJ250918 *Brassica napus*
DESCRIPTION: endopolygalacturonase. pgaz.
- 40 AAA32914.1 L06094 *Persea americana*
DESCRIPTION: cell wall degradation. polygalacturonase.
- AAF71160.1 AF152758 *Actinidia chinensis*
DESCRIPTION: polygalacturonase A. PGA.
- 45 AAF61444.1 AF138858 *Lycopersicon esculentum*
DESCRIPTION: hydrolyses polygalacturonic acid. polygalacturonase.XOPG1.

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- 5 AAA34178.1 M37304 Lycopersicon esculentum
DESCRIPTION: polygalacturonase.
- 10 CAA32235.1 X14074 Lycopersicon esculentum
DESCRIPTION: polygalacturonase.
- 15 CAA29148.1 X05656 Lycopersicon esculentum
DESCRIPTION: polygalacturonase (AA 1-457).
- 20 AAD46483.1 AF128266 Glycine max
DESCRIPTION: polygalacturonase PG1.
- 25 BAA88472.1 AB035890 Cucumis sativus
DESCRIPTION: polygalacturonase. CUPG1.
- 30 AAD46484.1 AF128267 Glycine max
DESCRIPTION: polygalacturonase PG2.
- 35 CAA54448.1 X77231 Prunus persica
DESCRIPTION: polygalacturonase. PG.
- 44 CAA47055.1 X66426 Persea americana
DESCRIPTION: polygalacturonase.
- 40 CAA47052.1 X66422 Zea mays
DESCRIPTION: polygalacturonase. PG.
- 45 AAC61805.1 U28007 Lycopersicon esculentum
DESCRIPTION: serine/threonine protein kinase. Pto kinase interactor 1.
Pti1. Pti1 kinase.
- 45 BAB21241.1 AP002953 Oryza sativa
DESCRIPTION: Putative Pto kinase interactor 1. P0426D06.21. contains ESTs

AU108280(E0721),D48017(S13927).

5 AAF91337.1 AF249318 Glycine max
DESCRIPTION: Pti1 kinase-like protein. Pti1b. protein kinase.

10 AAF91336.1 AF249317 Glycine max
DESCRIPTION: Pti1 kinase-like protein. Pti1a. protein kinase.

15 BAA87853.1 AP000816 Oryza sativa
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).

20 BAB16871.1 AP002537 Oryza sativa
DESCRIPTION: putative protein kinase APK1A Arabidopsis thaliana.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

25 AAG16628.1 AY007545 Brassica napus
DESCRIPTION: protein serine/threonine kinase BNK1.

30 BAB39409.1 AP002901 Oryza sativa
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).

35 BAB39873.1 AP002882 Oryza sativa
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

40 AAC27894.1 AF023164 Zea mays
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. ltk1.

BAA94509.1 AB041503 Populus nigra
DESCRIPTION: protein kinase 1. PnPK1.

45 BAB07999.1 AP002525 Oryza sativa
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST

C22619(S11214).

- 5 BAB03429.1 AP002817 Oryza sativa
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
- 10 AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.
- 15 AAC27895.1 AF023165 Zea mays
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 2. ltk2.
- 20 AAK00425.1 AC069324 Oryza sativa
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- 25 BAB21240.1 AP002953 Oryza sativa
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
- 30 BAA94510.1 AB041504 Populus nigra
DESCRIPTION: protein kinase 2. PnPK2.
- 35 AAG03090.1 AC073405 Oryza sativa
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
- 40 AAG59657.1 AC084319 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
- 45 BAA78764.1 AB023482 Oryza sativa
DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).

AAG25966.1 AF302082 *Nicotiana tabacum*

DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase;
transcript abundance decreases rapidly after cytokinin treatment.

5

AAF43496.1 AF131222 *Lophopyrum elongatum*

DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by
salt stress, osmotic stress, and ABA treatment.

10

AAK11674.1 AF339747 *Lophopyrum elongatum*

DESCRIPTION: protein kinase. ESI47.

15

AAB09771.1 U67422 *Zea mays*

DESCRIPTION: CRINKLY4 precursor. cr4. receptor kinase homolog.

20

CAA97692.1 Z73295 *Catharanthus roseus*

DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation
predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.

25

BAA90808.1 AP001168 *Oryza sativa*

DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).

30

AAB47421.1 U59316 *Lycopersicon esculentum*

DESCRIPTION: serine/threonine protein kinase Pto. pto. allele of Pto
bacterial speck disease resistance gene in tomato.

35

AAF76313.1 AF220603 *Lycopersicon esculentum*

DESCRIPTION: Pto kinase. LescPth5.

40

CAB51834.1 00069 *Oryza sativa*

DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.

AAB47423.1 U59315 *Lycopersicon pimpinellifolium*

DESCRIPTION: serine/threonine protein kinase Pto. Pto. bacterial speck
disease resistance in tomato; disease resistance gene.

45

AAF76306.1 AF220602 *Lycopersicon pimpinellifolium*

DESCRIPTION: Pto kinase.

5 AAC48914.1 U02271 *Lycopersicon pimpinellifolium*
DESCRIPTION: protein kinase.

10 BAA92221.1 AP001278 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC F12L6
genomic sequence, putative protein kinase. (AC004218).

15 BAA87852.1 AP000816 *Oryza sativa*
DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).

20 AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.

25 AAK11566.1 AF318490 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase E. LhirPtoE. confers resistance to
bacterial speck disease.

AAK11567.1 AF318491 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase F. LhirPtoF.

30 CAB51836.1 AJ243961 *Oryza sativa*
DESCRIPTION: Putitive Ser/Thr protein kinase. 11332.7.

35 AAD38286.1 AC007789 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0049B20.13.

40 BAB40081.1 AP003074 *Oryza sativa*
DESCRIPTION: putative receptor protein kinase. OSJNBa0004G10.30.

BAB18321.1 AP002865 *Oryza sativa*
DESCRIPTION: putative receptor protein kinase. P0034C11.11.

45 BAA92836.1 AB032473 *Brassica oleracea*

DESCRIPTION: S18 S-locus receptor kinase. SRK18.

45

5 AAB72110.1 U79958 Pisum sativum
DESCRIPTION: BP-80 vacuolar sorting receptor.

10 AAF80450.1 AF161719 Triticum aestivum
DESCRIPTION: vacuolar targeting receptor bp-80.

15 AAG60258.1 AY017377 Physcomitrella patens
DESCRIPTION: EGF receptor-like protein. ELP. PPELP; similar to putative
vacuolar sorting receptor.

20 AAF22842.1 AF209910 Prunus dulcis
DESCRIPTION: vacuolar sorting receptor protein. BP-80 type protein.

25 AAK31596.1 AY029172 Helianthus annuus
DESCRIPTION: EGF receptor-like protein. ELP.

30 AAB72113.1 U79961 Zea mays
DESCRIPTION: vacuolar sorting receptor homolog. similar to Pisum sativum
BP-80 vacuolar sorting receptor, GenBank Accession Number U79958.

35 BAA92985.1 AP001550 Oryza sativa
DESCRIPTION: EST D15617(C0960A) corresponds to a region of the predicted
gene.; Similar to Arabidopsis thaliana chromosome 4, BAC clone F18F4;
vacuolar sorting receptor-like protein (AL021637).

47

40 BAA00885.1 D10001 Pisum sativum
DESCRIPTION: phenylalanine ammonia-lyase.

45 AAK15640.1 AF326116 Agastache rugosa
DESCRIPTION: phenylalanine ammonia-lyase. PAL.

CAB42794.1 AJ238754 Citrus clementina x Citrus reticulata

DESCRIPTION: phenylalanine-ammonia lyase. pal2.

5 BAA00886.1 D10002 Pisum sativum
DESCRIPTION: phenylalanine ammonia-lyase. PAL1.

10 BAA00887.1 D10003 Pisum sativum
DESCRIPTION: phenylalanine ammonia-lyase. PAL2.

AAB67733.1 U43338 Citrus limon
DESCRIPTION: phenylalanine ammonia-lyase. pal6.

15 AAF40224.1 AF237955 Rubus idaeus
DESCRIPTION: phenylalanine ammonia-lyase 2. PAL2. PAL;
phenylpropanoid;
multigene; flavonoid.

20 AAA17993.1 M91192 Trifolium subterraneum
DESCRIPTION: phenylalanine ammonia-lyase. PAL1.

25 CAA57057.1 X81159 Petroselinum crispum
DESCRIPTION: phenylalanine ammonia-lyase 3. PAL3. tetramere subunit.

30 AAF40223.1 AF237954 Rubus idaeus
DESCRIPTION: phenylalanine ammonia-lyase 1. PAL1. PAL;
phenylpropanoid;
multigene; flavonoid.

35 CAA68938.1 Y07654 Petroselinum crispum
DESCRIPTION: PAL1 protein. pal1 gene.

40 CAA57056.1 X81158 Petroselinum crispum
DESCRIPTION: phenylalanine ammonia-lyase 2. PAL2. deaminase subunit.

45 CAB60719.1 AJ250836 Cicer arietinum
DESCRIPTION: phenylpropanoid pathway. phenylalanine ammonia-lyase. pal.

[illegible]

AAC78457.1 AF036948 *Prunus avium*
DESCRIPTION: phenylalanine ammonia-lyase. PAL1.

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CAA73065.1 Y12461 *Helianthus annuus*

DESCRIPTION: phenylalanine ammonia lyase. PAL.

5 BAA95629.1 AB042520 Catharanthus roseus
DESCRIPTION: phenylalanine ammonia lyase.

10 BAA05643.1 D26596 Camellia sinensis
DESCRIPTION: phenylalanine ammonia-lyase.

15 BAA24929.1 D83076 Lithospermum erythrorhizon
DESCRIPTION: phenylalanine ammonia-lyase.

20 BAA21643.1 D30656 Populus kitakamiensis
DESCRIPTION: phenylalanine ammonia-lyase.

25 CAA37129.1 X52953 Glycine max
DESCRIPTION: phenylalanine ammonia-lyase. PAL1.

30 AAA34122.1 M84466 Nicotiana tabacum
DESCRIPTION: phenylalanine ammonia lyase. tpa1.

35 BAA22948.1 AB008200 Nicotiana tabacum
DESCRIPTION: phenylalanine ammonia-lyase. palB.

40 AAA99500.1 L36822 Stylosanthes humilis
DESCRIPTION: phenylalanine ammonia lyase. PAL17.1.

45 CAB42793.1 AJ238753 Citrus clementina x Citrus reticulata
DESCRIPTION: phenylalanine-ammonia lyase. pal1.

50 AAG49585.1 AF325496 Ipomoea nil
DESCRIPTION: phenylalanine ammonia-lyase.

55 CAA55075.1 X78269 Nicotiana tabacum
DESCRIPTION: phenylalanine ammonia-lyase.

- BAA22963.1 D17467 *Nicotiana tabacum*
 DESCRIPTION: phenylalanine ammonia-lyase. TOBPAL1.
- 5
- BAA22947.1 AB008199 *Nicotiana tabacum*
 DESCRIPTION: phenylalanine ammonia-lyase. palA.
- 10
- AAA34179.2 M83314 *Lycopersicon esculentum*
 DESCRIPTION: deamination of phenylalanine to coumarate. phenylalanine
 ammonia lyase. pal.
- 15
- BAA11459.1 D78640 *Ipomoea batatas*
 DESCRIPTION: Phenylalanine Ammonia-Lyase.
- 20
- AAA33389.1 M29232 *Ipomoea batatas*
 DESCRIPTION: phenylalanine ammonia-lyase.
- 25
- CAA68036.1 X99705 *Triticum aestivum*
 DESCRIPTION: phenylalanine ammonia-lyase. PAL.
- 30
- CAA61198.1 X87946 *Oryza sativa*
 DESCRIPTION: phenylalanine ammonia-lyase. ZB8.
- 35
- BAA06337.1 D30657 *Populus kitakamiensis*
 DESCRIPTION: phenylalanine ammonia-lyase.
- 40
- AAD45384.1 AF165998 *Vigna unguiculata*
 DESCRIPTION: phenylalanine ammonia-lyase.
- 45
- CAA53733.1 X76130 *Cucumis melo*
 DESCRIPTION: phenylalanine ammonia-lyase. pal.
- AAA51873.1 U16130 *Persea americana*
 DESCRIPTION: phenylalanine ammonia lyase. PAL.

BAB19128.1 AB041361 *Dianthus caryophyllus*
DESCRIPTION: phenylalanine ammonia-lyase. Dcpal1.

5 CAA34715.1 X16772 *Petroselinum crispum*
DESCRIPTION: phenylalanine ammonia-lyase (AA 137 - 716) (1 is 3rd base in codon).

10 BAA07861.1 D43803 *Populus kitakamiensis*
DESCRIPTION: phenylalanine ammonia-lyase.

48

15 CAB94692.1 AJ242742 *Ipomoea batatas*
DESCRIPTION: Removal of H₂O₂, oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.

20 AAD37430.1 AF149280 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 5 precursor. FBP5. secretory peroxidase.

CAA66037.1 X97351 *Populus balsamifera* subsp. *trichocarpa*
25 DESCRIPTION: signal for ER. peroxidase.

BAA06335.1 D30653 *Populus kitakamiensis*
DESCRIPTION: peroxidase.

30

AAA34108.1 J02979 *Nicotiana tabacum*
DESCRIPTION: lignin-forming peroxidase precursor (EC 1.11.1.7).

35

BAA01992.1 D11396 *Nicotiana tabacum*
DESCRIPTION: 'peroxidase'.

40 CAA50597.1 X71593 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. CEVI-1.

CAB67121.1 Y19023 *Lycopersicon esculentum*
45 DESCRIPTION: peroxidase. cevi-1.

BAA11853.1 D83225 *Populus nigra*

DESCRIPTION: peroxidase.

5

CAA66034.1 X97348 *Populus balsamifera* subsp. *trichocarpa*

DESCRIPTION: signal for ER. peroxidase.

10 BAA01877.1 D11102 *Populus kitakamiensis*

DESCRIPTION: peroxidase. prxA1.

BAA11852.1 D83224 *Populus nigra*

15 DESCRIPTION: peroxidase.

CAA66035.1 X97349 *Populus balsamifera* subsp. *trichocarpa*

20 DESCRIPTION: signal for ER. peroxidase.

AAB47602.1 L07554 *Linum usitatissimum*

DESCRIPTION: peroxidase. FLXPER1.

25

AAD37427.1 AF149277 *Phaseolus vulgaris*

DESCRIPTION: peroxidase I precursor. FBP1. secretory peroxidase.

30 CAA66036.1 X97350 *Populus balsamifera* subsp. *trichocarpa*

DESCRIPTION: signal for ER. peroxidase.

AAB97734.1 AF014502 *Glycine max*

35 DESCRIPTION: seed coat peroxidase precursor. Ep. H₂O₂ oxidoreductase;
class III plant peroxidase.

BAA06334.1 D30652 *Populus kitakamiensis*

40 DESCRIPTION: peroxidase.

BAA07241.1 D38051 *Populus kitakamiensis*

45 DESCRIPTION: peroxidase. prxA4a.

CAA62226.1 X90693 Medicago sativa
DESCRIPTION: peroxidase1B. prx1B.

5 CAA62225.1 X90692 Medicago sativa
DESCRIPTION: peroxidase1A. prx1A.

10 CAA62227.1 X90694 Medicago sativa
DESCRIPTION: peroxidase1C. prx1C.

15 AAB41811.1 L36157 Medicago sativa
DESCRIPTION: peroxidase. pxdC. amino acid feature: conserved domains, aa
123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 ..
73.

20 AAB41810.1 L36156 Medicago sativa
DESCRIPTION: peroxidase. pxdA. amino acid feature: conserved motifs, aa
181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.

25 AAC98519.1 AF007211 Glycine max
DESCRIPTION: peroxidase precursor. GMIPER1. pathogen-induced.

30 BAA02840.1 D13683 Populus kitakamiensis
DESCRIPTION: peroxidase. HPOX14.

BAA14144.1 D90116 Armoracia rusticana
DESCRIPTION: peroxidase isozyme.

35 AAA33129.1 M91372 Cucumis sativus
DESCRIPTION: peroxidase. pre-peroxidase.

40 BAA14143.1 D90115 Armoracia rusticana
DESCRIPTION: peroxidase isozyme.

45 BAA08499.1 D49551 Oryza sativa
DESCRIPTION: peroxidase. poxN.

- BAA03373.1 D14482 *Oryza sativa*
DESCRIPTION: putative peroxidase.
- 5 AAA34101.1 L02124 *Nicotiana tabacum*
DESCRIPTION: peroxidase.
- 10 BAA82306.1 AB027752 *Nicotiana tabacum*
DESCRIPTION: peroxidase.
- 15 CAA40796.1 X57564 *Armoracia rusticana*
DESCRIPTION: peroxidase. peroxidase precursor.
- 20 AAA33121.1 M32742 *Cucumis sativus*
DESCRIPTION: peroxidase (CuPer2).
- CAA76680.1 Y17192 *Cucurbita pepo*
DESCRIPTION: peroxidase. aprx. type III peroxidase.
- 25 BAA92500.1 AP001383 *Oryza sativa*
DESCRIPTION: ESTs D39300(R3292),AU030751(E60187) correspond to a
region
of the predicted gene. Similar to peroxidase ATP6a. (X98774).
- 30 BAA77388.1 AB024438 *Scutellaria baicalensis*
DESCRIPTION: peroxidase 2.
- 35 AAA33127.1 M91373 *Cucumis sativus*
DESCRIPTION: peroxidase. pre-peroxidase. putative.
- 40 AAD43561.1 AF155124 *Gossypium hirsutum*
DESCRIPTION: bacterial-induced peroxidase precursor. Perx_Goshiko.
- 45 AAB06183.1 M37636 *Arachis hypogaea*
DESCRIPTION: cationic peroxidase. PNC1.

AAF63027.1 AF244924 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx15 precursor.
type III peroxidase.

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CAA71492.1 Y10466 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr5.

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AAB02554.1 L37790 *Stylosanthes humilis*
DESCRIPTION: cationic peroxidase.

15 BAA94962.1 AB042103 *Asparagus officinalis*
DESCRIPTION: peroxidase. AspPOX1.

20 BAA77389.1 AB024439 *Scutellaria baicalensis*
DESCRIPTION: peroxidase 3.

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25 CAA40796.1 X57564 *Armoracia rusticana*
DESCRIPTION: peroxidase. peroxidase precursor.

BAA03373.1 D14482 *Oryza sativa*
DESCRIPTION: putative peroxidase.

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BAA08499.1 D49551 *Oryza sativa*
DESCRIPTION: peroxidase. poxN.

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CAA66037.1 X97351 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.

40 BAA84764.1 D84400 *Oryza sativa*
DESCRIPTION: peroxidase. poxA.

45 BAA03372.1 D14481 *Oryza sativa*
DESCRIPTION: putative peroxidase.

- 5 CAB94692.1 AJ242742 *Ipomoea batatas*
DESCRIPTION: Removal of H₂O₂, oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
- 10 BAA06335.1 D30653 *Populus kitakamiensis*
DESCRIPTION: peroxidase.
- 15 AAD37427.1 AF149277 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 1 precursor. FBP1. secretory peroxidase.
- 20 AAD37430.1 AF149280 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 5 precursor. FBP5. secretory peroxidase.
- 25 BAA11852.1 D83224 *Populus nigra*
DESCRIPTION: peroxidase.
- 30 CAA66035.1 X97349 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.
- 35 BAA07241.1 D38051 *Populus kitakamiensis*
DESCRIPTION: peroxidase. prxA4a.
- 40 BAA92500.1 AP001383 *Oryza sativa*
DESCRIPTION: ESTs D39300(R3292),AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).
- 45 CAA50597.1 X71593 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. CEVI-1.

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AAC98519.1 AF007211 Glycine max
DESCRIPTION: peroxidase precursor. GMIPER1. pathogen-induced.

- BAA14143.1 D90115 *Armoracia rusticana*
DESCRIPTION: peroxidase isozyme.
- 5 AAB97734.1 AF014502 *Glycine max*
DESCRIPTION: seed coat peroxidase precursor. Ep. H₂O₂ oxidoreductase;
class III plant peroxidase.
- 10 AAF63027.1 AF244924 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx15 precursor.
type III peroxidase.
- 15 CAA62225.1 X90692 *Medicago sativa*
DESCRIPTION: peroxidase1A. prx1A.
- 20 BAA01877.1 D11102 *Populus kitakamiensis*
DESCRIPTION: peroxidase. prxA1.
- 25 AAF63026.1 AF244923 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx14 precursor.
type III peroxidase.
- 30 BAA14144.1 D90116 *Armoracia rusticana*
DESCRIPTION: peroxidase isozyme.
- 35 AAB41810.1 L36156 *Medicago sativa*
DESCRIPTION: peroxidase. pxdA. amino acid feature: conserved motifs, aa
181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
- 40 AAA34050.1 M74103 *Nicotiana sylvestris*
DESCRIPTION: anionic peroxidase.
- CAA62597.1 X91172 *Raphanus sativus*
DESCRIPTION: korean-radish isoperoxidase. prxk1.
- 45 AAB02554.1 L37790 *Stylosanthes humilis*
DESCRIPTION: cationic peroxidase.

- CAA76680.1 Y17192 Cucurbita pepo
DESCRIPTION: peroxidase. aprx. type III peroxidase.
- 5
- CAA71492.1 Y10466 Spinacia oleracea
DESCRIPTION: peroxidase. prxr5.
- 10
- BAA94962.1 AB042103 Asparagus officinalis
DESCRIPTION: peroxidase. AspPOX1.
- 15
- BAA77389.1 AB024439 Scutellaria baicalensis
DESCRIPTION: peroxidase 3.
- 20
- AAD37428.1 AF149278 Phaseolus vulgaris
DESCRIPTION: peroxidase 3 precursor. FBP3. secretory peroxidase.
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- AAB41811.1 L36157 Medicago sativa
DESCRIPTION: peroxidase. pxdC. amino acid feature: conserved domains, aa 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 .. 73.
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- AAB06183.1 M37636 Arachis hypogaea
DESCRIPTION: cationic peroxidase. PNC1.
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- BAA02112.1 D12544 Pisum sativum
DESCRIPTION: GTP-binding protein.
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- CAA98184.1 Z73956 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB11H. rab11H.
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- AAK15703.1 AF327517 Oryza sativa
DESCRIPTION: GTP-binding protein.
- BAA02904.1 D13758 Oryza sativa

DESCRIPTION: ras-related GTP binding protein. ss230.

5 BAA02111.1 D12543 Pisum sativum
DESCRIPTION: GTP-binding protein.

10 BAA02113.1 D12545 Pisum sativum
DESCRIPTION: GTP-binding protein.

CAA98180.1 Z73952 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB11D. rab11D.

15 CAB65172.1 AJ245570 Lycopersicon esculentum
DESCRIPTION: putative role in secretion of cell wall modifying enzymes.
Rab11 GTPase. Rab11a.

20 BAA02114.1 D12546 Pisum sativum
DESCRIPTION: GTP-binding protein.

25 CAA98181.1 Z73953 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB11E. rab11E.

30 CAA95859.1 Z71276 Mangifera indica
DESCRIPTION: small GTPase. rabX. homologous to Rab11.

35 CAA55865.1 X79278 Medicago sativa
DESCRIPTION: GTP binding protein. Rab.

CAA89049.1 Z49190 Beta vulgaris
DESCRIPTION: GTP-binding. small G protein.

40 CAA98179.1 Z73951 Lotus japonicus
DESCRIPTION: GTP-binding protein. RAB11C. rab11C.

45 BAA02437.1 D13152 Oryza sativa
DESCRIPTION: GTP binding protein. rgp2.

BAA06701.1 D31905 Zea mays
 DESCRIPTION: mgp1 GTP-binding protein. mgp1.
 5

BAA06702.1 D31906 Zea mays
 DESCRIPTION: mgp2 GTP-binding protein. mgp2.

10 BAA02110.1 D12542 Pisum sativum
 DESCRIPTION: GTP-binding protein.

15 CAA98177.1 Z73949 Lotus japonicus
 DESCRIPTION: GTP-binding protein. RAB11A. rab11A.

20 CAA41966.1 X59276 Oryza sativa
 DESCRIPTION: GTP-binding protein. rgp1.

25 AAB97114.1 U58853 Glycine max
 DESCRIPTION: small GTP-binding protein. sral.

CAA98185.1 Z73957 Lotus japonicus
 DESCRIPTION: GTP-binding protein. RAB11I. rab11I.

30 CAA67153.1 X98540 Fagus sylvatica
 DESCRIPTION: FSGTP1.

35 CAA98183.1 Z73955 Lotus japonicus
 DESCRIPTION: GTP-binding protein. RAB11G. rab11G.

40 CAA98182.1 Z73954 Lotus japonicus
 DESCRIPTION: GTP-binding protein. RAB11F. rab11F.

45 CAA54506.1 X77301 Glycine max
 DESCRIPTION: GTPase. gmr2.

[illegible]

DESCRIPTION: vesicular transport. guanine nucleotide regulatory protein.
rab2. GTP-binding protein; soyrab.

5 AAA63902.1 U22433 Zea mays
DESCRIPTION: GTP binding protein. rab2.

53

10 CAA64327.1 X94624 Brassica napus
DESCRIPTION: acyl-CoA synthetase.

15 CAA96523.1 Z72153 Brassica napus
DESCRIPTION: acyl CoA synthetase.

20 CAC19877.1 AJ401089 Brassica napus
DESCRIPTION: activation of free fatty acids. long chain acyl-CoA
synthetase. acs6. activity confirmed by expression in E. coli.

25 CAA06820.1 AJ006025 Cicer arietinum
DESCRIPTION: acyl-coA synthetase.

30 BAA08365.1 D49366 Lithospermum erythrorhizon
DESCRIPTION: 4-coumarate:CoA ligase.

CAA36850.1 X52623 Oryza sativa
DESCRIPTION: 4-coumarate-CoA ligase.

35 AAF37734.1 AF052223 Lolium perenne
DESCRIPTION: 4-coumarate--CoA ligase 4CL3.

40 AAF91309.1 AF239686 Rubus idaeus
DESCRIPTION: 4-coumarate:coA ligase 2. adenylate-forming enzyme; 4CL2.

45 AAC24503.1 AF041049 Populus tremuloides
DESCRIPTION: 4-coumarate:CoA ligase.

BAA08366.2 D49367 *Lithospermum erythrorhizon*
DESCRIPTION: 4-coumarate:CoA ligase.

5 AAF91308.1 AF239685 *Rubus idaeus*
DESCRIPTION: 4-coumarate:coA ligase 3. adenylate-forming enzyme; 4CL3.

10 AAC39366.1 AF008184 *Populus x generosa*
DESCRIPTION: 4-coumarate:CoA ligase 1. 4CL1.

15 CAA31696.1 X13324 *Petroselinum crispum*
DESCRIPTION: 4-coumarate:CoA ligase Pc4Cl-1 (AA 1-544).

AAC39365.1 AF008183 *Populus x generosa*
DESCRIPTION: 4-coumarate:CoA ligase 2. 4CL2.

20 AAA33842.1 M62755 *Solanum tuberosum*
DESCRIPTION: 4-coumarate--CoA ligase. St4Cl-1.

25 CAA31697.1 X13325 *Petroselinum crispum*
DESCRIPTION: 4-coumarate:CoA ligase Pc4Cl-2 (AA 1-544).

30 AAB42383.1 U39405 *Pinus taeda*
DESCRIPTION: 4-coumarate:CoA ligase. lp4CL-1.

35 AAB42382.1 U39404 *Pinus taeda*
DESCRIPTION: 4-coumarate:CoA ligase. lp4CL-2.

AAA92669.1 U12013 *Pinus taeda*
DESCRIPTION: 4-coumarate-CoA ligase enzyme.

40 AAF91310.1 AF239687 *Rubus idaeus*
DESCRIPTION: 4-coumarate:coA ligase 1. adenylate-forming enzyme; 4CL1.

45 AAA92668.1 U12012 *Pinus taeda*
DESCRIPTION: 4-coumarate-CoA ligase enzyme.

5 AAF37732.1 AF052221 *Lolium perenne*
DESCRIPTION: 4-coumarate--CoA ligase 4CL1.

CAA49575.1 X69954 *Glycine max*
DESCRIPTION: 4-coumarate--CoA ligase.

10 AAC24504.1 AF041050 *Populus tremuloides*
DESCRIPTION: 4-coumarate:CoA ligase.

15 AAF37733.1 AF052222 *Lolium perenne*
DESCRIPTION: 4-coumarate--CoA ligase 4CL2.

20 CAB97359.1 AJ278455 *Juglans nigra*
DESCRIPTION: 4-coumarate-CoA ligase. 4CL.

25 AAA69580.1 L43362 *Oryza sativa*
DESCRIPTION: 4-coumarate:CoA ligase isoform 2. 4cl.2. putative.

AAG46175.1 AC018727 *Oryza sativa*
DESCRIPTION: putative 4-coumarate CoA ligase. OSJNBa0056G17.30.

30 AAF73997.2 AF144504 *Picea smithiana*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

35 AAF73995.2 AF144502 *Pinus armandii*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

40 AAF73998.2 AF144505 *Cathaya argyrophylla*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

45 AAF73994.2 AF144501 *Pinus armandii*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

AAF73996.2 AF144503 Pinus armandii
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

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CAA87068.1 Z46944 Citrus sinensis
DESCRIPTION: non-photosynthetic ferredoxin.

10 AAK15005.1 AF233452 Impatiens balsamina
DESCRIPTION: ferredoxin. plastidal protein.

15 AAA33461.1 M73831 Zea mays
DESCRIPTION: ferredoxin.

20 CAB65696.1 AJ270962 Lycopersicon esculentum
DESCRIPTION: electron transfer. putative ferredoxin. ferredoxin.

BAA90760.1 AB038037 Ipomoea nil
DESCRIPTION: non-photosynthetic ferredoxin.

25 BAA06456.1 D30794 Oryza sativa
DESCRIPTION: ferredoxin.

30 AAB61593.1 AF003125 Mesembryanthemum crystallinum
DESCRIPTION: ferredoxin I precursor.

35 AAA33665.1 M31713 Pisum sativum
DESCRIPTION: ferredoxin I precursor.

40 AAD02175.1 AF039662 Capsicum annuum
DESCRIPTION: delays the harpin-mediated hypersensitive response.
ferredoxin-like protein. ap1.

45 CAA73265.1 Y12734 Physcomitrella patens
DESCRIPTION: ferredoxin.

CAA52980.1 X75089 *Triticum aestivum*
DESCRIPTION: ferredoxin. petF.

5 BAA06436.1 D30763 *Oryza sativa*
DESCRIPTION: ferredoxin.

10 CAA99756.1 Z75520 *Lycopersicon esculentum*
DESCRIPTION: transfer of electrons in a wide variety of metabolic
reactions. ferredoxin-I. precursor.

15 AAA33462.1 M73828 *Zea mays*
DESCRIPTION: ferredoxin.

20 AAA34028.1 M35660 *Spinacia oleracea*
DESCRIPTION: ferredoxin I precursor.

CAA26281.1 X02432 *Silene latifolia* subsp. *alba*
DESCRIPTION: ferredoxin precursor.

25 AAA33459.1 M73829 *Zea mays*
DESCRIPTION: ferredoxin.

30 AAA33460.1 M73830 *Zea mays*
DESCRIPTION: ferredoxin.

35 BAA32348.1 AB016810 *Zea mays*
DESCRIPTION: ferredoxin. pFD2.

40 BAA19865.1 D83660 *Oryza sativa*
DESCRIPTION: root ferredoxin.

AAA33085.1 L10349 *Chlamydomonas reinhardtii*
DESCRIPTION: ferredoxin. precursor.

45 AAC49171.1 U29516 *Chlamydomonas reinhardtii*

DESCRIPTION: ferredoxin precursor. Method: conceptual translation
supplied by author.

5 AAB65699.1 AF010320 Oryza sativa
DESCRIPTION: ferredoxin.

10 AAK14422.1 AC087851 Oryza sativa
DESCRIPTION: putative ferredoxin. OSJNBb0072E24.16.

57

15 CAB94692.1 AJ242742 Ipomoea batatas
DESCRIPTION: Removal of H₂O₂, oxidation of toxic reductants, defence
response toward wounding. peroxidase. pod.

20 AAD37430.1 AF149280 Phaseolus vulgaris
DESCRIPTION: peroxidase 5 precursor. FBP5. secretory peroxidase.

25 CAA66037.1 X97351 Populus balsamifera subsp. trichocarpa
DESCRIPTION: signal for ER. peroxidase.

BAA06335.1 D30653 Populus kitakamiensis
DESCRIPTION: peroxidase.

30 AAA34108.1 J02979 Nicotiana tabacum
DESCRIPTION: lignin-forming peroxidase precursor (EC 1.11.1.7).

35 BAA01992.1 D11396 Nicotiana tabacum
DESCRIPTION: 'peroxidase'.

40 CAA66034.1 X97348 Populus balsamifera subsp. trichocarpa
DESCRIPTION: signal for ER. peroxidase.

45 AAB47602.1 L07554 Linum usitatissimum
DESCRIPTION: peroxidase. FLXPER1.

10 CAB67121.1 Y19023 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. cevi-1.

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25 BAA01877.1 D11102 *Populus kitakamiensis*
DESCRIPTION: peroxidase. prxA1.

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DESCRIPTION: peroxidase1C. prx1C.

5 BAA06334.1 D30652 Populus kitakamiensis
DESCRIPTION: peroxidase.

10 BAA07241.1 D38051 Populus kitakamiensis
DESCRIPTION: peroxidase. prxA4a.

15 AAB41810.1 L36156 Medicago sativa
DESCRIPTION: peroxidase. pxdA. amino acid feature: conserved motifs, aa
181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.

20 AAB41811.1 L36157 Medicago sativa
DESCRIPTION: peroxidase. pxdC. amino acid feature: conserved domains, aa
123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 ..
73.

25 BAA14144.1 D90116 Armoracia rusticana
DESCRIPTION: peroxidase isozyme.

30 AAC98519.1 AF007211 Glycine max
DESCRIPTION: peroxidase precursor. GMIPER1. pathogen-induced.

BAA02840.1 D13683 Populus kitakamiensis
DESCRIPTION: peroxidase. HPOX14.

35 BAA14143.1 D90115 Armoracia rusticana
DESCRIPTION: peroxidase isozyme.

40 AAA33129.1 M91372 Cucumis sativus
DESCRIPTION: peroxidase. pre-peroxidase.

45 BAA08499.1 D49551 Oryza sativa
DESCRIPTION: peroxidase. poxN.

BAA03373.1 D14482 *Oryza sativa*
DESCRIPTION: putative peroxidase.

5 AAA34101.1 L02124 *Nicotiana tabacum*
DESCRIPTION: peroxidase.

10 CAA76680.1 Y17192 *Cucurbita pepo*
DESCRIPTION: peroxidase. aprx. type III peroxidase.

15 CAA40796.1 X57564 *Armoracia rusticana*
DESCRIPTION: peroxidase. peroxidase precursor.

20 AAA33121.1 M32742 *Cucumis sativus*
DESCRIPTION: peroxidase (CuPer2).

BAA82306.1 AB027752 *Nicotiana tabacum*
DESCRIPTION: peroxidase.

25 AAD43561.1 AF155124 *Gossypium hirsutum*
DESCRIPTION: bacterial-induced peroxidase precursor. Perx_Goshiko.

30 AAB06183.1 M37636 *Arachis hypogaea*
DESCRIPTION: cationic peroxidase. PNC1.

35 AAA33127.1 M91373 *Cucumis sativus*
DESCRIPTION: peroxidase. pre-peroxidase. putative.

CAA71492.1 Y10466 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr5.

40 AAF63027.1 AF244924 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx15 precursor.
type III peroxidase.

45 AAA33128.1 M91374 *Cucumis sativus*

DESCRIPTION: peroxidase. putative.

BAA77389.1 AB024439 *Scutellaria baicalensis*

5 DESCRIPTION: peroxidase 3.

BAA77388.1 AB024438 *Scutellaria baicalensis*

10 DESCRIPTION: peroxidase 2.

AAB02554.1 L37790 *Stylosanthes humilis*

DESCRIPTION: cationic peroxidase.

15 AAF63026.1 AF244923 *Spinacia oleracea*

DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx14 precursor.
type III peroxidase.

20 58

AAG49002.1 AY013246 *Hordeum vulgare*

DESCRIPTION: putative ABC transporter. 635P2.4a; GC splice donor
confirmed by cDNA and comparative sequencing.

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AAG45492.1 AY013245 *Oryza sativa*

DESCRIPTION: 36I5.4. putative ABC transporter; GC splice donor confirmed
by cDNA alignment and comparative sequence.

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AAG49003.1 AY013246 *Hordeum vulgare*

DESCRIPTION: putative ABC transporter. 635P2.4b; GC splice donor
confirmed by cDNA alignment and comparative sequence.

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BAA83352.1 AP000391 *Oryza sativa*

DESCRIPTION: ESTs AU067992(C11433),AU077424(C11433) correspond to
a

40 region of the predicted gene.; Similar to ABC transporter-7 (U43892).

BAB17113.1 AP002866 *Oryza sativa*

DESCRIPTION: putative white protein; ATP-binding cassette transporter.
P0410E01.34.

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- 5 BAA90508.1 AP001111 *Oryza sativa*
DESCRIPTION: similar to ABC transporter of *Arabidopsis thaliana* (AC004697).
- 10 BAA90507.1 AP001111 *Oryza sativa*
DESCRIPTION: similar to ABC transporter of *Arabidopsis thaliana* (AC004697).
- 15 BAB40032.1 AP003046 *Oryza sativa*
DESCRIPTION: putative ABC transporter. P0445D12.3.
- 20 BAB16495.1 AP002861 *Oryza sativa*
DESCRIPTION: putative ABC transporter ATP-binding protein. P0665D10.21.
- 25 BAA94511.1 AB041505 *Populus nigra*
DESCRIPTION: ABC transporter homolog. PnATH.
- 30 BAB21275.1 AP002844 *Oryza sativa*
DESCRIPTION: putative ABC transporter protein. P0410E03.6.
- 35 BAB21276.1 AP002844 *Oryza sativa*
DESCRIPTION: putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
- 40 BAB21279.1 AP002844 *Oryza sativa*
DESCRIPTION: putative ABC transporter protein. P0410E03.10. contains ESTs AU065360(R3463),AU101680(R3463).
- 45 CAA94437.1 Z70524 *Spirodela polyrrhiza*
DESCRIPTION: multidrug resistance protein. PDR5-like ABC transporter.
- 59 BAB21273.1 AP002844 *Oryza sativa*
DESCRIPTION: putative ABC transporter protein. P0410E03.4.

CAA71369.1 Y10338 Solanum tuberosum
DESCRIPTION: chloride channel Stclcl. putative.

5 AAD29679.1 AF133209 Nicotiana tabacum
DESCRIPTION: CLC-Nt2 protein. putative chloride channel.

60

10 BAB40094.1 AP003210 Oryza sativa
DESCRIPTION: putative receptor protein kinase. OSJNBa0010K01.7.

15 AAG52992.1 U77888 Ipomoea nil
DESCRIPTION: receptor-like protein kinase INRPK1a. inrpk1.

20 AAF59906.1 AF197947 Glycine max
DESCRIPTION: receptor protein kinase-like protein. CLV1B.

AAC36318.1 AF053127 Malus x domestica
DESCRIPTION: leucine-rich receptor-like protein kinase. LRPKml.

25 AAF91323.1 AF244889 Glycine max
DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.

30 AAF91324.1 AF244890 Glycine max
DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.

35 AAB36558.1 U77888 Ipomoea nil
DESCRIPTION: receptor-like protein kinase INRPK1. inrpk1. leucine-rich repeat.

40 BAA83373.1 AP000391 Oryza sativa
DESCRIPTION: ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

45 BAA84787.1 AP000559 Oryza sativa

DESCRIPTION: ESTs C22557(S0014),C22656(S0014) correspond to a region
of
the predicted gene.; Similar to receptor protein kinase, ERECTA
(AC004484).

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AAF91322.1 AF244888 Glycine max
DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.

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AAF59905.1 AF197946 Glycine max
DESCRIPTION: receptor protein kinase-like protein. CLV1A.

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AAB61708.1 U93048 Daucus carota
DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.

20

CAB51480.1 Y14600 Sorghum bicolor
DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates
in mesophyll cells.

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CAC20842.1 AJ250467 Pinus sylvestris
DESCRIPTION: receptor protein kinase. upk.

30

CAA61510.1 X89226 Oryza sativa
DESCRIPTION: leucine-rich repeat/receptor protein kinase. lrk2.

35

BAB19337.1 AP003044 Oryza sativa
DESCRIPTION: putative protein kinase. P0038C05.10. contains ESTs
AU056335(S20481),AU056336(S20481).

40

AAG52994.1 U77888 Ipomoea nil
DESCRIPTION: receptor-like protein kinase INRPK1c. inrpk1.

BAB40081.1 AP003074 Oryza sativa
DESCRIPTION: putative receptor protein kinase. OSJNBa0004G10.30.

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BAB18321.1 AP002865 Oryza sativa
DESCRIPTION: putative receptor protein kinase. P0034C11.11.

AAD38286.1 AC007789 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0049B20.13.

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BAB07903.1 AP002835 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0417G05.10. contains ESTs
AU032341(R3918),AU071016(R10613).

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AAF34426.1 AF172282 *Oryza sativa*
DESCRIPTION: leucine rich repeat containing protein kinase. DUPR11.16.

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BAA94519.1 AP001800 *Oryza sativa*
DESCRIPTION: ESTs AU032341(R3918),AU071016(R10613) correspond to a
region
of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 4, BAC
F9D16; putative receptor kinase (AL035394).

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AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.

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BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

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BAA82393.1 AP000367 *Oryza sativa*
DESCRIPTION: EST C96716(C10608) corresponds to a region of the predicted
gene.; Similar to putative receptor protein kinase. (AC002334).

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BAB03631.1 AP002522 *Oryza sativa*
DESCRIPTION: putative protein kinase Xa21. P0009G03.32.

40

AAB82755.1 U72725 *Oryza longistaminata*
DESCRIPTION: receptor kinase-like protein. Xa21 gene family member A1;
downstream of microsatellite region; disease resistance gene family
member.

45

AAK00425.1 AC069324 *Oryza sativa*
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

5 AAK27817.1 AC022457 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0006L06.16.

10 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).

15 BAB03621.1 AP002522 *Oryza sativa*
DESCRIPTION: putative protein kinase Xa21. P0009G03.21.

20 AAG59657.1 AC084319 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.

25 BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

30 BAB03429.1 AP002817 *Oryza sativa*
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted
gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12;
putative protein kinase (AC006587).

35 BAB07999.1 AP002525 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST
C22619(S11214).

40 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.

45 AAG16628.1 AY007545 *Brassica napus*
DESCRIPTION: protein serine/threonine kinase BNK1.

BAA94509.1 AB041503 *Populus nigra*
DESCRIPTION: protein kinase 1. PnPK1.

5 BAB39421.1 AP002901 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0456F08.21.

10 BAA94510.1 AB041504 *Populus nigra*
DESCRIPTION: protein kinase 2. PnPK2.

15 CAB51836.1 AJ243961 *Oryza sativa*
DESCRIPTION: Putitive Ser/Thr protein kinase. I1332.7.

BAB17139.1 AP002867 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0463F06.31.

20 BAB07904.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.12.

25 BAB39409.1 AP002901 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).

62
30 -----
BAA25753.1 AB012932 *Vigna radiata*
DESCRIPTION: Ca²⁺/H⁺ exchanger. VCAX1.

35 AAF91350.1 AF256229 *Zea mays*
DESCRIPTION: calcium/proton exchanger CAX1-like protein.

40 BAA75232.1 AB018526 *Ipomoea nil*
DESCRIPTION: H⁺/Ca²⁺ exchanger 2. CAX2.

63

45 BAA85655.1 AB026297 *Pisum sativum*
DESCRIPTION: elicitor-responsive Dof protein ERDP.

- 5 AAB70119.1 U82230 Zea mays
DESCRIPTION: transcription factor. prolamin box binding factor. PBF.
endosperm-specific DOF protein; DNA binding.
- 10 CAB89831.1 AJ242853 Solanum tuberosum
DESCRIPTION: DNA binding protein. Dof zinc finger protein. dof1.
- 15 CAA08755.1 AJ009594 Nicotiana tabacum
DESCRIPTION: Dof zinc finger protein. BBF1.
- 20 CAA66601.1 X97942 Nicotiana tabacum
DESCRIPTION: Zn finger protein. NtBBF1.1.
- 25 CAA66604.1 X97945 Nicotiana tabacum
DESCRIPTION: Zn finger protein. NtBBF2a.
- 30 BAA78575.1 AB028132 Oryza sativa
DESCRIPTION: Dof zinc finger protein.
- 35 BAA78572.1 AB028129 Oryza sativa
DESCRIPTION: Dof zinc finger protein.
- 40 BAA78573.1 AB028130 Oryza sativa
DESCRIPTION: Dof zinc finger protein.
- 45 CAA66606.1 X97947 Nicotiana tabacum
DESCRIPTION: Zn finger protein. NtBBF3.
- CAA66605.1 X97946 Nicotiana tabacum
DESCRIPTION: Zn finger protein. NtBBF2b.
- BAA78574.1 AB028131 Oryza sativa
DESCRIPTION: Dof zinc finger protein. Rice cDNA for protein that binds to
AT-rich sequence of rice carboxypeptidase-3 promoter.

CAA56287.1 X79934 Zea mays
DESCRIPTION: Dof2. No start codon.

5

CAA56288.1 X79935 Zea mays
DESCRIPTION: Dof3 gene. no start codon.

10 BAA78576.1 AB028133 Oryza sativa
DESCRIPTION: Dof zinc finger protein.

64

15 CAA11219.1 AJ223281 Manihot esculenta
DESCRIPTION: alpha-hydroxynitrile lyase. HNL4.

20 BAB19413.1 AP002870 Oryza sativa
DESCRIPTION: putative acetone-cyanohydrin lyase. P0458A05.22.

25 AAC49184.1 U40402 Hevea brasiliensis
DESCRIPTION: hydroxynitrile lyase. hnl.

CAA82334.1 Z29091 Manihot esculenta
DESCRIPTION: alpha-hydroxynitrile lyase.

30

CAA11428.1 AJ223506 Manihot esculenta
DESCRIPTION: alpha-hydroxynitrile lyase. HNL24.

67

35 CAB89831.1 AJ242853 Solanum tuberosum
DESCRIPTION: DNA binding protein. Dof zinc finger protein. dof1.

40 CAA56288.1 X79935 Zea mays
DESCRIPTION: Dof3 gene. no start codon.

45 BAA85655.1 AB026297 Pisum sativum
DESCRIPTION: elicitor-responsive Dof protein ERDP.

BAA78575.1 AB028132 Oryza sativa
DESCRIPTION: Dof zinc finger protein.

5

AAB70119.1 U82230 Zea mays
DESCRIPTION: transcription factor. prolamin box binding factor. PBF.
endosperm-specific DOF protein; DNA binding.

10

CAA08755.1 AJ009594 Nicotiana tabacum
DESCRIPTION: Dof zinc finger protein. BBF1.

15

CAA66601.1 X97942 Nicotiana tabacum
DESCRIPTION: Zn finger protein. NtBBF1.1.

20

CAA66606.1 X97947 Nicotiana tabacum
DESCRIPTION: Zn finger protein. NtBBF3.

25

BAA78573.1 AB028130 Oryza sativa
DESCRIPTION: Dof zinc finger protein.

BAA78572.1 AB028129 Oryza sativa
DESCRIPTION: Dof zinc finger protein.

30

CAA56287.1 X79934 Zea mays
DESCRIPTION: Dof2. No start codon.

35

CAA66604.1 X97945 Nicotiana tabacum
DESCRIPTION: Zn finger protein. NtBBF2a.

40

CAA66605.1 X97946 Nicotiana tabacum
DESCRIPTION: Zn finger protein. NtBBF2b.

45

BAA78574.1 AB028131 Oryza sativa
DESCRIPTION: Dof zinc finger protein. Rice cDNA for protein that binds to
AT-rich sequence of rice carboxypeptidase-3 promoter.

BAA78576.1 AB028133 *Oryza sativa*
DESCRIPTION: Dof zinc finger protein.

5 68

CAA83453.1 Z31581 *Pisum sativum*
DESCRIPTION: chloroplast outer envelope protein 86.

10

AAA53276.1 L36857 *Pisum sativum*
DESCRIPTION: component of chloroplast outer membrane protein import
apparatus. GTP-binding protein. IAP86.

15

AAF75761.1 AF262939 *Pisum sativum*
DESCRIPTION: chloroplast protein import component Toc159. major receptor
of the chloroplast outer envelope membrane protein import apparatus.

20

AAG48839.1 AC084218 *Oryza sativa*
DESCRIPTION: similar to *Arabidopsis thaliana* putative chloroplast outer
envelope 86-like protein (AC002330).

25

AAC25785.1 L36856 *Pisum sativum*
DESCRIPTION: component of chloroplast outer membrane protein import
apparatus. GTP-binding protein. IAP34.

30

CAB77551.1 AJ271049 *Zea mays*
DESCRIPTION: a component of the protein translocon at the outer envelope
of chloroplast. Toc34-2 protein. toc34B.

35

CAB65537.1 AJ245968 *Zea mays*
DESCRIPTION: a component of the protein translocon at the outer envelope
of chloroplast. Toc34-1 protein. toc34A.

40 70

AAB71887.1 AF020791 *Hordeum vulgare*
DESCRIPTION: inserts Fe²⁺ into protoporphyrin IX. ferrochelatase. hemH.
protoheme IX ferro-lyase.

45

- BAA05101.1 D26105 *Hordeum vulgare*
DESCRIPTION: ferrochelatase. hemH.
- 5 BAA05102.1 D26106 *Cucumis sativus*
DESCRIPTION: ferrochelatase. hemH.
- 10 BAB20760.1 AB037113 *Cucumis sativus*
DESCRIPTION: ferrochelatase. hemH.
- 15 BAA22284.1 AB007120 *Oryza sativa*
DESCRIPTION: ferrochelatase. hemH.
- CAA06705.1 AJ005802 *Solanum tuberosum*
DESCRIPTION: tetrapyrrole biosynthesis. ferrochelatase.
- 20 AAK16728.1 AF332962 *Chlamydomonas reinhardtii*
DESCRIPTION: ferrochelatase.
- 25 AAK16729.1 AF332963 *Polytomella* sp. 'Pringsheim 198.80'
DESCRIPTION: ferrochelatase.
- 30 AAC84139.1 AF101426 *Cichorium intybus*
DESCRIPTION: ferrochelatase.
- 71
-
- 35 CAA64442.1 X94986 *Manihot esculenta*
DESCRIPTION: beta glucosidase. bglA.
- 40 AAB22162.1 S35175 *Manihot esculenta*
DESCRIPTION: linamarase. linamarase. beta-glucosidase; Method: conceptual translation with partial peptide sequencing; This sequence comes from Fig. 4.
- 45 AAA93032.1 U50201 *Prunus serotina*
DESCRIPTION: hydrolysis of the cyanogenic glucoside (R)-prunasin. prunasin hydrolase precursor. located in protein bodies of *Prunus* seeds;

encodes 8 putative N-glycosylation sites (N-X-S/T); encodes NEP and ITENG motifs characteristic of the BGA family of beta-glucosidases.

- 5 AAA91166.1 U39228 *Prunus avium*
 DESCRIPTION: beta-glucosidase.
- 10 AAF34650.1 AF221526 *Prunus serotina*
 DESCRIPTION: hydrolysis of the cyanogenic glucoside (R)-prunasin.
 prunasin hydrolase isoform PHA precursor. beta-glucosidase; contains 6
 potential N-glycosylation sites (N-X-S/T); glycosyl hydrolase family 1
 member.
- 15 AAF03675.1 AF149311 *Rauvolfia serpentina*
 DESCRIPTION: hydrolyses the glucoalkaloid raucaffricine.
 raucaffricine-O-beta-D-glucosidase. beta glucosidase; RG; part of the
 Ajmaline biosynthesis pathway; belongs to family 1 of the glucosyl
20 hydrolases.
- 25 CAA57913.1 X82577 *Brassica napus*
 DESCRIPTION: beta-glucosidase. bgl.
- 30 BAA78708.1 AB003089 *Polygonum tinctorium*
 DESCRIPTION: beta-glucosidase.
- 35 BAA11831.1 D83177 *Costus speciosus*
 DESCRIPTION: saponin metabolite. furostanol glycoside
 26-O-beta-glucosidase (F26G). functional expression in *E. coli*; one of the
 F26G isozymes.
- 40 AAG25897.1 AF170087 *Cucurbita pepo*
 DESCRIPTION: silverleaf whitefly-induced protein 3. SLW3. similar to
 beta-glucosidase.
- 45 AAF04007.1 AF163097 *Dalbergia cochinchinensis*
 DESCRIPTION: beta-fucosidase beta-glucosidase. dalcochinin
 8'-O-beta-glucoside beta-glucosidase precursor. BGLU1. rotenoid
 beta-glucosidase.

- AAC69619.1 AF072736 *Pinus contorta*
DESCRIPTION: beta-glucosidase.
- 5 AAB38784.1 U72154 *Brassica nigra*
DESCRIPTION: beta-glucosidase. psr3.1. PSR3.1; phosphate-starvation responsive enzyme.
- 10 AAD02839.1 AF082991 *Avena sativa*
DESCRIPTION: beta-D-glucosidase beta subunit precursor. P60b. avenacosidase.
- 15 AAA87339.1 L41869 *Hordeum vulgare*
DESCRIPTION: beta-glucosidase. BGQ60. expression specific to starchy endosperm of seed.
- 20 AAB71381.1 U95298 *Manihot esculenta*
DESCRIPTION: linamarase. pLIN-GEN. beta-glucosidase.
- 25 CAA55196.1 X78433 *Avena sativa*
DESCRIPTION: beta-D-glucosidase.
- 30 AAC49177.1 U33817 *Sorghum bicolor*
DESCRIPTION: beta-glucosidase, catalyzes the hydrolysis of the cyanogenic beta-glucoside dhurrin. dhurrinase.
- 35 AAD09850.1 U44087 *Zea mays*
DESCRIPTION: beta-D-glucosidase precursor. glu2. product subunit structure: autodimer of 58.4 kDa monomers Allele: glu2-B73.
- 40 AAG00614.1 AF293849 *Secale cereale*
DESCRIPTION: beta-glucosidase.
- 45 AAF28800.1 AF112888 *Catharanthus roseus*
DESCRIPTION: plays a role in secondary metabolism by hydrolyzing strictosidine to cathenamine during indole alkaloid biosynthesis. strictosidine beta-glucosidase. localized in the endoplasmic reticulum.

- CAA40058.1 X56734 *Trifolium repens*
DESCRIPTION: beta-glucosidase. non-cyanogenic.
- CAA40057.1 X56733 *Trifolium repens*
DESCRIPTION: beta-glucosidase. Li.
- AAD10503.1 U33816 *Zea mays*
DESCRIPTION: functions in defense of young plant parts against pests via the production of hydroxamic acids from hydroxamic acid glucosides. beta-D-glucosidase.
- AAA65946.1 U25157 *Zea mays*
DESCRIPTION: functions in defense of young plant parts against pests via the production of hydroxamic acids from hydroxamic acid glucosides. beta-D-glucosidase.
- CAA52293.1 X74217 *Zea mays*
DESCRIPTION: beta-glucosidase. p60.1.
- AAB03266.1 U44773 *Zea mays*
DESCRIPTION: beta-D-glucosidase. glu1. autodimer of 58.4 kD monomers.
- AAK07429.1 AF321287 *Musa acuminata*
DESCRIPTION: beta-glucosidase.
- CAA79989.2 Z21977 *Brassica napus*
DESCRIPTION: beta thioglucosidase. myrosinase, thioglucoside glucohydrolase. Myr1.Bn1.
- AAF34651.1 AF221527 *Prunus serotina*
DESCRIPTION: putative prunasin hydrolase precursor. beta-glucosidase; glycosyl hydrolase family 1 member.
- AAA84906.1 U28047 *Oryza sativa*
DESCRIPTION: catalyzes the release of either giberellin or cyanogenic

substances from their glucoconjugates. beta glucosidase. beta-D-glucoside
glucohydrolase; dimer of 60 kDa monomers; localized in the plastid.

- 5 CAC08209.1 AJ005950 *Cicer arietinum*
DESCRIPTION: beta-glucosidase.

72

- 10 CAA56570.1 X80301 *Nicotiana tabacum*
DESCRIPTION: axi 1.

- 15 AAB72114.1 U81288 *Pisum sativum*
DESCRIPTION: PsRT17-1. similar to the *Nicotiana tabacum* axi 1 gene
product encoded by the sequence presented in GenBank Accession Number
X80301.

74

- 20 AAG23130.1 AF198260 *Lycopersicon esculentum*
DESCRIPTION: diacylglycerol kinase variant A. Dgk1. DGK-1; alternatively
spliced.

- 25 AAG23129.1 AF198259 *Lycopersicon esculentum*
DESCRIPTION: phosphorylates diacylglycerol to yield phosphatidic acid.
diacylglycerol kinase. DGK1. LeDGK1; lipid kinase; non-calmodulin-binding
isoform; alternatively spliced product.

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- AAG23131.1 AF198260 *Lycopersicon esculentum*
DESCRIPTION: diacylglycerol kinase variant B. Dgk1. CBDGK;
calmodulin-binding; alternatively spliced.

35

- AAG23128.1 AF198258 *Lycopersicon esculentum*
DESCRIPTION: phosphorylates diacylglycerol to yield phosphatidic acid.
calmodulin-binding diacylglycerol kinase. DGK1. LeCBDGK; lipid kinase;
alternatively spliced product.

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- 45 CAC09580.1 AJ298992 *Fagus sylvatica*
DESCRIPTION: Absciscic acid (ABA) and calcium induced protein kinase.
protein kinase (PK). pk1.

- 5 AAA34002.1 M67449 Glycine max
DESCRIPTION: protein kinase. PK6.
- 10 AAG31141.1 AF305911 Oryza sativa
DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
- 15 AAG31142.1 AF305912 Hordeum vulgare
DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
- 20 CAA73722.1 Y13273 Lycopersicon esculentum
DESCRIPTION: putative protein kinase.
- 25 AAD46406.1 AF096250 Lycopersicon esculentum
DESCRIPTION: ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.
- 30 AAD10056.1 AF110518 Lycopersicon esculentum
DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.
- 35 AAD10057.1 AF110519 Lycopersicon esculentum
DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.
- 40 CAA06334.1 AJ005077 Lycopersicon esculentum
DESCRIPTION: protein kinase. TCTR2 protein. TCTR2.
- 45 AAK30005.1 AY029067 Rosa hybrid cultivar

[illegible]

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BAB17348.1 AP002747 *Oryza sativa*
DESCRIPTION: putative receptor kinase. P0698G03.32.

CAA57898.1 X82548 Hordeum vulgare
DESCRIPTION: SNF1-related protein kinase. BKIN2.

5

BAB17345.1 AP002747 Oryza sativa
DESCRIPTION: putative receptor kinase. P0698G03.29.

10 BAB17116.1 AP002867 Oryza sativa
DESCRIPTION: putative receptor kinase. P0463F06.3.

15 BAB39441.1 AP003338 Oryza sativa
DESCRIPTION: putative receptor kinase. OJ1212_B09.11.

20 CAC20842.1 AJ250467 Pinus sylvestris
DESCRIPTION: receptor protein kinase. upk.

AAD52097.1 AF088885 Nicotiana tabacum
DESCRIPTION: receptor-like kinase CHRK1. Chrkl.

25 BAB16918.1 AP002863 Oryza sativa
DESCRIPTION: putative protein kinase. P0005A05.22.

30 AAF91322.1 AF244888 Glycine max
DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.

35 BAB17342.1 AP002747 Oryza sativa
DESCRIPTION: putative receptor kinase. P0698G03.26.

40 AAF78044.1 AF248493 Oryza sativa
DESCRIPTION: receptor-like kinase. RLG18. protein kinase.

AAF91324.1 AF244890 Glycine max
DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.

45 AAF59905.1 AF197946 Glycine max

DESCRIPTION: receptor protein kinase-like protein. CLV1A.

AAAF91323.1 AF244889 Glycine max

5 DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.

AAD46917.1 AF164021 Oryza sativa

10 DESCRIPTION: receptor kinase.

AAF59906.1 AF197947 Glycine max

DESCRIPTION: receptor protein kinase-like protein. CLV1B.

AAAF78018.1 AF238474 Oryza sativa

15 DESCRIPTION: receptor-like kinase. RLG16. protein kinase.

BAB39438.1 AP003338 Oryza sativa

20 DESCRIPTION: putative receptor kinase. OJ1212_B09.7.

BAA05649.1 D26602 Nicotiana tabacum

25 DESCRIPTION: protein kinase.

AAC01746.1 AF044489 Oryza sativa

30 DESCRIPTION: receptor-like protein kinase. drpk1.

CAA71142.1 Y10036 Cucumis sativus

DESCRIPTION: SNF1-related protein kinase.

AAA62232.1 U00443 Brassica napus

35 DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like domain.

CAA61510.1 X89226 Oryza sativa

40 DESCRIPTION: leucine-rich repeat/receptor protein kinase. lrk2.

77

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AAD03693.1 AF084554 Brassica napus

DESCRIPTION: fibrillin.

CAA10372.1 AJ131455 Plastid Solanum demissum
5 DESCRIPTION: carotenoid-associated. fibrillin. c40.4.

CAA50750.1 X71952 Capsicum annuum
10 DESCRIPTION: fibrillin.
79

AAB53155.1 U43629 Beta vulgaris
15 DESCRIPTION: putative sugar transporter. integral membrane protein.
member of major facilitator superfamily.

AAF74566.1 AF215852 Nicotiana tabacum
20 DESCRIPTION: transport of hexoses across the plastid inner envelope
membrane. hexose transporter. pGlcT.

AAG00995.1 AF286906 Mesembryanthemum crystallinum
25 DESCRIPTION: putative glucose translocator. metabolite transporter;
targeted to plastid inner envelope membrane.

AAF74565.1 AF215851 Spinacia oleracea
30 DESCRIPTION: transport of hexoses across the plastid inner envelope
membrane. hexose transporter. pGlcT.

AAF74567.1 AF215853 Solanum tuberosum
35 DESCRIPTION: transport of hexoses across the plastid inner envelope
membrane. hexose transporter. pGlcT.

AAF74568.1 AF215854 Zea mays
40 DESCRIPTION: transport of hexoses across the plastid inner envelope
membrane. hexose transporter. pGlcT.

AAG46179.1 AC018727 Oryza sativa
45 DESCRIPTION: putative sugar transporter protein. OSJNBa0056G17.3.

AAB88879.1 AF000952 *Prunus armeniaca*
DESCRIPTION: putative sugar transporter.

5 AAG43998.1 AF215837 *Apium graveolens* var. dulce
DESCRIPTION: mannitol transporter. Mat1.

10 CAA68813.1 Y07520 *Chlorella kessleri*
DESCRIPTION: H(+)/hexose cotransporter (AA 1-533).

15 CAA53192.1 X75440 *Chlorella kessleri*
DESCRIPTION: hexose transporter like protein. HUP3.

CAB52689.1 AJ132224 *Lycopersicon esculentum*
DESCRIPTION: hexose transporter. ht2.

20 CAA39036.1 X55349 *Chlorella kessleri*
DESCRIPTION: H(+)/hexose-cotransporter. HUP1.

25 CAA47324.1 X66856 *Nicotiana tabacum*
DESCRIPTION: monosaccharid transporter. MST1.

30 AAB68028.1 U64902 *Beta vulgaris*
DESCRIPTION: BvcDNA-205. putative sugar transporter; member of major facilitative superfamily; integral membrane protein.

35 AAB68029.1 U64903 *Beta vulgaris*
DESCRIPTION: BvcDNA-397. putative sugar transporter; member of major facilitative superfamily; integral membrane protein.

40 CAA09419.1 AJ010942 *Lycopersicon esculentum*
DESCRIPTION: hexose transporter protein.

45 CAB07812.1 Z93775 *Vicia faba*
DESCRIPTION: sugar transport. monosaccharid transport protein. hext.

BAB19864.1 AB052885 *Oryza sativa*
DESCRIPTION: monosaccharide transporter 3. OsMST3.

5 AAA79761.1 L08196 *Ricinus communis*
DESCRIPTION: hexose transport. sugar carrier protein. RCSTC.

10 AAK13147.1 AC083945 *Oryza sativa*
DESCRIPTION: Putative sugar transporter. OSJNBa0058E19.22.

15 AAB06594.1 U38651 *Medicago truncatula*
DESCRIPTION: sugar transporter.

CAA04511.1 AJ001061 *Vitis vinifera*
DESCRIPTION: hexose uptake. hexose transporter.

20 AAC61852.1 AF061106 *Petunia x hybrida*
DESCRIPTION: putative monosaccharide transporter 1. pmt1. similar to
hexose transporter protein; PMT1.

25 CAA70777.1 Y09590 *Vitis vinifera*
DESCRIPTION: hexose transporter.

30 AAA79769.1 L08197 *Ricinus communis*
DESCRIPTION: sugar transport. sugar carrier protein. RCSTA. putative.

35 CAB06079.1 Z83829 *Picea abies*
DESCRIPTION: monosaccharide transporter. PaMst-1. PaMst-1.

40 AAA18534.1 L21753 *Saccharum hybrid cultivar H65-7052*
DESCRIPTION: glucose transporter. putative.

CAC00697.1 AJ278765 *Lycopersicon esculentum*
DESCRIPTION: putative sugar transporter. st3.

45 AAA79857.1 L08188 *Ricinus communis*

DESCRIPTION: hexose transport. hexose carrier protein. HEX6.

BAB19863.1 AB052884 *Oryza sativa*

5 DESCRIPTION: monosaccharide transporter 2. OsMST2.

BAB19862.1 AB052883 *Oryza sativa*

10 DESCRIPTION: monosaccharide transporter 1. OsMST1.

AAF91432.1 AF280432 *Mesembryanthemum crystallinum*

15 DESCRIPTION: putative Na⁺/myo-inositol symporter. Itr2. membrane transport protein.

CAB52688.1 AJ132223 *Lycopersicon esculentum*

20 DESCRIPTION: hexose transporter. ht1.

BAA85398.1 AP000615 *Oryza sativa*

25 DESCRIPTION: similar to sugar transporter protein. (AL022604).

AAG46115.1 AC073166 *Oryza sativa*

30 DESCRIPTION: putative sugar transporter. OSJNBb0064P21.3.

CAB52690.1 AJ132225 *Lycopersicon esculentum*

35 DESCRIPTION: hexose transporter. ht3.

AAA18533.1 L21752 *Saccharum hybrid cultivar H65-7052*

40 DESCRIPTION: glucose transporter. putative.

AAD55054.1 AF173655 *Beta vulgaris*

45 DESCRIPTION: glucose transporter. Gt.

BAB39246.1 AP002869 *Oryza sativa*

50 DESCRIPTION: putative transport protein homolog. P0554D10.30.

AAA79764.1 L08191 *Ricinus communis*

55 DESCRIPTION: sugar transport. sugar carrier protein. RCSTC. Nucleotides 1

to 23 and 226 to 246 are originated from degenerated primers; putative.

- 5 AAA79762.1 L08189 Ricinus communis
DESCRIPTION: sugar transport. sugar carrier protein. RCSTA. Nucleotides 1 to 23 and 226 to 246 are originated from degenerated primers; putative.

- 10 AAA79767.1 L08194 Ricinus communis
DESCRIPTION: sugar transport. sugar carrier protein. RCSTG. Nucleotides 1 to 23 and 226 to 246 are originated from degenerated primers; putative.

- 15 AAA79766.1 L08193 Ricinus communis
DESCRIPTION: sugar transport. sugar carrier protein. RCSTF. Nucleotides 1 to 23 and 226 to 246 are originated from degenerated primers; putative.

82

- 20 CAA78386.1 Z13996 Petunia x hybrida
DESCRIPTION: DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.

25

- CAB43399.1 AJ006292 Antirrhinum majus
DESCRIPTION: Myb-related transcription factor mixta-like 1. mybm11.

30

- CAA67600.1 X99210 Lycopersicon esculentum
DESCRIPTION: myb-related transcription factor. THM16.

- 35 BAA93038.1 AP001552 Oryza sativa
DESCRIPTION: EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).

40

- BAA23337.1 D88617 Oryza sativa
DESCRIPTION: transfactor. OSMYB1. Osmby1.

- 45 CAA64614.1 X95296 Lycopersicon esculentum
DESCRIPTION: transcription factor. THM27. myb-related.

- CAA72186.1 Y11351 *Oryza sativa*
DESCRIPTION: myb factor. myb.
5
- AAF22256.1 AF161711 *Pimpinella brachycarpa*
DESCRIPTION: myb-related transcription factor.
10
- AAC04720.1 AF034134 *Gossypium hirsutum*
DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-binding
domain protein. Cmy-O. similar to MYB A encoded by GenBank Accession
15 Number L04497.
- AAA82943.1 U39448 *Picea mariana*
DESCRIPTION: MYB-like transcriptional factor MBF1. putative DNA binding
20 region highly similar to the maize C1.
- BAB39987.1 AP003020 *Oryza sativa*
DESCRIPTION: putative transcription factor (myb). P0498A12.16. contains
25 ESTs AU097474(S5087),D40175(S1959).
- BAB39972.1 AP003018 *Oryza sativa*
DESCRIPTION: putative transcription factor (myb). OSJNBa0004B13.27.
30 contains ESTs AU097474(S5087),D40175(S1959).
- BAA23338.1 D88618 *Oryza sativa*
DESCRIPTION: transfactor. OSMYB2. Osmyb2.
35
- CAA67575.1 X99134 *Lycopersicon esculentum*
DESCRIPTION: transcription factor. THM6. myb-related.
40
- CAA78387.1 Z13997 *Petunia x hybrida*
DESCRIPTION: DNA-binding protein, transcriptional activator. protein 2.
myb.Ph2. related to animal myb proto-oncoproteins.
45
- AAA19821.1 L19495 *Zea mays*

DESCRIPTION: transcriptional activator for anthocyanin synthesis.
transcriptional activator.

5 AAC49394.1 U57002 Zea mays

DESCRIPTION: P protein. P. allele P-wr; Myb-like transcriptional
regulator with a putative zinc-finger at the C-terminal.

10 AAA33500.1 M73028 Zea mays

DESCRIPTION: myb-like transcription factor. P.

AAG36774.1 AF210616 Zea mays

15 DESCRIPTION: P2 protein. P2. myb-like transcriptional factor; similar to
Zea mays P gene.

BAA88222.1 AB028650 Nicotiana tabacum

20 DESCRIPTION: myb-related transcription factor LBM2. lbm2.

CAA72185.1 Y11350 Oryza sativa

25 DESCRIPTION: myb factor. myb.

AAG13574.1 AC037425 Oryza sativa

DESCRIPTION: myb factor. OSJNBa0055P24.4.

30

AAB41101.1 U72762 Nicotiana tabacum

DESCRIPTION: transcription factor Myb1. myb1. TMV-inducible Myb
homolog;

contains helix-turn-helix motif; contains redox-sensitive cysteine.

35

BAA88223.1 AB028651 Nicotiana tabacum

DESCRIPTION: myb-related transcription factor LBM3. lbm3.

40

AAA19819.1 L19496 Zea mays

DESCRIPTION: transcriptional activator for anthocyanin synthesis.
transcriptional activator.

45

BAA88224.1 AB028652 Nicotiana tabacum

DESCRIPTION: myb-related transcription factor LBM4. lbm4.

AAB67720.1 AF015268 Zea mays

5 DESCRIPTION: activator of anthocyanin structural genes. PL transcription factor. Pl.

AAA33492.1 L13454 Zea mays

10 DESCRIPTION: transcriptional activator for anthocyanin biosynthesis. Pl-Bh (Blotched1).

83

15 CAA78387.1 Z13997 Petunia x hybrida

DESCRIPTION: DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.

20 BAA81736.1 AB029165 Glycine max

DESCRIPTION: GmMYB29B2.

BAA81732.1 AB029161 Glycine max

25 DESCRIPTION: GmMYB29A2.

BAA81731.1 AB029160 Glycine max

30 DESCRIPTION: GmMYB29A1.

BAA81730.1 AB029159 Glycine max

DESCRIPTION: GmMYB29A1.

35

BAA88221.1 AB028649 Nicotiana tabacum

DESCRIPTION: myb-related transcription factor LBM1. lbm1.

40 BAA88224.1 AB028652 Nicotiana tabacum

DESCRIPTION: myb-related transcription factor LBM4. lbm4.

CAA66952.1 X98308 Lycopersicon esculentum

45 DESCRIPTION: THM18. myb-related transcription factor.

- BAA81733.2 AB029162 Glycine max
DESCRIPTION: GmMYB29A2.
- 5 CAA72217.1 Y11414 Oryza sativa
DESCRIPTION: myb.
- 10 BAA88222.1 AB028650 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM2. lbm2.
- 15 AAB41101.1 U72762 Nicotiana tabacum
DESCRIPTION: transcription factor Myb1. myb1. TMV-inducible Myb
homolog;
contains helix-turn-helix motif; contains redox-sensitive cysteine.
- 20 BAA88223.1 AB028651 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM3. lbm3.
- 25 CAA72185.1 Y11350 Oryza sativa
DESCRIPTION: myb factor. myb.
- 30 AAG13574.1 AC037425 Oryza sativa
DESCRIPTION: myb factor. OSJNBa0055P24.4.
- 35 AAK19616.1 AF336283 Gossypium hirsutum
DESCRIPTION: GHMYB25. ghmyb25. similar to myb; contains an unspliced
intron.
- 40 CAA78386.1 Z13996 Petunia x hybrida
DESCRIPTION: DNA binding protein; transcriptional activator. protein 1.
myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from
nucleotide 992 is not included in clone cPF1 and has been obtained by PCR
amplification of cDNA.
- 45 CAA72218.1 Y11415 Oryza sativa
DESCRIPTION: myb.

AAA33067.1 L04497 *Gossypium hirsutum*
DESCRIPTION: MYB A; putative.

5

CAA68235.1 X99973 *Hordeum vulgare*
DESCRIPTION: myb4 transcription factor. myb4.

10

AAC49394.1 U57002 *Zea mays*
DESCRIPTION: P protein. P. allele P-wr; Myb-like transcriptional
regulator with a putative zinc-finger at the C-terminal.

15

AAA33500.1 M73028 *Zea mays*
DESCRIPTION: myb-like transcription factor. P.

20

CAA67600.1 X99210 *Lycopersicon esculentum*
DESCRIPTION: myb-related transcription factor. THM16.

25

AAG36774.1 AF210616 *Zea mays*
DESCRIPTION: P2 protein. P2. myb-like transcriptional factor; similar to
Zea mays P gene.

30

AAF22256.1 AF161711 *Pimpinella brachycarpa*
DESCRIPTION: myb-related transcription factor.

35

CAA72187.1 Y11352 *Oryza sativa*
DESCRIPTION: myb factor. myb.

AAC04718.1 AF034132 *Gossypium hirsutum*
DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-
binding
domain protein. CmY-J. similar to MYB A encoded by GenBank Accession
Number L04497.

40

45

CAB43399.1 AJ006292 *Antirrhinum majus*
DESCRIPTION: Myb-related transcription factor mixta-like 1. mybml1.

AAK19615.1 AF336282 *Gossypium hirsutum*
DESCRIPTION: GHMYB10. ghmyb10. similar to myb.

5 AAK19618.1 AF336285 *Gossypium hirsutum*
DESCRIPTION: GHMYB38. ghmyb38. similar to myb.

10 CAA72186.1 Y11351 *Oryza sativa*
DESCRIPTION: myb factor. myb.

15 CAA64614.1 X95296 *Lycopersicon esculentum*
DESCRIPTION: transcription factor. THM27. myb-related.

CAA50221.1 X70876 *Hordeum vulgare*
DESCRIPTION: MybHv5. myb2.

20 BAA23338.1 D88618 *Oryza sativa*
DESCRIPTION: transfactor. OSMYB2. Osmyb2.

25 AAK19619.1 AF336286 *Gossypium hirsutum*
DESCRIPTION: GHMYB9. ghmyb9. similar to myb.

30 AAA82943.1 U39448 *Picea mariana*
DESCRIPTION: MYB-like transcriptional factor MBF1. putative DNA binding
region highly similar to the maize C1.

35 AAC04720.1 AF034134 *Gossypium hirsutum*
DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-
binding
domain protein. CmY-O. similar to MYB A encoded by GenBank Accession
Number L04497.

40 AAK19611.1 AF336278 *Gossypium hirsutum*
DESCRIPTION: BNLGHi233. bnlghi6233. similar to myb.

45 BAA23337.1 D88617 *Oryza sativa*
DESCRIPTION: transfactor. OSMYB1. Osmyb1.

5 BAB39987.1 AP003020 Oryza sativa
DESCRIPTION: putative transcription factor (myb). P0498A12.16. contains
ESTs AU097474(S5087),D40175(S1959).

10 BAB39972.1 AP003018 Oryza sativa
DESCRIPTION: putative transcription factor (myb). OSJNBa0004B13.27.
contains ESTs AU097474(S5087),D40175(S1959).

15 CAA65525.1 X96749 Oryza sativa
DESCRIPTION: myb7.

20 AAK19617.1 AF336284 Gossypium hirsutum
DESCRIPTION: GHMYB36. ghmyb36. similar to myb.

CAA67575.1 X99134 Lycopersicon esculentum
DESCRIPTION: transcription factor. THM6. myb-related.

25 CAA50224.1 X70879 Hordeum vulgare
DESCRIPTION: MybHv1. myb1.

84

30 BAA88222.1 AB028650 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM2. lbm2.

35 BAA88221.1 AB028649 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM1. lbm1.

40 BAA88224.1 AB028652 Nicotiana tabacum
DESCRIPTION: myb-related transcription factor LBM4. lbm4.

45 CAA78387.1 Z13997 Petunia x hybrida
DESCRIPTION: DNA-binding protein, transcriptional activator. protein 2.
myb.Ph2. related to animal myb proto-oncoproteins.

CAA66952.1 X98308 *Lycopersicon esculentum*
DESCRIPTION: THM18. myb-related transcription factor.

5 AAB41101.1 U72762 *Nicotiana tabacum*
DESCRIPTION: transcription factor Myb1. myb1. TMV-inducible Myb
homolog;
contains helix-turn-helix motif; contains redox-sensitive cysteine.

10 BAA88223.1 AB028651 *Nicotiana tabacum*
DESCRIPTION: myb-related transcription factor LBM3. lbm3.

15 BAA81733.2 AB029162 *Glycine max*
DESCRIPTION: GmMYB29A2.

20 BAA81731.1 AB029160 *Glycine max*
DESCRIPTION: GmMYB29A1.

25 BAA81730.1 AB029159 *Glycine max*
DESCRIPTION: GmMYB29A1.

BAA81736.1 AB029165 *Glycine max*
DESCRIPTION: GmMYB29B2.

30 CAA72217.1 Y11414 *Oryza sativa*
DESCRIPTION: myb.

35 BAA81732.1 AB029161 *Glycine max*
DESCRIPTION: GmMYB29A2.

40 CAA72185.1 Y11350 *Oryza sativa*
DESCRIPTION: myb factor. myb.

45 AAG13574.1 AC037425 *Oryza sativa*
DESCRIPTION: myb factor. OSJNBa0055P24.4.

CAA72218.1 Y11415 Oryza sativa
DESCRIPTION: myb.

5 CAA78386.1 Z13996 Petunia x hybrida
DESCRIPTION: DNA binding protein; transcriptional activator. protein 1.
myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from
nucleotide 992 is not included in clone cPF1 and has been obtained by PCR
amplification of cDNA.

10

AAC49394.1 U57002 Zea mays
DESCRIPTION: P protein. P. allele P-wr; Myb-like transcriptional
regulator with a putative zinc-finger at the C-terminal.

15

CAB43399.1 AJ006292 Antirrhinum majus
DESCRIPTION: Myb-related transcription factor mixta-like 1. mybml1.

20

AAK19616.1 AF336283 Gossypium hirsutum
DESCRIPTION: GHMYB25. ghmyb25. similar to myb; contains an unspliced
intron.

25

AAG36774.1 AF210616 Zea mays
DESCRIPTION: P2 protein. P2. myb-like transcriptional factor; similar to
Zea mays P gene.

30

AAA33500.1 M73028 Zea mays
DESCRIPTION: myb-like transcription factor. P.

35 CAA68235.1 X99973 Hordeum vulgare
DESCRIPTION: myb4 transcription factor. myb4.

40 CAA72187.1 Y11352 Oryza sativa
DESCRIPTION: myb factor. myb.

AAA33067.1 L04497 Gossypium hirsutum
DESCRIPTION: MYB A; putative.

45

- CAA72186.1 Y11351 *Oryza sativa*
DESCRIPTION: myb factor. myb.
- 5 CAA67600.1 X99210 *Lycopersicon esculentum*
DESCRIPTION: myb-related transcription factor. THM16.
- 10 AAK19618.1 AF336285 *Gossypium hirsutum*
DESCRIPTION: GHMYB38. ghmyb38. similar to myb.
- 15 AAK19611.1 AF336278 *Gossypium hirsutum*
DESCRIPTION: BNLGHi233. bnlghi6233. similar to myb.
- 20 AAC04718.1 AF034132 *Gossypium hirsutum*
DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-J. similar to MYB A encoded by GenBank Accession Number L04497.
- 25 AAK19619.1 AF336286 *Gossypium hirsutum*
DESCRIPTION: GHMYB9. ghmyb9. similar to myb.
- 30 AAK19615.1 AF336282 *Gossypium hirsutum*
DESCRIPTION: GHMYB10. ghmyb10. similar to myb.
- 35 CAA64614.1 X95296 *Lycopersicon esculentum*
DESCRIPTION: transcription factor. THM27. myb-related.
- 40 BAA23338.1 D88618 *Oryza sativa*
DESCRIPTION: transfactor. OSMYB2. Osmyb2.
- 45 BAA23337.1 D88617 *Oryza sativa*
DESCRIPTION: transfactor. OSMYB1. Osmyb1.
- CAA67575.1 X99134 *Lycopersicon esculentum*
DESCRIPTION: transcription factor. THM6. myb-related.

CAA65525.1 X96749 Oryza sativa
DESCRIPTION: myb7.

5

BAB39987.1 AP003020 Oryza sativa
DESCRIPTION: putative transcription factor (myb). P0498A12.16. contains
ESTs AU097474(S5087),D40175(S1959).

10

BAB39972.1 AP003018 Oryza sativa
DESCRIPTION: putative transcription factor (myb). OSJNBa0004B13.27.
contains ESTs AU097474(S5087),D40175(S1959).

15

CAA50221.1 X70876 Hordeum vulgare
DESCRIPTION: MybHv5. myb2.

20

AAA82943.1 U39448 Picea mariana
DESCRIPTION: MYB-like transcriptional factor MBF1. putative DNA binding
region highly similar to the maize C1.

25

AAF22256.1 AF161711 Pimpinella brachycarpa
DESCRIPTION: myb-related transcription factor.

30

AAK19617.1 AF336284 Gossypium hirsutum
DESCRIPTION: GHMYB36. ghmyb36. similar to myb.

35

CAA50222.1 X70877 Hordeum vulgare
DESCRIPTION: MybHv1. myb1.

40

CAA50224.1 X70879 Hordeum vulgare
DESCRIPTION: MybHv1. myb1.

AAD11575.1 AF064029 Helianthus tuberosus
DESCRIPTION: lectin 1. LECHeltubal; agglutinin.

45

AAD11578.1 AF064030 Helianthus tuberosus

DESCRIPTION: lectin 2. LECHeltuba2; agglutinin.

5 AAD11577.1 AF064032 Helianthus tuberosus
DESCRIPTION: lectin HE17.

10 AAG10403.1 AF233284 Convolvulus arvensis
DESCRIPTION: mannose-binding lectin. cr8. Conarva.

15 AAD11576.1 AF064031 Helianthus tuberosus
DESCRIPTION: lectin 3.

20 AAB82776.2 AF001527 Musa acuminata
DESCRIPTION: ripening-associated protein. similar to lectin.

25 AAC49564.1 U56820 Calystegia sepium
DESCRIPTION: lectin.

88 CAB40792.1 AJ237754 Hordeum vulgare
DESCRIPTION: putative lectin. hl#2.

30 AAB65163.1 AF002692 Solanum commersonii
DESCRIPTION: glutathione S-transferase, class-phi. GST1. low temperature
induced.

35 CAA55039.1 X78203 Hyoscyamus muticus
DESCRIPTION: glutathione transferase.

40 AAA33930.1 M84968 Silene vulgaris
DESCRIPTION: glutathione-S-transferase.

45 AAA33931.1 M84969 Silene vulgaris
DESCRIPTION: glutathione-S-transferase.

AAF65767.1 AF242309 Euphorbia esula

DESCRIPTION: glutathione S-transferase. putative auxin-binding GST.

- 5 BAA01394.1 D10524 *Nicotiana tabacum*
DESCRIPTION: glutathione S-transferase. parB.
- 10 CAA96431.1 Z71749 *Nicotiana plumbaginifolia*
DESCRIPTION: glutathione S-transferase.
- 15 AAF61392.1 AF133894 *Persea americana*
DESCRIPTION: glutathione S-transferase. GTH.
- 20 CAB38119.1 AJ010296 *Zea mays*
DESCRIPTION: Glutathione transferase III(b). gst3b.
- 25 CAB38118.1 AJ010295 *Zea mays*
DESCRIPTION: Glutathione transferase III(a). gst3a.
- 30 BAB39935.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.17.
- CAA09190.1 AJ010451 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2a.
- 35 CAA09192.1 AJ010453 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2c.
- 40 CAA09193.1 AJ010454 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2d.
- 45 CAA09191.1 AJ010452 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2b.
- BAB39941.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.23.

Abstract

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- 538 -

CAA39480.1 X56004 *Triticum aestivum*
DESCRIPTION: glutathione transferase. gstA2.

5 AAA33469.1 M16902 *Zea mays*
DESCRIPTION: glutathione S-transferase I.

10 AAG32475.1 AF309382 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTF5.

15 AAA33470.1 M16901 *Zea mays*
DESCRIPTION: glutathione S-transferase I.

AAG32477.1 AF309384 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTF3.

20 CAA68993.1 Y07721 *Petunia x hybrida*
DESCRIPTION: conjugates glutathione to anthocyanin to facilitate
transport to the vacuole. glutathione S-transferase. an9 locus.

25 BAB39940.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.22.

30 AAC64007.1 AF062403 *Oryza sativa*
DESCRIPTION: glutathione S-transferase II.

35 AAG34823.1 AF244680 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 15.

40 AAG34817.1 AF244674 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 9.

CAB66333.1 AJ279691 *Betula pendula*
DESCRIPTION: glutathione-S-transferase. gst.

45 AAG34820.1 AF244677 *Zea mays*

DESCRIPTION: glutathione S-transferase GST 11.

AAG34821.1 AF244678 Zea mays

5 DESCRIPTION: glutathione S-transferase GST 13.

CAA05354.1 AJ002380 Oryza sativa

10 DESCRIPTION: glutathione S-transferase. Rgst I.

AAG34816.1 AF244673 Zea mays

DESCRIPTION: glutathione S-transferase GST 8.

15

AAG34818.1 AF244675 Zea mays

DESCRIPTION: glutathione S-transferase GST 10.

20 CAA05355.1 AJ002381 Oryza sativa

DESCRIPTION: glutathione S-transferase. Rgst II.

AAG34824.1 AF244681 Zea mays

25 DESCRIPTION: glutathione S-transferase GST 16.

91

AAG34695.1 AF313492 Matthiola incana

30 DESCRIPTION: putative cytochrome P450.

CAA71516.1 Y10492 Glycine max

35 DESCRIPTION: putative cytochrome P450.

BAA12159.1 D83968 Glycine max

DESCRIPTION: Cytochrome P-450 (CYP93A1).

40

AAC32274.1 AF081575 Petunia x hybrida

DESCRIPTION: flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.

45 AAA32913.1 M32885 Persea americana

DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).

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- 541 -

- 5 BAA74466.1 AB022733 Glycyrrhiza echinata
DESCRIPTION: cytochrome P450. CYP Ge-51.
- CAA50648.1 X71657 Solanum melongena
DESCRIPTION: P450 hydroxylase.
- 10 BAA22423.1 AB001380 Glycyrrhiza echinata
DESCRIPTION: cytochrome P450. CYP93B1.
- 15 BAB40324.1 AB037245 Asparagus officinalis
DESCRIPTION: cytochrome P450. ASPI-2.
- 20 AAB94588.1 AF022459 Glycine max
DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
- 25 AAG14961.1 AF214007 Brassica napus
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H1.
- BAB40323.1 AB037244 Asparagus officinalis
DESCRIPTION: cytochrome P450. ASPI-1.
- 30 AAB61965.1 U48435 Solanum chacoense
DESCRIPTION: putative cytochrome P450.
- 35 AAC39452.1 AF014800 Eschscholzia californica
DESCRIPTION: hydroxylase involved in the biosynthesis of
tetrahydrobenzylisoquinoline alkaloids in plants. (S)-N-methylcoclaurine
3'-hydroxylase. CYP80B1. cytochrome P-450-dependent monooxygenase;
CYP80B1v1.
- 40 AAG14962.1 AF214008 Brassica napus
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H2.
- 45 BAA84072.1 AB028152 Torenia hybrida

DESCRIPTION: flavone synthase II. cytochrome P450. TFNS5.

- 5 AAC39453.1 AF014801 *Eschscholzia californica*
DESCRIPTION: hydroxylase involved in the biosynthesis of
tetrahydrobenzylisoquinoline alkaloids in plants. (S)-N-methylcoclaurine
3'-hydroxylase. CYP80B1. cytochrome P-450-dependent monooxygenase;
CYP80B1v2.
- 10 AAD47832.1 AF166332 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450.
- 92
- 15 -----
AAG42490.1 AF321001 *Suaeda maritima* subsp. *salsa*
DESCRIPTION: S-adenosylmethionine synthetase 2.
- 20 AAG17666.1 AF271220 *Brassica juncea*
DESCRIPTION: S-adenosylmethionine synthetase. MSAMS2.
- 25 BAA96637.1 AP002482 *Oryza sativa*
DESCRIPTION: Similar to *Oryza sativa* S-adenosylmethionine synthetase 1
(P46611).
- 30 AAG17036.1 AF187821 *Pinus contorta*
DESCRIPTION: catalyzes the reaction between methionine and ATP to
S-adenosylmethionine. S-adenosylmethionine synthetase. sams2.
- 35 BAA94605.1 AB041534 *Camellia sinensis*
DESCRIPTION: s-adenosylmethionine synthetase. SAM.
- 40 AAA81377.1 U17239 *Actinidia chinensis*
DESCRIPTION: S-adenosylmethionine synthetase.
- 45 AAB38500.1 U79767 *Mesembryanthemum crystallinum*
DESCRIPTION: S-adenosylmethionine synthetase. methionine
adenosyltransferase.

AAA81378.1 U17240 Actinidia chinensis
DESCRIPTION: S-adenosylmethionine synthetase.

5 BAA09895.1 D63835 Hordeum vulgare
DESCRIPTION: S-adenosylmethionine synthetase.

10 AAA33274.1 M61882 Dianthus caryophyllus
DESCRIPTION: S-adenosylmethionine synthetase. CARSAM2.

15 AAA58773.1 L36681 Pisum sativum
DESCRIPTION: S-adenosylmethionine synthase. precursor for ethylene and
polyamine biosynthesis.

20 AAA58772.1 L36680 Pisum sativum
DESCRIPTION: precursor for ethylene and polyamine biosynthesis.
S-adenosylmethionine synthase.

25 AAA81379.1 U17241 Actinidia chinensis
DESCRIPTION: S-adenosylmethionine synthetase.

30 AAA33857.1 M62758 Petroselinum crispum
DESCRIPTION: S-adenosylmethionine synthetase. SMS-1.

35 AAG17035.1 AF187820 Pinus contorta
DESCRIPTION: catalyzes the reaction between methionine and ATP to
S-adenosylmethionine. S-adenosylmethionine synthetase. sams1.

AAB71833.1 AF008568 Chlamydomonas reinhardtii
DESCRIPTION: S-adenosylmethionine synthetase. CHRSAMS.

40 AAA33858.1 M62757 Petroselinum crispum
DESCRIPTION: S-adenosylmethionine synthetase. SMS-2.

45 BAA21726.1 AB006187 Nicotiana tabacum
DESCRIPTION: S-adenosylmethionine synthase. BYJ90.

AAAF78525.1 AF195233 *Pyrus pyrifolia*
DESCRIPTION: S-adenosylmethionine synthase. SAMS.

5 94

AAB36543.1 U77935 Phaseolus vulgaris
DESCRIPTION: DnaJ-like protein. synthesis and expression are regulated by heavy metal stress, virus infection and wounding treatment, suggesting that DnaJ-like protein plays a role in plant defense.

95

AAB36546.1 U77940 Phaseolus vulgaris
DESCRIPTION: polyubiquitin. expression is regulated by heavy metal stress, UV, virus infection, heat shock and wounding treatment, this suggests that ubiquitin plays a role in plant defense.

98

AA22109.1 AF119411 *Lupinus albus*
DESCRIPTION: ethylene biosynthesis enzyme.
1-aminocyclopropane-1-carboxylate synthase 1. ACS1. ACC synthase;
S-adenosyl-L-methionine methylthioadenosine-lyase.

AAC83146.1 AF057562 *Nicotiana glutinosa*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. ACS1. ACC synthase.

AAB06724.1 U64804 Petunia x hybrida
DESCRIPTION: ethylene biosynthesis enzyme.
1-aminocyclopropane-1-carboxylate synthase. PH-ACS1.

CAA79478.1 Z18953 Petunia x hybrida
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.

AAB17279.1 U72390 *Lycopersicon esculentum*
DESCRIPTION: converts S-adenosylmethionine to
 1-aminocyclopropane-1-carboxylate hormone biosynthesis.
 1-aminocyclopropane-1-carboxylate synthase. LE-ACS1B.

45

BAA94600.1 AB033503 *Populus euramericana*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. peacs-2.

5 BAA96743.1 AB044662 *Prunus persica*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. PP-ACS1.

CAB60831.1 AJ012696 *Citrus sinensis*

10 DESCRIPTION: ACC synthase. acs2.

CAA09477.1 AJ011095 *Citrus sinensis*

DESCRIPTION: ACC synthase. acs-1.

15

CAA41855.1 X59139 *Lycopersicon esculentum*

DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase. LE-Acc2.

20

BAA90549.1 AB031026 *Prunus mume*

DESCRIPTION: ACC synthase. PM-ACS1. 1-aminocyclopropane-1-carboxylic
acid
synthase.

25

AAA81580.1 M34289 *Lycopersicon esculentum*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.

30

CAA44397.1 X62536 *Lycopersicon esculentum*

DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

35 CAA46797.1 X65982 *Nicotiana tabacum*

DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

BAA78333.1 AB015625 *Pyrus pyrifolia*

40 DESCRIPTION: 1-aminocyclopropane-1-carboxylic acid synthase. pPPACS3.

CAA41856.1 X59145 *Lycopersicon esculentum*

DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase. LE-ACC2.

45

099972206201

- 5 AAB17278.1 U72389 *Lycopersicon esculentum*
DESCRIPTION: converts S-adenosylmethionine to
1-aminocyclopropane-1-carboxylate hormone biosynthesis.
1-aminocyclopropane-1-carboxylate synthase. LE-ACS1A.
- 10 AAF97614.1 U18056 *Lycopersicon esculentum*
DESCRIPTION: converts SAM to ACC; plant hormone biosynthesis.
1-amino-cyclopropane-1-carboxylate synthase. LE-ACS1A. ACC synthase;
direct precursor of ethylene; one member of a multigene family.
- 15 BAB16433.1 AB041521 *Solanum tuberosum*
DESCRIPTION: ACC synthase. ppACS1.
- 20 BAA34923.1 AB013100 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. LE-ACS6. ACC
synthase.
- 25 BAA25916.1 AB013346 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.
- 30 AAF97615.1 U18057 *Lycopersicon esculentum*
DESCRIPTION: converts SAM to ACC; plant hormone biosynthesis.
1-amino-cyclopropane-1-carboxylate synthase. LE-ACS1B. ACC synthase;
direct precursor of ethylene; one member of a multigene family.
- 35 BAA92350.1 AB034992 *Malus x domestica*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. MdACS-5A.
- 40 BAA92351.1 AB034993 *Malus x domestica*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. MdACS-5B.
- 45 BAA93712.1 AB032935 *Cucumis melo*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CMe-ACS1.
- BAA94599.1 AB033502 *Populus euphratica*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. peacs-1.

BAA33374.1 AB006803 Cucumis sativus
DESCRIPTION: ACC synthase. CS-ACS1.

5

BAA93714.1 AB032937 Cucumis sativus
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CS-ACS1.

10 AAC49153.1 U17229 Pelargonium x hortorum
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase. ACC synthase.

CAA06288.1 AJ005002 Nicotiana tabacum
15 DESCRIPTION: 1-cyclopropane-1-carboxylate synthase. acs2.

CAB65314.1 AJ131836 Nicotiana tabacum
20 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. acs2.

AAC15777.1 AF061605 Nicotiana glutinosa
DESCRIPTION: ACC synthase. ACS3.

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AAC83147.1 AF057563 Nicotiana glutinosa
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. ACS2. ACC
synthase.

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BAA06464.1 D30805 Cucumis melo
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.

35 BAA83618.1 AB025906 Cucumis melo
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CMe-ACS1
(ME-ACS1).

40 AAB70885.1 U88971 Pelargonium x hortorum
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. GACS2. similar
to Pelargonium hortorum clone pGAC-2, Genbank Accession Number U17231.

45 AAA33113.1 M58323 Cucurbita pepo
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.

5
AAA33111.1 M61195 Cucurbita pepo
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CP-ACC1A.

10
CAA57724.1 X82273 Brassica oleracea
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.

15
CAA47474.1 X67100 Glycine max
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

20
AAC98809.1 U68216 Carica papaya
DESCRIPTION: ACC synthase. fruit specific; ripening related.

25
CAA51227.1 X72676 Brassica juncea
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. MACC.

30
BAA00838.1 D01032 Cucurbita maxima
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. accW.

35
AAA34131.1 M63490 Lycopersicon esculentum
DESCRIPTION: enzyme. 1-aminocyclopropane-1-carboxylate synthase.

40
AAA03164.1 M88487 Lycopersicon esculentum
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. ACC4.

45
CAA41857.1 X59146 Lycopersicon esculentum
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase. LE-ACC4.

50
CAA77688.1 Z11613 Vigna radiata
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

CAA67118.1 X98492 *Nicotiana tabacum*
DESCRIPTION: ACC synthase. ACCS2.

99

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BAA22976.1 D63457 *Arabis gemmifera*
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

10 BAA22973.1 D63454 *Arabis gemmifera*
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

15 AAF23537.1 AF110439 *Arabis glabra*
DESCRIPTION: alcohol dehydrogenase.

20 BAA22978.1 D63459 *Arabis gemmifera*
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

25 BAA22974.1 D63455 *Arabis gemmifera*
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

AAF23540.1 AF110442 *Arabidopsis halleri*
DESCRIPTION: alcohol dehydrogenase.

30 AAF23551.1 AF110453 *Arabidopsis lyrata* subsp. *petraea*
DESCRIPTION: alcohol dehydrogenase.

35 AAF23539.1 AF110441 *Halimolobos perplexa* var. *lemhiensis*
DESCRIPTION: alcohol dehydrogenase.

40 BAA22975.1 D63456 *Arabis gemmifera*
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

AAF23546.1 AF110448 *Arabis lyallii*
DESCRIPTION: alcohol dehydrogenase.

45 AAF23548.1 AF110450 *Arabis parishii*

DESCRIPTION: alcohol dehydrogenase.

5 AAF23550.1 AF110452 *Arabidopsis lyrata* subsp. *petraea*
DESCRIPTION: alcohol dehydrogenase.

10 BAA22972.1 D63453 *Arabis gemmifera*
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

BAA22971.1 D63452 *Arabis gemmifera*
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

15 BAA22977.1 D63458 *Arabis gemmifera*
DESCRIPTION: alcohol dehydrogenase. Adh. ADH.

20 AAF23549.1 AF110451 *Arabis pauciflora*
DESCRIPTION: alcohol dehydrogenase.

25 AAF23545.1 AF110447 *Arabis lignifera*
DESCRIPTION: alcohol dehydrogenase.

30 AAF23536.1 AF110438 *Arabis fendleri*
DESCRIPTION: alcohol dehydrogenase.

AAF23541.1 AF110443 *Arabis hirsuta*
DESCRIPTION: alcohol dehydrogenase.

35 AAF23531.1 AF110433 *Arabis blepharophylla*
DESCRIPTION: alcohol dehydrogenase.

40 AAF23530.1 AF110432 *Arabis blepharophylla*
DESCRIPTION: alcohol dehydrogenase.

45 AAF23523.1 AF110425 *Aubrieta deltoidea*
DESCRIPTION: alcohol dehydrogenase.

AAF23547.1 AF110449 *Arabidopsis lyrata* subsp. *lyrata*
DESCRIPTION: alcohol dehydrogenase.

15

AAF23534.1 AF110436 *Arabis drummondii*
DESCRIPTION: alcohol dehydrogenase.

AAF23532.1 AF110434 Brassica oleracea
DESCRIPTION: alcohol dehydrogenase.

25

AAF23555.1 AF110457 *Arabis turrita*
DESCRIPTION: alcohol dehydrogenase.

35

AAF23524.1 AF110426 *Arabis alpina*
DESCRIPTION: alcohol dehydrogenase.

AAF23543.1 AF110445 *Arabis hirsuta*
DESCRIPTION: alcohol dehydrogenase.

45

AAF23527.1 AF110429 Arabis alpina

DESCRIPTION: alcohol dehydrogenase.

5 AAF23535.1 AF110437 *Arabis drummondii*
DESCRIPTION: alcohol dehydrogenase.

10 AAF23553.1 AF110455 *Arabis procurrens*
DESCRIPTION: alcohol dehydrogenase.

AAF23544.1 AF110446 *Arabis jacquinii*
DESCRIPTION: alcohol dehydrogenase.

15 AAF23526.1 AF110428 *Arabis alpina*
DESCRIPTION: alcohol dehydrogenase.

20 AAF23528.1 AF110430 *Cardamine amara*
DESCRIPTION: alcohol dehydrogenase.

25 AAF23552.1 AF110454 *Arabis procurrens*
DESCRIPTION: alcohol dehydrogenase.

30 AAF23542.1 AF110444 *Arabis hirsuta*
DESCRIPTION: alcohol dehydrogenase.

AAC79418.1 AF037560 *Leavenworthia stylosa*
DESCRIPTION: alcohol dehydrogenase 3. Adh3.

35 BAA34682.1 AB015504 *Arabidopsis griffithiana*
DESCRIPTION: alcohol dehydrogenase. Adh.

40 BAA34685.1 AB015507 *Arabidopsis suecica*
DESCRIPTION: alcohol dehydrogenase. Adh.

45 BAA34683.1 AB015505 *Arabidopsis korshinskyi*
DESCRIPTION: alcohol dehydrogenase. Adh.

CAB72921.1 AJ251281 *Arabidopsis lyrata* subsp. *petraea*
DESCRIPTION: alcohol dehydrogenase. adh.

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CAB72920.1 AJ251280 *Arabidopsis lyrata* subsp. *petraea*
DESCRIPTION: alcohol dehydrogenase. adh.

10 CAB72919.1 AJ251279 *Arabidopsis lyrata* subsp. *petraea*
DESCRIPTION: alcohol dehydrogenase. adh.

15 CAB72918.1 AJ251278 *Arabidopsis lyrata* subsp. *petraea*
DESCRIPTION: alcohol dehydrogenase. adh.

20 CAB72917.1 AJ251277 *Arabidopsis lyrata* subsp. *petraea*
DESCRIPTION: alcohol dehydrogenase. adh.

100

25 AAD09518.1 U64925 *Nicotiana tabacum*
DESCRIPTION: NTGP4. similar to AIG1; geranylgeranylated protein.

102

30 BAA12039.1 D83669 *Spinacia oleracea*
DESCRIPTION: stromal ascorbate peroxidase.

35 BAA19611.1 D77997 *Spinacia oleracea*
DESCRIPTION: thylakoid-bound ascorbate peroxidase.

BAA24610.1 AB002467 *Spinacia oleracea*
DESCRIPTION: stromal ascorbate peroxidase. APX2.

40 BAA24609.1 AB002467 *Spinacia oleracea*
DESCRIPTION: thylakoid-bound ascorbate peroxidase. APX2.

45 AAC19394.1 AF069316 *Mesembryanthemum crystallinum*
DESCRIPTION: stromal L-ascorbate peroxidase precursor.

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- AAC19393.1 AF069315 *Mesembryanthemum crystallinum*
DESCRIPTION: thylakoid-bound L-ascorbate peroxidase precursor.
- 5 BAA78553.1 AB022274 *Chloroplast Nicotiana tabacum*
DESCRIPTION: stromal ascorbate peroxidase.
- 10 BAA78552.1 AB022273 *Chloroplast Nicotiana tabacum*
DESCRIPTION: thylakoid-bound ascorbate peroxidase.
- 15 BAA22196.1 D88420 *Cucurbita* sp.
DESCRIPTION: a hydrogen peroxide-scavenging enzyme. stromal ascorbate peroxidase.
- 20 BAA12029.1 D83656 *Cucurbita* sp.
DESCRIPTION: $2\text{AsA} + \text{H}_2\text{O}_2 \rightarrow 2\text{MDA} + 2\text{H}_2\text{O}$. thylakoid-bound ascorbate peroxidase.
- 25 CAA11265.1 AJ223325 *Chlamydomonas reinhardtii*
DESCRIPTION: ascorbate peroxidase. apx1.
- 30 BAA83595.1 AB009084 *Chlamydomonas* sp. W80
DESCRIPTION: chloroplast ascorbate peroxidase.
- 35 AAD30294.1 AF139190 *Mesembryanthemum crystallinum*
DESCRIPTION: cytosolic ascorbate peroxidase. similar to L0-328, R6-3, L72-2.
- 40 AAB52954.1 U37060 *Gossypium hirsutum*
DESCRIPTION: ascorbate peroxidase. glyoxysomal membrane-bound protein.
- 45 AAD43334.1 AF159254 *Zantedeschia aethiopica*
DESCRIPTION: ascorbate peroxidase. apx2. putative glyoxysomal membrane-bound protein.
- AAC08576.1 AF053474 *Zantedeschia aethiopica*

DESCRIPTION: cytosolic ascorbate peroxidase. apx.

5 AAD43338.1 AF158654 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase APX26.

10 AAD43336.1 AF158652 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. ApxSC. corresponds to mRNA
sequence deposited in GenBank Accession Number AF039953.

15 AAB95222.1 AF039953 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. ApxSC.

20 AAD41408.1 AF159633 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. APX.

AAD41407.1 AF159632 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. APX.

25 AAD41403.1 AF159628 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. APX.

30 AAD41402.1 AF159627 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. APX.

35 AAD43337.1 AF158653 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase APX19.

AAD41406.1 AF159631 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. APX.

40 AAD41404.1 AF159629 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. APX.

45 AAB94574.1 AF022213 Fragaria x ananassa
DESCRIPTION: cytosolic ascorbate peroxidase. APX-c.

- 5 AAD41405.1 AF159630 *Fragaria x ananassa*
DESCRIPTION: cytosolic ascorbate peroxidase. APX.
- 10 BAA08264.1 D45423 *Oryza sativa*
DESCRIPTION: ascorbate peroxidase.
- 15 BAA13671.1 D88649 *Cucumis sativus*
DESCRIPTION: cytosolic ascorbate peroxidase.
- 20 CAA55209.1 X78452 *Raphanus sativus*
DESCRIPTION: L-ascorbate peroxidase. APX.
- 25 BAA12890.1 D85864 *Spinacia oleracea*
DESCRIPTION: cytosolic ascorbate peroxidase.
- AAA99518.1 L20864 *Spinacia oleracea*
DESCRIPTION: ascorbate peroxidase.
- 30 BAA12918.1 D85912 *Nicotiana tabacum*
DESCRIPTION: cytosolic ascorbate peroxidase.
- AAB03844.1 U61379 *Vigna unguiculata*
DESCRIPTION: ascorbate peroxidase.
- 35 CAB58361.1 Y16773 *Lycopersicon esculentum*
DESCRIPTION: ascorbate peroxidase. Apx. H2O2 scavenger, cytosolic protein.
- 40 CAA57140.1 X81376 *Capsicum annuum*
DESCRIPTION: L-ascorbate peroxidase.
- 45 CAA06996.1 AJ006358 *Hordeum vulgare*
DESCRIPTION: ascorbate peroxidase. apx.

AAF22246.1 AF159380 *Pimpinella brachycarpa*
DESCRIPTION: ascorbate peroxidase. APX.

5

AAA86689.1 U15933 *Nicotiana tabacum*
DESCRIPTION: reduction of hydrogen peroxide. ascorbate peroxidase. APX.

10

CAA84406.1 Z34934 *Zea mays*
DESCRIPTION: cytosolic ascorbate peroxidase. apx.

15

CAA43992.1 X62077 *Pisum sativum*
DESCRIPTION: L-ascorbate peroxidase. AppxI.

20

AAA33645.1 M93051 *Pisum sativum*
DESCRIPTION: hydrogen peroxide removal; oxidative stress. ascorbate
peroxidase. ApxI.

25

AAB01221.1 U56634 *Glycine max*
DESCRIPTION: ascorbate peroxidase 2. APx2.

30

AAA61779.1 L10292 *Glycine max*
DESCRIPTION: ascorbate peroxidase. Automated Edman sequencing of the
N-terminal amino acids confirmed that the protein was authentic ascorbate
peroxidase; putative.

35

BAB20889.1 AB053297 *Oryza sativa*
DESCRIPTION: L-ascorbate peroxidase. APXb.

40

CAA72247.1 Y11461 *Brassica napus*
DESCRIPTION: L-ascorbate peroxidase. APX.

45

AAD20022.1 AF127804 *Glycine max*
DESCRIPTION: ascorbate peroxidase. apx1. AsPOX; cytosolic.

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- 559 -

- AAC83147.1 AF057563 *Nicotiana glutinosa*
 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. ACS2. ACC synthase.
- 5 CAB60722.1 AJ012551 *Citrus sinensis*
 DESCRIPTION: ACC synthase. acs1.
- 10 CAB60721.1 AJ012550 *Citrus sinensis*
 DESCRIPTION: ACC synthase. acs1.
- 15 CAA06288.1 AJ005002 *Nicotiana tabacum*
 DESCRIPTION: 1-cyclopropane-1-carboxylate synthase. acs2.
- 20 CAB65314.1 AJ131836 *Nicotiana tabacum*
 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. acs2.
- BAA78333.1 AB015625 *Pyrus pyrifolia*
 DESCRIPTION: 1-aminocyclopropane-1-carboxylic acid synthase. pPPACS3.
- 25 AAB17279.1 U72390 *Lycopersicon esculentum*
 DESCRIPTION: converts S-adenosylmethionine to
 1-aminocyclopropane-1-carboxylate hormone biosynthesis.
 1-aminocyclopropane-1-carboxylate synthase. LE-ACS1B.
- 30 AAF97614.1 U18056 *Lycopersicon esculentum*
 DESCRIPTION: converts SAM to ACC; plant hormone biosynthesis.
 1-amino-cyclopropane-1-carboxylate synthase. LE-ACS1A. ACC synthase;
 35 direct precursor of ethylene; one member of a multigene family.
- 40 AAF97615.1 U18057 *Lycopersicon esculentum*
 DESCRIPTION: converts SAM to ACC; plant hormone biosynthesis.
 1-amino-cyclopropane-1-carboxylate synthase. LE-ACS1B. ACC synthase;
 direct precursor of ethylene; one member of a multigene family.
- 45 AAB17278.1 U72389 *Lycopersicon esculentum*
 DESCRIPTION: converts S-adenosylmethionine to
 1-aminocyclopropane-1-carboxylate hormone biosynthesis.

1-aminocyclopropane-1-carboxylate synthase. LE-ACS1A.

CAA46797.1 X65982 Nicotiana tabacum
5 DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

BAA06464.1 D30805 Cucumis melo
10 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.

AAB06724.1 U64804 Petunia x hybrida
DESCRIPTION: ethylene biosynthesis enzyme.
1-aminocyclopropane-1-carboxylate synthase. PH-ACS1.
15

CAA79478.1 Z18953 Petunia x hybrida
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.
20

BAA94599.1 AB033502 Populus euphratica
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. peacs-1.

CAA67118.1 X98492 Nicotiana tabacum
25 DESCRIPTION: ACC synthase. ACCS2.

CAA79477.1 Z18952 Dianthus caryophyllus
30 DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

AAA33275.1 M66619 Dianthus caryophyllus
35 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CARACC.

BAA83618.1 AB025906 Cucumis melo
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CMe-ACS1
(ME-ACS1).
40

BAA34923.1 AB013100 Lycopersicon esculentum
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. LE-ACS6. ACC
synthase.
45

BAA25916.1 AB013346 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.

5 CAB60831.1 AJ012696 *Citrus sinensis*
DESCRIPTION: ACC synthase. acs2.

10 CAA41855.1 X59139 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase. LE-Acc2.

15 CAA44397.1 X62536 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

CAA41856.1 X59145 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase. LE-ACC2.

20 AAA81580.1 M34289 *Lycopersicon esculentum*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.

25 AAC98809.1 U68216 *Carica papaya*
DESCRIPTION: ACC synthase. fruit specific; ripening related.

30 BAA92350.1 AB034992 *Malus x domestica*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. MdACS-5A.

35 BAA92351.1 AB034993 *Malus x domestica*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. MdACS-5B.

BAA94600.1 AB033503 *Populus euramericana*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. peacs-2.

40 CAA77688.1 Z11613 *Vigna radiata*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

45 CAA47474.1 X67100 *Glycine max*
DESCRIPTION: 1-aminocyclopropane 1-carboxylate synthase.

- AAB70885.1 U88971 *Pelargonium x hortorum*
 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. GACS2. similar
 5 to *Pelargonium hortorum* clone pGAC-2, Genbank Accession Number U17231.
- AAD04199.1 AF016459 *Pisum sativum*
 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. ACS2. ACC
 10 synthase.
- BAB18464.1 D86242 *Cucumis melo*
 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CMe-ACS2
 15 (ME-ACS2).
- BAA93713.1 AB032936 *Cucumis melo*
 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CMe-ACS2.
 20
- BAA93715.1 AB032938 *Cucumis sativus*
 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CS-ACS2.
 25
- BAA33375.1 AB006804 *Cucumis sativus*
 DESCRIPTION: ACC synthase. CS-ACS2.
- 30 BAB16433.1 AB041521 *Solanum tuberosum*
 DESCRIPTION: ACC synthase. ppACS1.
- AAC15777.1 AF061605 *Nicotiana glutinosa*
 35 DESCRIPTION: ACC synthase. ACS3.
- CAA72191.1 Y11357 *Carica papaya*
 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase.
 40
- BAA96743.1 AB044662 *Prunus persica*
 DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. PP-ACS1.
 45
- BAA90549.1 AB031026 *Prunus mume*

DESCRIPTION: ACC synthase. PM-ACS1. 1-aminocyclopropane-1-carboxylic acid synthase.

5

BAA93712.1 AB032935 Cucumis melo

DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CMe-ACS1.

10

AAF22109.1 AF119411 Lupinus albus

DESCRIPTION: ethylene biosynthesis enzyme.

1-aminocyclopropane-1-carboxylate synthase 1. ACS1. ACC synthase;

S-adenosyl-L-methionine methylthioadenosine-lyase.

15

AAC83146.1 AF057562 Nicotiana glutinosa

DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. ACS1. ACC synthase.

20

CAA09477.1 AJ011095 Citrus sinensis

DESCRIPTION: ACC synthase. acs-1.

25

BAA93714.1 AB032937 Cucumis sativus

DESCRIPTION: 1-aminocyclopropane-1-carboxylate synthase. CS-ACS1.

106

30

AAF63205.1 AF245119 Mesembryanthemum crystallinum

DESCRIPTION: AP2-related transcription factor. CDBP. stress induced transcription factor.

35

BAA97122.1 AB016264 Nicotiana glauca

DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.

40

AAC50047.1 U89255 Lycopersicon esculentum

DESCRIPTION: binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti4.

45

BAA07321.1 D38123 Nicotiana tabacum

DESCRIPTION: ERF1. ethylene-responsive transcription factor.

- 5 AAC62619.1 AF057373 *Nicotiana tabacum*
DESCRIPTION: transcription factor. ethylene response element binding protein 1. EREBP1.
- 10 BAA87068.1 AB035270 *Matricaria chamomilla*
DESCRIPTION: ethylene-responsive element binding protein1 homolog. McEREBP1.
- 15 AAC49740.1 U89256 *Lycopersicon esculentum*
DESCRIPTION: binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti5.
- 20 AAG43545.1 AF211527 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.
- 25 BAA97124.1 AB016266 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
- 30 CAB96900.1 AJ251250 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.
- 35 CAB96899.1 AJ251249 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.
- 40 AAB38748.1 U81157 *Nicotiana tabacum*
DESCRIPTION: S25-XP1 DNA binding protein.
- 45 AAG60182.1 AC084763 *Oryza sativa*
DESCRIPTION: putative ethylene-responsive element binding protein. OSJNBa0027P10.12.

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AAK31279.1 AC079890 *Oryza sativa*

DESCRIPTION: putative ethylene-responsive element binding protein.
OSJNBb0089A17.16.

5

CAB93940.1 AJ238740 *Catharanthus roseus*

DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
protein. orca2.

10

AAC49741.1 U89257 *Lycopersicon esculentum*

DESCRIPTION: DNA-binding protein binds the GCC box pathogenesis-related
promoter element. Pti6.

15

CAC12822.1 AJ299252 *Nicotiana tabacum*

DESCRIPTION: AP2 domain-containing transcription factor. ap2.

20

BAB03248.1 AB037183 *Oryza sativa*

DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive
element binding factor3. osERF3.

25

AAC14323.1 AF058827 *Nicotiana tabacum*

DESCRIPTION: TSI1. Tsi1. contains putative AP2 DNA-binding domain;
similar to Pti6.

30

BAA97123.1 AB016265 *Nicotiana sylvestris*

DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
element binding factor. nserf3.

35

AAD00708.1 U91857 *Stylosanthes hamata*

DESCRIPTION: ethylene-responsive element binding protein homolog. similar
to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers
D38123, D38126, D38124, and D38125 respectively.

40

AAF05606.1 AF190770 *Oryza sativa*

DESCRIPTION: EREBP-like protein. tsh1. TSH1; induced by ethylene.

45

BAA76734.1 AB024575 *Nicotiana tabacum*

DESCRIPTION: ethylene responsive element binding factor.

5 AAC29516.1 U77655 Solanum tuberosum
DESCRIPTION: DNA binding protein homolog. STWAAEIRD.

10 AAF23899.1 AF193803 Oryza sativa
DESCRIPTION: transcription factor EREBP1. EREBP/AP2-like transcription factor.

15 CAB93939.1 AJ238739 Catharanthus roseus
DESCRIPTION: putative transcription factor. AP2-domain DNA-binding protein. orcal.

20 AAD45623.1 AF084185 Brassica napus
DESCRIPTION: dehydration responsive element binding protein. DNA binding protein; DRE binding protein.

25 AAK31271.1 AC079890 Oryza sativa
DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.

30 AAG43548.1 AF211530 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.

35 BAB21218.1 AP002913 Oryza sativa
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.24.

40 AAG43549.1 AF211531 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.

45 BAB21211.1 AP002913 Oryza sativa
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.17.

AAK01088.1 AF298230 Hordeum vulgare

DESCRIPTION: CBF1-like protein BCBF1. BCBF1. AP2 domain protein;
putative
DRE binding factor.

5

AAK01089.1 AF298231 *Hordeum vulgare*
DESCRIPTION: CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE
binding factor.

10 107

AAF63205.1 AF245119 *Mesembryanthemum crystallinum*
DESCRIPTION: AP2-related transcription factor. CDBP. stress induced
transcription factor.

15

AAC50047.1 U89255 *Lycopersicon esculentum*
DESCRIPTION: binds the GCC box pathogenesis-related promoter element
DNA-binding protein. Pti4.

20

BAA97122.1 AB016264 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
element binding factor. nserf2.

25

BAA07321.1 D38123 *Nicotiana tabacum*
DESCRIPTION: ERF1. ethylene-responsive transcription factor.

30

AAC62619.1 AF057373 *Nicotiana tabacum*
DESCRIPTION: transcription factor. ethylene response element binding
protein 1. EREBP1.

35

BAA87068.1 AB035270 *Matricaria chamomilla*
DESCRIPTION: ethylene-responsive element binding protein1 homolog.
McEREBP1.

40

CAB96899.1 AJ251249 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

45

CAB96900.1 AJ251250 *Catharanthus roseus*

DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

5 AAB38748.1 U81157 *Nicotiana tabacum*
DESCRIPTION: S25-XP1 DNA binding protein.

10 AAC49740.1 U89256 *Lycopersicon esculentum*
DESCRIPTION: binds the GCC box pathogenesis-related promoter element
DNA-binding protein. Pti5.

15 CAB93940.1 AJ238740 *Catharanthus roseus*
DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
protein. orca2.

20 AAG43545.1 AF211527 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to
EREBP transcription factors.

25 BAA97124.1 AB016266 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
element binding factor. nserf4.

30 AAG60182.1 AC084763 *Oryza sativa*
DESCRIPTION: putative ethylene-responsive element binding protein.
OSJNBa0027P10.12.

35 AAK31279.1 AC079890 *Oryza sativa*
DESCRIPTION: putative ethylene-responsive element binding protein.
OSJNBb0089A17.16.

40 BAA97123.1 AB016265 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
element binding factor. nserf3.

45 AAD00708.1 U91857 *Stylosanthes hamata*
DESCRIPTION: ethylene-responsive element binding protein homolog. similar

to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.

- 5 AAC14323.1 AF058827 *Nicotiana tabacum*
DESCRIPTION: TSI1. Tsi1. contains putative AP2 DNA-binding domain;
similar to Pti6.
- 10 CAC12822.1 AJ299252 *Nicotiana tabacum*
DESCRIPTION: AP2 domain-containing transcription factor. ap2.
- 15 BAB03248.1 AB037183 *Oryza sativa*
DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive
element binding factor3. osERF3.
- 20 AAF05606.1 AF190770 *Oryza sativa*
DESCRIPTION: EREBP-like protein. tsh1. TSH1; induced by ethylene.
- 25 BAA76734.1 AB024575 *Nicotiana tabacum*
DESCRIPTION: ethylene responsive element binding factor.
- 30 AAC49741.1 U89257 *Lycopersicon esculentum*
DESCRIPTION: DNA-binding protein binds the GCC box pathogenesis-related
promoter element. Pti6.
- 35 AAF23899.1 AF193803 *Oryza sativa*
DESCRIPTION: transcription factor EREBP1. EREBP/AP2-like transcription
factor.
- 40 AAC29516.1 U77655 *Solanum tuberosum*
DESCRIPTION: DNA binding protein homolog. STWAAEIRD.
- 45 CAB93939.1 AJ238739 *Catharanthus roseus*
DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
protein. orcal.
- BAA78738.1 AB023482 *Oryza sativa*

DESCRIPTION: EST AU055776(S20048) corresponds to a region of the predicted gene.; Similar to Arabidopsis thaliana AP2 domain containing protein RAP2.10 mRNA, partial cds.(AF003103).

5

AAD45623.1 AF084185 Brassica napus

DESCRIPTION: dehydration responsive element binding protein. DNA binding protein; DRE binding protein.

10

AAG43548.1 AF211530 Nicotiana tabacum

DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.

15

AAG43549.1 AF211531 Nicotiana tabacum

DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.

20

BAA99376.1 AP002526 Oryza sativa

DESCRIPTION: ESTs AU093391(E60370),AU091593(C60458), AU093392(E60370)

25

correspond to a region of the predicted gene. Similar to Arabidopsis thaliana BAC F21J9; AP2 domain protein. (AC000103).

BAB21218.1 AP002913 Oryza sativa

DESCRIPTION: putative DNA binding protein RAV2. P0480E02.24.

30

AAK31271.1 AC079890 Oryza sativa

DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.

35

BAB21211.1 AP002913 Oryza sativa

DESCRIPTION: putative DNA binding protein RAV2. P0480E02.17.

40

AAK01088.1 AF298230 Hordeum vulgare

DESCRIPTION: CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.

45

AAG59618.1 AF239616 Hordeum vulgare

DESCRIPTION: CRT/DRE-binding factor. CBF.

- 5 AAK01089.1 AF298231 *Hordeum vulgare*
DESCRIPTION: CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.

109

- 10 BAA97124.1 AB016266 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.

- 15 AAG43545.1 AF211527 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.

- 20 AAK31279.1 AC079890 *Oryza sativa*
DESCRIPTION: putative ethylene-responsive element binding protein. OSJNBb0089A17.16.

- 25 AAG60182.1 AC084763 *Oryza sativa*
DESCRIPTION: putative ethylene-responsive element binding protein. OSJNBa0027P10.12.

- 30 BAA87068.1 AB035270 *Matricaria chamomilla*
DESCRIPTION: ethylene-responsive element binding protein1 homolog. McEREBP1.

- 35 AAF63205.1 AF245119 *Mesembryanthemum crystallinum*
DESCRIPTION: AP2-related transcription factor. CDBP. stress induced transcription factor.

- 40 AAC50047.1 U89255 *Lycopersicon esculentum*
DESCRIPTION: binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti4.

- 45 BAA97122.1 AB016264 *Nicotiana sylvestris*

DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.

5

BAA07321.1 D38123 *Nicotiana tabacum*

DESCRIPTION: ERF1. ethylene-responsive transcription factor.

10

CAB93940.1 AJ238740 *Catharanthus roseus*

DESCRIPTION: putative transcription factor. AP2-domain DNA-binding protein. orca2.

15

AAC49740.1 U89256 *Lycopersicon esculentum*

DESCRIPTION: binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti5.

20

AAC62619.1 AF057373 *Nicotiana tabacum*

DESCRIPTION: transcription factor. ethylene response element binding protein 1. EREBP1.

25

AAB38748.1 U81157 *Nicotiana tabacum*

DESCRIPTION: S25-XP1 DNA binding protein.

30

CAC12822.1 AJ299252 *Nicotiana tabacum*

DESCRIPTION: AP2 domain-containing transcription factor. ap2.

35

CAB96900.1 AJ251250 *Catharanthus roseus*

DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

40

CAB96899.1 AJ251249 *Catharanthus roseus*

DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

45

BAA97123.1 AB016265 *Nicotiana sylvestris*

DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.

BAB03248.1 AB037183 *Oryza sativa*

DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.

5

AAD00708.1 U91857 *Stylosanthes hamata*

DESCRIPTION: ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.

10

AAC14323.1 AF058827 *Nicotiana tabacum*

DESCRIPTION: TSI1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pti6.

15

AAC49741.1 U89257 *Lycopersicon esculentum*

DESCRIPTION: DNA-binding protein binds the GCC box pathogenesis-related promoter element. Pti6.

20

AAC29516.1 U77655 *Solanum tuberosum*

DESCRIPTION: DNA binding protein homolog. STWAAEIRD.

25

AAF05606.1 AF190770 *Oryza sativa*

DESCRIPTION: EREBP-like protein. tsh1. TSH1; induced by ethylene.

30

BAA76734.1 AB024575 *Nicotiana tabacum*

DESCRIPTION: ethylene responsive element binding factor.

35

AAF23899.1 AF193803 *Oryza sativa*

DESCRIPTION: transcription factor EREBP1. EREBP/AP2-like transcription factor.

40

BAA78738.1 AB023482 *Oryza sativa*

DESCRIPTION: EST AU055776(S20048) corresponds to a region of the predicted gene.; Similar to *Arabidopsis thaliana* AP2 domain containing protein RAP2.10 mRNA, partial cds.(AF003103).

45

CAB93939.1 AJ238739 *Catharanthus roseus*

DESCRIPTION: putative transcription factor. AP2-domain DNA-binding

protein. orcal.

- 5 AAD45623.1 AF084185 Brassica napus
DESCRIPTION: dehydration responsive element binding protein. DNA binding protein; DRE binding protein.
- 10 AAG43549.1 AF211531 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
- 15 AAG43548.1 AF211530 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
- 20 AAK31271.1 AC079890 Oryza sativa
DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.
- 25 AAK01088.1 AF298230 Hordeum vulgare
DESCRIPTION: CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
- 30 BAA99376.1 AP002526 Oryza sativa
DESCRIPTION: ESTs AU093391(E60370),AU091593(C60458), AU093392(E60370) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana BAC F21J9; AP2 domain protein. (AC000103).
- 35 AAG59619.1 AF243384 Oryza sativa
DESCRIPTION: CRT/DRE binding factor. CBF. DREB.
- 40 BAB21218.1 AP002913 Oryza sativa
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.24.
- 45 AAG32659.1 AF253971 Picea abies
DESCRIPTION: APETALA2-related transcription factor 2. AP2L2. PaAP2L2.

AAC49567.1 U41466 Zea mays

DESCRIPTION: Glossy15. Glossy15. AP2 DNA-binding domain protein; similar

5 to the Arabidopsis floral homeotic gene APETALA2; maize AP2-domain regulator of leaf epidermal traits; homeotic regulator of leaf epidermal cell identity; allele: W64A; putative transcription factor.

110

10

AAG43545.1 AF211527 Nicotiana tabacum

DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.

15

BAA97124.1 AB016266 Nicotiana glauca

DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.

20

AAK31279.1 AC079890 Oryza sativa

DESCRIPTION: putative ethylene-responsive element binding protein. OSJNBb0089A17.16.

25

AAG60182.1 AC084763 Oryza sativa

DESCRIPTION: putative ethylene-responsive element binding protein. OSJNBa0027P10.12.

30

AAF63205.1 AF245119 Mesembryanthemum crystallinum

DESCRIPTION: AP2-related transcription factor. CDBP. stress induced transcription factor.

35

BAA97122.1 AB016264 Nicotiana glauca

DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.

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BAA87068.1 AB035270 Matricaria chamomilla

DESCRIPTION: ethylene-responsive element binding protein1 homolog. McEREBP1.

45

- 5 AAC50047.1 U89255 *Lycopersicon esculentum*
DESCRIPTION: binds the GCC box pathogenesis-related promoter element
DNA-binding protein. Pti4.
- 10 BAA07321.1 D38123 *Nicotiana tabacum*
DESCRIPTION: ERF1. ethylene-responsive transcription factor.
- 15 AAC49740.1 U89256 *Lycopersicon esculentum*
DESCRIPTION: binds the GCC box pathogenesis-related promoter element
DNA-binding protein. Pti5.
- 20 CAB93940.1 AJ238740 *Catharanthus roseus*
DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
protein. orca2.
- 25 AAC62619.1 AF057373 *Nicotiana tabacum*
DESCRIPTION: transcription factor. ethylene response element binding
protein 1. EREBP1.
- 30 CAB96899.1 AJ251249 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.
- 35 CAB96900.1 AJ251250 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.
- 40 AAB38748.1 U81157 *Nicotiana tabacum*
DESCRIPTION: S25-XP1 DNA binding protein.
- 45 CAC12822.1 AJ299252 *Nicotiana tabacum*
DESCRIPTION: AP2 domain-containing transcription factor. ap2.
- AAF05606.1 AF190770 *Oryza sativa*
DESCRIPTION: EREBP-like protein. tsh1. TSH1; induced by ethylene.
- AAC29516.1 U77655 *Solanum tuberosum*

DESCRIPTION: DNA binding protein homolog. STWAAEIRD.

- 5 AAF23899.1 AF193803 *Oryza sativa*
DESCRIPTION: transcription factor EREBP1. EREBP/AP2-like transcription factor.
- 10 BAB03248.1 AB037183 *Oryza sativa*
DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
- 15 BAA97123.1 AB016265 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
- 20 BAA76734.1 AB024575 *Nicotiana tabacum*
DESCRIPTION: ethylene responsive element binding factor.
- 25 AAD00708.1 U91857 *Stylosanthes hamata*
DESCRIPTION: ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.
- 30 AAC49741.1 U89257 *Lycopersicon esculentum*
DESCRIPTION: DNA-binding protein binds the GCC box pathogenesis-related promoter element. Pti6.
- 35 AAC14323.1 AF058827 *Nicotiana tabacum*
DESCRIPTION: TSI1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pti6.
- 40 CAB93939.1 AJ238739 *Catharanthus roseus*
DESCRIPTION: putative transcription factor. AP2-domain DNA-binding protein. orcal.
- 45 AAD45623.1 AF084185 *Brassica napus*
DESCRIPTION: dehydration responsive element binding protein. DNA binding

protein; DRE binding protein.

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DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar
to EREBP transcription factors.

10 AAG43549.1 AF211531 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar
to EREBP transcription factors.

15 AAK31271.1 AC079890 *Oryza sativa*
DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.

20 BAB21218.1 AP002913 *Oryza sativa*
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.24.

25 AAK01088.1 AF298230 *Hordeum vulgare*
DESCRIPTION: CBF1-like protein BCBF1. BCBF1. AP2 domain protein;
putative
DRE binding factor.

30 AAG59619.1 AF243384 *Oryza sativa*
DESCRIPTION: CRT/DRE binding factor. CBF. DREB.

35 BAB21211.1 AP002913 *Oryza sativa*
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.17.

40 AAK01089.1 AF298231 *Hordeum vulgare*
DESCRIPTION: CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE
binding factor.

40 111

45 AAF87216.1 AF231351 *Nicotiana tabacum*
DESCRIPTION: plastidic glucose 6-phosphate dehydrogenase. G6PDHP2.

CAA67782.1 X99405 *Nicotiana tabacum*

DESCRIPTION: glucose-6-phosphate dehydrogenase. G6PD.

AAB69317.1 AF012861 *Petroselinum crispum*

5 DESCRIPTION: plastidic glucose-6-phosphate dehydrogenase. pG6PDH.

CAB52708.1 AJ010712 *Solanum tuberosum*

10 DESCRIPTION: glucose-6-phosphate 1-dehydrogenase. g6pd.

CAB52685.1 AJ132346 *Dunaliella bioculata*

DESCRIPTION: plastidic glucose-6-phosphate dehydrogenase. g6PD.

15 CAA04994.1 AJ001772 *Nicotiana tabacum*

DESCRIPTION: glucose-6-phosphate dehydrogenase. TCG18.

20 CAA58775.1 X83923 *Solanum tuberosum*

DESCRIPTION: glucose-6-phosphate dehydrogenase.

CAA03941.1 AJ000184 *Spinacia oleracea*

25 DESCRIPTION: Glucose-6-phosphate dehydrogenase. G6PD.

CAA03939.1 AJ000182 *Spinacia oleracea*

30 DESCRIPTION: Glucose-6-phosphate dehydrogenase. G6PD.

CAA03940.1 AJ000183 *Spinacia oleracea*

DESCRIPTION: Glucose-6-phosphate dehydrogenase. G6PD.

35 AAB41552.1 U18238 *Medicago sativa* subsp. *sativa*
DESCRIPTION: glucose-6-phosphate dehydrogenase.

40 AAD11426.1 AF097663 *Mesembryanthemum crystallinum*
DESCRIPTION: cytoplasmic glucose-6-phosphate 1-dehydrogenase. G6PD.

AAB69319.1 AF012863 *Petroselinum crispum*

45 DESCRIPTION: cytosolic glucose-6-phosphate dehydrogenase 2. cG6PDH2.

CAA52442.1 X74421 Solanum tuberosum
DESCRIPTION: glucose-6-phosphate 1-dehydrogenase. g6pdh. homotetramer.

5

AAB69318.1 AF012862 Petroselinum crispum
DESCRIPTION: cytosolic glucose-6-phosphate dehydrogenase 1. cG6PDH1.

10

BAA97662.1 AB029454 Triticum aestivum
DESCRIPTION: glucose-6-phosphate dehydrogenase. g6pdh.

15

BAA97663.1 AB029455 Triticum aestivum
DESCRIPTION: glucose-6-phosphate dehydrogenase. g6pdh.

20

CAA04993.1 AJ001770 Nicotiana tabacum
DESCRIPTION: glucose-6-phosphate dehydrogenase. TCG9.

25

CAA04992.1 AJ001769 Nicotiana tabacum
DESCRIPTION: glucose-6-phosphate dehydrogenase. TCG6.

30

BAA97664.1 AB029456 Triticum aestivum
DESCRIPTION: glucose-6-phosphate dehydrogenase. g6pdh.

AAG23802.1 AF260736 Cucurbita pepo
DESCRIPTION: plastidic glucose-6-phosphate dehydrogenase.

35

CAB66330.1 AJ279688 Betula pendula
DESCRIPTION: glucose-6-phosphate dehydrogenase. g6pd.

40

BAA82155.1 AB011441 Triticum aestivum
DESCRIPTION: glucose-6-phosphate dehydrogenase. WESR5. salt-stress
responding gene.

45

CAA06200.1 AJ004900 Glycine max
DESCRIPTION: pentose phosphate pathway oxidoreductase generating
NADPH.
glucose-6-phosphate-dehydrogenase.

- CAA48611.1 X68652 *Raphanus sativus*
5 DESCRIPTION: hydroxymethylglutaryl-CoA reductase (NADPH). HMG2.
- CAA48610.1 X68651 *Raphanus sativus*
10 DESCRIPTION: hydroxymethylglutaryl-CoA reductase (NADPH). HMG1.
- AAC05089.1 AF038046 *Gossypium hirsutum*
15 DESCRIPTION: catalyzes the synthesis of mevalonate from hmg-coA.
3-hydroxy-3-methylglutaryl-coenzyme A reductase 2. hmg2. hmg-coA reductase
2; HMGR2.
- AAA33108.1 M96068 *Catharanthus roseus*
20 DESCRIPTION: hydroxymethylglutaryl-CoA reductase. HMGR.
- BAA36291.1 AB021862 *Cucumis melo*
25 DESCRIPTION: HMG-CoA reductase. Cm-HMGR. putative.
- AAB52551.1 U51985 *Solanum tuberosum*
DESCRIPTION: HMG-CoA reductase.
- 30 AAA93498.1 L01400 *Solanum tuberosum*
DESCRIPTION: convert HMG-CoA into mevalonate. hydroxymethylglutaryl
coenzyme A reductase. hmgr. putative.
- 35 AAB87727.1 U60452 *Nicotiana tabacum*
DESCRIPTION: hydroxy-methylglutaryl-coenzyme A reductase. HMGR1.
- CAA70440.1 Y09238 *Zea mays*
40 DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.
- CAA45181.1 X63649 *Nicotiana glauca*
45 DESCRIPTION: catalyzes synthesis of mevalonate.
3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR. endoplasmic
reticulum location.

- AAD28179.1 AF110383 *Capsicum annuum*
 DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase.
 5 HMGR2M.
 HMGR.
- AAB52552.1 U51986 *Solanum tuberosum*
 10 DESCRIPTION: HMG-CoA reductase.
- BAA93631.1 AB022690 *Solanum tuberosum*
 DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.HMG3.
 15
- AAB62581.1 U68072 *Lycopersicon esculentum*
 DESCRIPTION: 3-hydroxy-3-methylglutaryl CoA reductase 2. HMG2.
 20
- AAB69726.1 U72145 *Camptotheca acuminata*
 DESCRIPTION: converts HMGCoA to mevalonate. 3-hydroxy-3-methylglutaryl
 coenzyme a reductase. hmg3. HMGR.
 25
- AAB53748.1 U95816 *Oryza sativa*
 DESCRIPTION: 3-hydroxy-3-methylglutaryl-CoA reductase. HMGR.
- 30 BAB20771.1 AB041031 *Solanum tuberosum*
 DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. HMG2.
- AAB69727.1 U72146 *Camptotheca acuminata*
 35 DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. converts
 HMGCoA in mevalonate precursor for isoprenoid compounds; HMGR; hmg2;
 similar to protein encoded by GenBank Accession Number L10390.
- 40 AAD47596.1 AF142473 *Artemisia annua*
 DESCRIPTION: HMG-CoA reductase. HMGR1.
- AAA34169.1 M63642 *Lycopersicon esculentum*
 45 DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. hmg2.

- AAA68966.1 U14625 *Artemisia annua*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM4.
- 5 AAA33358.1 M74798 *Hevea brasiliensis*
DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
- 10 AAA68965.1 U14624 *Artemisia annua*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM1.
- 15 AAD08820.1 U43961 *Oryza sativa*
DESCRIPTION: 3-hydroxy-3-methylglutaryl=CoA reductase. HMGR.
- 20 AAA33360.1 M74800 *Hevea brasiliensis*
DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
- CAA92821.1 Z68504 *Oryza sativa*
DESCRIPTION: 3-hydroxy-3-methylglutaryl-CoA reductase.
- 25 AAC05088.1 AF038045 *Gossypium hirsutum*
DESCRIPTION: catalyzes the synthesis of mevalonate from hmg-coA.
3-hydroxy-3-methylglutaryl-coenzyme A reductase 1. hmgl. hmg-coA reductase
1; HMGR1.
- 30 AAC15475.1 AF034760 *Tagetes erecta*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.
- 35 AAC15476.1 AF034761 *Tagetes erecta*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.
- 40 CAA38469.1 X54659 *Hevea brasiliensis*
DESCRIPTION: hydroxymethylglutaryl-CoA reductase. HMGR1.
- 45 CAA38467.1 X54657 *Hevea brasiliensis*
DESCRIPTION: hydroxymethylglutaryl-CoA reductase. HMGR1.

- 5 AAD38873.1 AF110382 *Oryza sativa*
DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR3G.
HMG-CoA reductase.
- 10 AAA33040.1 L10390 *Camptotheca acuminata*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coA reductase.
- 15 AAD03789.1 U43711 *Morus alba*
DESCRIPTION: catalyzes the final step in mevalonate pathway.
3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR.
- 20 AAA21720.1 L28995 *Oryza sativa*
DESCRIPTION: conversion of hydroxymethylglutaryl coenzyme A to
mevalonate. 3-hydroxy-3-methylglutaryl coenzyme A reductase. putative.
- 25 AAC72378.1 AF096838 *Solanum tuberosum*
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.
- 30 AAB04043.1 L40938 *Lycopersicon esculentum*
DESCRIPTION: HMGR CoA reductase. HMGR1.
- 35 CAA38468.1 X54658 *Hevea brasiliensis*
DESCRIPTION: hydroxymethylglutaryl-CoA reductase. HMGR2.
- 40 CAA52787.1 X74783 *Lithospermum erythrorhizon*
DESCRIPTION: 3-hydroxy-3-methyl glutaryl coenzyme A reductase. Lehmgr1.
- 45 AAD09278.1 U97683 *Glycine max*
DESCRIPTION: catalyzes the synthesis of mevalonate, the specific
precursor of all isoprenoid compounds present in plants.
3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMG-CoA reductase.
- AAG43469.1 AF196964 *Bixa orellana*
DESCRIPTION: catalyzes mevalonate synthesis from hmg-CoA.
3-hydroxy-3-methylglutaryl-coenzyme A reductase.

BAA09705.1 D63389 Cucumis sativus
DESCRIPTION: 3-hydroxy-3-methylglutaryl CoA reductase.

5

AAB47161.1 S82272 Gossypium barbadense
DESCRIPTION: 3-hydroxy-3-methylglutaryl coenzyme A reductase.
/gene="3-hydroxy-3-methylglutaryl coenzyme A reductase,. This
sequence comes from Fig. 2; 3-hydroxy-3-methylglutaryl CoA reductase;
10 HMGR.

AAA33359.1 M74799 Hevea brasiliensis
DESCRIPTION: 3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.

15

AAC37432.1 L34825 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

20

AAC37434.1 L34827 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

25

AAC37431.1 L34823 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

30

AAC37433.1 L34826 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

35

AAC37435.1 L34828 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

40

AAC37436.1 L34829 Solanum tuberosum
DESCRIPTION: HMG-CoA reductase. hmg1 gene family.

113

AAC49676.1 U77345 Zea mays
DESCRIPTION: lethal leaf-spot 1. lls1. Allele: wild-type; LLS1; similar
to bacterial ring-hydroxylating dioxygenase.

45

AAG03051.1 AF284781 *Oryza sativa*
DESCRIPTION: LLS1 protein. Lls1.

115

5

BAA82379.1 AP000367 *Oryza sativa*
DESCRIPTION: Similar to putative receptor kinase. (AC002332).

10 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).

15

AAG25966.1 AF302082 *Nicotiana tabacum*
DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase;
transcript abundance decreases rapidly after cytokinin treatment.

20

BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

25

AAC27894.1 AF023164 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. Itk1.

30

AAC27895.1 AF023165 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 2. Itk2.

35

BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

40

BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A*Arabidopsis thaliana*.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

45

BAB39409.1 AP002901 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).

- 5 AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.
- 10 CAB41878.1 Y18259 *Brassica oleracea*
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.
- 15 AAG59657.1 AC084319 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
- 20 BAB03429.1 AP002817 *Oryza sativa*
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
- 25 BAB07999.1 AP002525 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST C22619(S11214).
- 30 AAK00425.1 AC069324 *Oryza sativa*
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- 35 CAB41879.1 Y18260 *Brassica oleracea*
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.
- 40 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- 45 AAD21872.1 AF078082 *Phaseolus vulgaris*
DESCRIPTION: receptor-like protein kinase homolog RK20-1.
- CAA97692.1 Z73295 *Catharanthus roseus*
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.

CAA74661.1 Y14285 Brassica oleracea
DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain:
1343-1411; intracellular kinase domain: 1412-2554.

5

AAC23542.1 U20948 Ipomoea trifida
DESCRIPTION: receptor protein kinase. IRK1.

10

AAG16628.1 AY007545 Brassica napus
DESCRIPTION: protein serine/threonine kinase BNK1.

15

BAA94509.1 AB041503 Populus nigra
DESCRIPTION: protein kinase 1. PnPK1.

20

BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.

25

CAA47962.1 X67733 Zea mays
DESCRIPTION: receptor-like protein kinase. PK1.

CAA67145.1 X98520 Brassica oleracea
DESCRIPTION: receptor-like kinase. SFR2.

30

AAB09771.1 U67422 Zea mays
DESCRIPTION: CRINKLY4 precursor. cr4. receptor kinase homolog.

35

CAA74662.1 Y14286 Brassica oleracea
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane
domain: 1347-1412; intracellular kinase domain: from 1413.

40

BAA94510.1 AB041504 Populus nigra
DESCRIPTION: protein kinase 2. PnPK2.

45

AAB93834.1 U82481 Zea mays
DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
kinase; serine/threonine protein kinase.

CAA73133.1 Y12530 Brassica oleracea
DESCRIPTION: serine /threonine kinase. ARLK.

5

BAA06538.1 D31737 Nicotiana tabacum
DESCRIPTION: protein-serine/threonine kinase.

10 AAF43496.1 AF131222 Lophopyrum elongatum
DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by
salt stress, osmotic stress, and ABA treatment.

15 AAK11674.1 AF339747 Lophopyrum elongatum
DESCRIPTION: protein kinase. ESI47.

20 BAB21001.1 AB054061 Brassica rapa
DESCRIPTION: S locus receptor kinase. SRK22.

25 CAB51480.1 Y14600 Sorghum bicolor
DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates
in mesophyll cells.

30 BAA87852.1 AP000816 Oryza sativa
DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).

35 BAA92221.1 AP001278 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana chromosome II BAC F12L6
genomic sequence, putative protein kinase. (AC004218).

40 BAA78764.1 AB023482 Oryza sativa
DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region
of
the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein
tyrosine-serine-threonine kinase.(D12522).

45 BAA90808.1 AP001168 Oryza sativa
DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).

BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.

5

AAB47422.1 U59318 Lycopersicon esculentum
DESCRIPTION: serine/threonine protein kinase Fen. fen. allele of Fen,
fenthion sensitivity gene from tomato.

10

BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).

117

15

AAA34002.1 M67449 Glycine max
DESCRIPTION: protein kinase. PK6.

20

AAG31141.1 AF305911 Oryza sativa
DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
Arabidopsis
thaliana EDR1.

25

AAG31142.1 AF305912 Hordeum vulgare
DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
Arabidopsis
thaliana EDR1.

30

CAC09580.1 AJ298992 Fagus sylvatica
DESCRIPTION: Absciscic acid (ABA) and calcium induced protein kinase.
protein kinase (PK). pk1.

35

CAA06334.1 AJ005077 Lycopersicon esculentum
DESCRIPTION: protein kinase. TCTR2 protein. TCTR2.

40

AAD10057.1 AF110519 Lycopersicon esculentum
DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase
homolog; ethylene and fruit ripening inducible CTR1-like protein kinase;
TCTR1v.

45

- 5 AAD10056.1 AF110518 *Lycopersicon esculentum*
DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.
- 10 AAD46406.1 AF096250 *Lycopersicon esculentum*
DESCRIPTION: ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to *Arabidopsis thaliana* negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.
- 15 CAA73722.1 Y13273 *Lycopersicon esculentum*
DESCRIPTION: putative protein kinase.
- 20 AAK11734.1 AY027437 *Arachis hypogaea*
DESCRIPTION: serine/threonine/tyrosine kinase.
- 25 AAK30005.1 AY029067 *Rosa* hybrid cultivar
DESCRIPTION: CTR2 protein kinase.
- 30 AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.
- 35 CAA73068.1 Y12465 *Sorghum bicolor*
DESCRIPTION: serine/threonine kinase. SNFL2.
- 40 CAA61510.1 X89226 *Oryza sativa*
DESCRIPTION: leucine-rich repeat/receptor protein kinase. Irk2.
- 45 BAA83688.1 AB011967 *Oryza sativa*
DESCRIPTION: OsPK4. OsPK4. protein kinase.
- AAF34436.1 AF172282 *Oryza sativa*
DESCRIPTION: similar to mitogen-activated protein kinases. DUPR11.32.
- AAF22219.1 AF141378 *Zea mays*

DESCRIPTION: protein kinase PK4. ZmPK4.

BAA87852.1 AP000816 Oryza sativa

5 DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).

BAA92221.1 AP001278 Oryza sativa

10 DESCRIPTION: Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).

AAF91323.1 AF244889 Glycine max

15 DESCRIPTION: receptor-like protein kinase 2. RLK2. GmRLK2.

BAB40094.1 AP003210 Oryza sativa

20 DESCRIPTION: putative receptor protein kinase. OSJNBa0010K01.7.

AAF91324.1 AF244890 Glycine max

DESCRIPTION: receptor-like protein kinase 3. RLK3. GmRLK3.

25 BAA34675.1 AB011670 Triticum aestivum

DESCRIPTION: wpk4 protein kinase. wpk4.

BAA92970.1 AP001551 Oryza sativa

30 DESCRIPTION: Similar to Arabidopsis thaliana chromosome 4 BAC clone F28A21 ; putative protein kinase. (AL035526).

AAF91322.1 AF244888 Glycine max

35 DESCRIPTION: receptor-like protein kinase 1. RLK1. GmRLK1.

BAB07999.1 AP002525 Oryza sativa

40 DESCRIPTION: putative protein kinase. P0462H08.22. contains EST C22619(S11214).

BAB03429.1 AP002817 Oryza sativa

45 DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).

- CAA73067.1 Y12464 Sorghum bicolor
DESCRIPTION: serine/threonine kinase. SNFL1.
- 5
- AAF59906.1 AF197947 Glycine max
DESCRIPTION: receptor protein kinase-like protein. CLV1B.
- 10
- AAF59905.1 AF197946 Glycine max
DESCRIPTION: receptor protein kinase-like protein. CLV1A.
- 15
- BAB16918.1 AP002863 Oryza sativa
DESCRIPTION: putative protein kinase. P0005A05.22.
- 20
- AAC36318.1 AF053127 Malus x domestica
DESCRIPTION: leucine-rich receptor-like protein kinase. LRPKml.
- 25
- BAA83689.1 AB011968 Oryza sativa
DESCRIPTION: OsPK7. OsPK7. protein kinase.
- 30
- CAA74646.1 Y14274 Sorghum bicolor
DESCRIPTION: putative serine/threonine protein kinase. SNFL3.
- 35
- BAA95893.1 AP002071 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana wak4 gene; wall-associated kinase 4. (AJ009695).
- 40
- BAA92954.1 AP001551 Oryza sativa
DESCRIPTION: Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
- 45
- AAC83393.1 U83625 Zea mays
DESCRIPTION: protein kinase ZmMEK1. mitogen-activated; ERK-activating protein kinase (MEK) homolog.
- BAA92972.1 AP001551 Oryza sativa

DESCRIPTION: ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4 BAC clone F6I18 ; putative protein kinase. (AL022198).

5

BAB18292.1 AP002860 Oryza sativa

DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

10

BAB40015.1 AP003021 Oryza sativa

DESCRIPTION: putative wall-associated kinase 1. P0503E05.18.

15

BAA05648.1 D26601 Nicotiana tabacum

DESCRIPTION: protein kinase.

20

AAC27489.1 AF077130 Oryza sativa

DESCRIPTION: receptor-like protein kinase.

25

AAC02535.1 AF044260 Oryza sativa

DESCRIPTION: receptor serine/threonine kinase. protein kinase.

30

AAG40578.1 AF216314 Oryza sativa

DESCRIPTION: MAP kinase kinase 1. protein kinase; MEK1.

CAA08997.1 AJ010093 Brassica napus

DESCRIPTION: MAP3K beta 1 protein kinase. MAP3K beta 1.

118

35

AAD21199.1 AF127797 Capsicum chinense

DESCRIPTION: putative bZIP DNA-binding protein.

40

CAC00658.1 AJ292745 Petroselinum crispum

DESCRIPTION: bZIP type transcription factor. common plant regulatory factor 7. cprf7.

45

CAC00657.1 AJ292744 Petroselinum crispum

DESCRIPTION: bZIP type transcription factor. common plant regulatory factor 6. cprf6.

- CAA74023.1 Y13676 *Antirrhinum majus*
DESCRIPTION: bZIP DNA-binding protein.
5
- CAA74022.1 Y13675 *Antirrhinum majus*
DESCRIPTION: bZIP DNA-binding protein.
10
- BAA22204.1 D63951 *Nicotiana tabacum*
DESCRIPTION: TBZ17. tbz17. bZIP protein.
15
- AAD55394.1 AF176641 *Lycopersicon esculentum*
DESCRIPTION: bZIP DNA-binding protein.
20
- CAA44607.1 X62745 *Zea mays*
DESCRIPTION: ocs-binding factor 1. OBF1.
25
- AAK25822.1 AF350505 *Phaseolus vulgaris*
DESCRIPTION: bZip transcription factor.
30
- AAK01953.1 AY026054 *Phaseolus acutifolius*
DESCRIPTION: bZIP. transcription factor.
35
- CAA71687.1 Y10685 *Glycine max*
DESCRIPTION: bZIP DNA-binding protein. G/HBF-1. G/HBF-1.
40
- AAC37418.1 L34551 *Oryza sativa*
DESCRIPTION: transcriptional activator protein. RITA-1.
45
- BAA36492.1 AB021736 *Oryza sativa*
DESCRIPTION: bZIP protein.
- BAA11431.1 D78609 *Oryza sativa*
DESCRIPTION: bZIP protein.

CAA41453.1 X58577 Petroselinum crispum
DESCRIPTION: DNA-binding protein; bZIP type. CPRF2.

5 CAA71768.1 Y10809 Petroselinum crispum
DESCRIPTION: bZIP DNA-binding protein. CPRF4a.

AAD42938.1 AF084972 Catharanthus roseus
10 DESCRIPTION: G-Box binding protein 2. GBF2. basic leucine zipper;
trans-regulatory factor.

AAC49556.1 U04295 Oryza sativa
15 DESCRIPTION: DNA-binding factor of bZIP class. osZIP-1a.

BAA07289.1 D38111 Triticum aestivum
20 DESCRIPTION: transcription factor HBP-1a(17).

CAA71795.1 Y10834 Hordeum vulgare
DESCRIPTION: bZIP transcription factor 2. Blz2.
25

CAA70216.1 Y09013 Triticum aestivum
DESCRIPTION: transcriptional activator. SPA.

30 CAA40101.1 X56781 Triticum aestivum
DESCRIPTION: transcription factor. HBP-1a. la-17.

AAA80169.1 U10270 Zea mays
35 DESCRIPTION: G-box binding factor 1. GBF1.

CAA11499.1 AJ223624 Spinacia oleracea
40 DESCRIPTION: basic leucine zipper protein. bZIP.

AAC49474.1 U41817 Phaseolus vulgaris
DESCRIPTION: regulator of MAT2. ROM2. Repressor of seed-specific lectin
(phytohemagglutinin) gene; bZIP transcriptional repressor.
45

AAB40291.1 U42208 *Oryza sativa*
DESCRIPTION: OSBZ8. G-box binding protein; GBF type bZIP protein.

- 5 BAA02304.1 D12920 *Triticum aestivum*
DESCRIPTION: transcription factor HBP-1a(c14).

119

- 10 BAA96200.1 AP002093 *Oryza sativa*
DESCRIPTION: EST D40368(S2303) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome II putative cytochrome P450 (AC004077).

- 15 BAA96158.1 AP002092 *Oryza sativa*
DESCRIPTION: EST D40368(S2303) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome II BAC T31E10; putative cytochrome P450 (AC004077).

20

- BAA96196.1 AP002093 *Oryza sativa*
DESCRIPTION: ESTs AU086027(S2303),D40339(S2251) correspond to a region of
25 the predicted gene. Similar to *Arabidopsis thaliana* chromosome II BAC T31E10; putative cytochrome P450 (AC004077).

- BAA96154.1 AP002092 *Oryza sativa*
30 DESCRIPTION: ESTs AU086027(S2303),D40339(S2251) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome II BAC T31E10; putative cytochrome P450 (AC004077).

35

- BAA96193.1 AP002093 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC T31E10; putative cytochrome P450 (AC004077).

40

- BAA96151.1 AP002092 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC T31E10; putative cytochrome P450 (AC004077).

45

- BAA96194.1 AP002093 *Oryza sativa*

DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC T31E10; putative cytochrome P450 (AC004077).

- 5 BAA96152.1 AP002092 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC T31E10; putative cytochrome P450 (AC004077).
- 10 AAG41777.1 AF212991 *Cucurbita maxima*
DESCRIPTION: ent-kaurene oxidase. CYP88A2. cytochrome P450; similar to maize Dwarf3 protein.
- 15 AAK11616.1 AF326277 *Hordeum vulgare*
DESCRIPTION: ent-kaurenoic acid oxidase. KAO1. cytochrome P450; CYP88A; HvKAO1.
- 20 AAK00946.1 AF318211 *Taxus cuspidata*
DESCRIPTION: 5-alpha-taxadienol-10-beta-hydroxylase. cytochrome P450-like protein.
- 25 AAC49659.1 U74319 *Sorghum bicolor*
DESCRIPTION: obtusifolios 14-alpha demethylase CYP51. CYP51. cytochrome P450 catalyzing the 14-alpha demethylation of obtusifolios in plants.
- 30 AAA17746.1 L19075 *Catharanthus roseus*
DESCRIPTION: cytochrome P450. CYP72C. putative.
- 35 AAA33106.1 L10081 *Catharanthus roseus*
DESCRIPTION: cytochrome P-450 protein. CYP72. putative; CYP72 protein.
- 40 AAA17732.1 L19074 *Catharanthus roseus*
DESCRIPTION: cytochrome P450. CYP72B.
- 45 CAB56503.1 AJ238612 *Catharanthus roseus*
DESCRIPTION: cytochrome P450.

AAB17070.1 U54770 *Lycopersicon esculentum*
DESCRIPTION: cytochrome P450 homolog. dwarf.

5 CAB41490.1 AJ238439 *Cicer arietinum*
DESCRIPTION: cytochrome P450 monooxygenase. cyp81E3v2.

BAB19089.1 AP002744 *Oryza sativa*
10 DESCRIPTION: putative cytochrome P450. P0006C01.31. contains ESTs
D24685(R2374),AU031882(R2374).

AAD44150.1 AF124815 *Mentha spicata*
15 DESCRIPTION: cytochrome p450.

BAB19110.1 AP002839 *Oryza sativa*
20 DESCRIPTION: putative cytochrome P450. P0688A04.16. contains ESTs
D24685(R2374),AU031882(R2374).

BAA74465.1 AB022732 *Glycyrrhiza echinata*
25 DESCRIPTION: cytochrome P450. CYP Ge-31.

BAA22422.1 AB001379 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP81E1.

30 CAA10067.1 AJ012581 *Cicer arietinum*
DESCRIPTION: cytochrome P450. cyp81E3.

35 BAB40322.1 AB036772 *Triticum aestivum*
DESCRIPTION: cytochrome P450. N-1.

CAB43505.1 AJ239051 *Cicer arietinum*
40 DESCRIPTION: cytochrome P450. cyp81E2.

CAB56742.1 AJ249800 *Cicer arietinum*
45 DESCRIPTION: cytochrome P450 monooxygenase. cyp81E5.

AAF89209.1 AF279252 *Vigna radiata*
DESCRIPTION: cytochrome P450. CipCYP.

5 BAA93634.1 AB025016 *Lotus japonicus*
DESCRIPTION: cytochrome P450.

10 BAB19107.1 AP002839 *Oryza sativa*
DESCRIPTION: putative cytochrome P450. P0688A04.13. contains ESTs
AU100635(C10787),D22354(C10787).

15 BAB19086.1 AP002744 *Oryza sativa*
DESCRIPTION: putative cytochrome P450. P0006C01.28. contains ESTs
AU100635(C10787),D22354(C10787).

20 CAA04116.1 AJ000477 *Helianthus tuberosus*
DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

25 CAA04117.1 AJ000478 *Helianthus tuberosus*
DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l.
chimeric sequence (from 5'-race).

30 CAA71517.1 Y10493 *Glycine max*
DESCRIPTION: putative cytochrome P450.

BAB21156.1 AP002899 *Oryza sativa*
DESCRIPTION: putative cytochrome P450. P0456A01.12.

35 AAG13498.1 AC068924 *Oryza sativa*
DESCRIPTION: putative cytochrome P450. OSJNBa0026L12.20.

40 AAF34534.1 AF195813 *Lupinus albus*
DESCRIPTION: isoflavone synthase 1. ifs1. cytochrome P450.

45 CAA83941.1 Z33875 *Mentha x piperita*
DESCRIPTION: cytochrome P-450 oxidase.

AAF34533.1 AF195812 Pisum sativum
DESCRIPTION: isoflavone synthase 1. ifs1. cytochrome P450.

5

AAF45142.1 AF195818 Glycine max
DESCRIPTION: isoflavone synthase 1. ifs1. cytochrome P450.

120

10

CAB42052.1 AJ242045 Lycopersicon esculentum
DESCRIPTION: nicotianamine synthase. chln.

15

BAA74581.1 AB011264 Hordeum vulgare
DESCRIPTION: nicotianamine synthase 3. hvnas3.

20

AAD32651.1 AF136942 Hordeum vulgare
DESCRIPTION: nicotianamine synthase 2. nashor2.

25

BAA74582.1 AB011265 Hordeum vulgare
DESCRIPTION: nicotianamine synthase 2. hvnas2.

30

BAB17824.1 AB023819 Oryza sativa
DESCRIPTION: nicotianamine synthase 3. osnas3.

35

BAA74583.1 AB011266 Hordeum vulgare
DESCRIPTION: nicotianamine Synthase 4. hvnas4.

40

BAA74586.1 AB011269 Hordeum vulgare
DESCRIPTION: nicotianamine Synthase 6. hvnas6.

45

BAA74587.1 AB019525 Hordeum vulgare
DESCRIPTION: nicotianamine synthase 7. hvnas7.

BAB17826.1 AB046401 Oryza sativa
DESCRIPTION: nicotianamine synthase 2. OsNAS2.

5 BAB17823.1 AB023818 Oryza sativa
DESCRIPTION: nicotianamine synthase 2. osnas2.

10 BAB17825.1 AB046401 Oryza sativa
DESCRIPTION: nicotianamine synthase 1. OsNAS1.

15 BAA74588.2 AB021746 Oryza sativa
DESCRIPTION: nicotianamine synthase 1. osnas1.

BAA74580.1 AB010086 Hordeum vulgare
DESCRIPTION: nicotianamine synthase 1. hvnas1.

20 BAA74585.1 AB011268 Hordeum vulgare
DESCRIPTION: nicotianamine Synthase 5-2. hvnas5-2.

25 BAA74584.1 AB011267 Hordeum vulgare
DESCRIPTION: nicotianamine synthase 5-1. hvnas5-1.

122

30 AAD01804.1 AF026480 Dianthus caryophyllus
DESCRIPTION: lipase. lipid-protein-particle associated.

35 BAB39417.1 AP002901 Oryza sativa
DESCRIPTION: putative lipase. P0456F08.17. contains ESTs
C99390(E11001),AU101109(E0858),AU101332(E11001).

40 AAB07724.1 U55867 Ipomoea nil
DESCRIPTION: Pn47p. lipase-like protein.

45 AAK31273.1 AC079890 Oryza sativa
DESCRIPTION: putative lipase. OSJNBb0089A17.13.

123

BAA21923.1 AB006601 Petunia x hybrida
DESCRIPTION: ZPT2-14. C2H2 zinc finger protein, 2 finger.

5

BAA21922.1 AB006600 Petunia x hybrida
DESCRIPTION: ZPT2-13. C2H2 zinc finger protein, 2finger.

10

BAA21921.1 AB006599 Petunia x hybrida
DESCRIPTION: ZPT2-12. C2H2 zinc finger protein, 2 finger.

15

BAA19110.1 AB000451 Petunia x hybrida
DESCRIPTION: PETHy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.

20

BAA21926.1 AB006604 Petunia x hybrida
DESCRIPTION: ZPT2-9. C2H2 zinc finger protein, 2 finger.

25

BAA21925.1 AB006603 Petunia x hybrida
DESCRIPTION: ZPT2-8. C2H2 zinc finger protein, 2 finger.

30

BAA21924.1 AB006602 Petunia x hybrida
DESCRIPTION: ZPT2-7. C2H2 zinc finger protein, 2finger.

BAA21920.1 AB006598 Petunia x hybrida
DESCRIPTION: ZPT2-11. C2H2 zinc finger protein, 2finger.

35

CAA60828.1 X87374 Pisum sativum
DESCRIPTION: putative zinc finger protein.

40

BAA19111.1 AB000452 Petunia x hybrida
DESCRIPTION: PETHy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.

45

CAB77055.1 Y18788 Medicago sativa
DESCRIPTION: putative TFIIIA (or kruppel)-like zinc finger protein.

BAA96071.1 AB035133 Petunia x hybrida

DESCRIPTION: C2H2 zinc-finger protein ZPT3-3. ZPT3-3.

5 BAA21927.1 AB006605 Petunia x hybrida
DESCRIPTION: ZPT3-3. C2H2 zinc finger protein, 3 finger.

10 BAA96070.1 AB035132 Petunia x hybrida
DESCRIPTION: C2H2 zinc-finger protein ZPT2-10. PEThy;ZPT2-10.

15 BAA21919.1 AB006597 Petunia x hybrida
DESCRIPTION: ZPT2-10. C2H2 zinc finger protein, 2 finger.

20 AAK01713.1 AF332876 Oryza sativa
DESCRIPTION: zinc finger transcription factor ZF1.

25 AAC06243.1 AF053077 Nicotiana tabacum
DESCRIPTION: transcription factor. osmotic stress-induced zinc-finger
protein. zfp.

30 BAA05079.1 D26086 Petunia x hybrida
DESCRIPTION: zinc-finger protein.

35 BAA05078.1 D26085 Petunia x hybrida
DESCRIPTION: zinc-finger DNA binding protein.

40 AAB39638.1 U68763 Glycine max
DESCRIPTION: putative transcription factor. SCOF-1. scof-1. zinc-finger
protein.

45 BAA05076.1 D26083 Petunia x hybrida
DESCRIPTION: zinc-finger DNA binding protein.

BAA05077.1 D26084 Petunia x hybrida
DESCRIPTION: zinc-finger DNA binding protein.

45 BAA21928.1 AB006606 Petunia x hybrida

DESCRIPTION: ZPT4-4. C2H2 zinc finger protein, 4 finger.

5 BAA19114.1 AB000455 Petunia x hybrida
DESCRIPTION: PETHy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.

10 AAD26942.1 AF119050 Datisca glomerata
DESCRIPTION: zinc-finger protein 1. zfp1. DgZFP1.

15 BAA19112.1 AB000453 Petunia x hybrida
DESCRIPTION: PETHy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.

20 AAB53260.1 U76554 Brassica rapa
DESCRIPTION: transcription factor. zinc-finger protein-1. BR42.

25 AAB53261.1 U76555 Brassica rapa
DESCRIPTION: zinc-finger protein BcZFP1. BcZFP1(3-2z).

30 BAA19926.1 AB000456 Petunia x hybrida
DESCRIPTION: PETHy; ZPT4-2. C2H2 zinc finger protein, 4 finger.

126

35 CAA10134.1 AJ012693 Cicer arietinum
DESCRIPTION: basic blue copper protein.

40 CAB65280.1 AJ248323 Medicago sativa subsp. x varia
DESCRIPTION: basic blue protein. babl.

45 AAC32448.1 U76296 Spinacia oleracea
DESCRIPTION: plantacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytocyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Plantacyanins; non-glycosylated.

50 AAF66243.1 AF243181 Lycopersicon esculentum
DESCRIPTION: plantacyanin. naturally occurring cupredoxin with a Val

residue in the position of the axial ligand Met; member of the plantacyanin subfamily of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins.

- 5
AAD10251.1 AF031195 *Triticum aestivum*
DESCRIPTION: blue copper-binding protein homolog. S85.
- 10
AAF66242.1 AF243180 *Lycopersicon esculentum*
DESCRIPTION: dicyanin. binuclear blue copper protein; contains two stellacyanins linked together.
- 15
CAA80963.1 Z25471 *Pisum sativum*
DESCRIPTION: blue copper protein.
- 20
AAC64163.1 AF093537 *Zea mays*
DESCRIPTION: blue copper protein. similar to pea blue copper protein in GenBank Accession Number Z25471.
- 25
AAC32421.1 U65511 *Cucumis sativus*
DESCRIPTION: putative oxygen activation and/or lignin formation. stellacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Stellacyanins; similar to *Rhus vernicifera* stellacyanin: SwissProt Accession Number P00302; similar to umecyanin: SwissProt Accession Number P42849; similar to mavicyanin; SwissProt Accession Number P80728; similar to BCB encoded by GenBank Accession Number Z15058; similar to F18A8.9, encoded by GenBank Accession Number AC003105; similar to F7F1.27 encoded by GenBank Accession Number AC004669; similar to F9D12.16 encoded by GenBank Accession Number AF077407; glycoprotein.
- 35
- 127

- 40
AAA17000.1 L08632 *Glycine max*
DESCRIPTION: pyruvate kinase.
- 45
CAA37727.1 X53688 *Solanum tuberosum*
DESCRIPTION: pyruvate kinase.

Figure 1 consists of 12 histograms arranged vertically, labeled $k=0$ through $k=11$. Each histogram shows the frequency of the number of non-zero elements in the vector x_k . The x-axis for all plots is 'Number of non-zero elements' with ticks at 0, 20, 40, 60, 80, and 100. The y-axis is 'Frequency' with ticks at 0, 2, 4, 6, 8, and 10. The distributions are as follows:

- $k=0$: A single bar at 0 with frequency 10.
- $k=1$: A single bar at 1 with frequency 10.
- $k=2$: A single bar at 2 with frequency 10.
- $k=3$: A single bar at 3 with frequency 10.
- $k=4$: A single bar at 4 with frequency 10.
- $k=5$: A single bar at 5 with frequency 10.
- $k=6$: A single bar at 6 with frequency 10.
- $k=7$: A single bar at 7 with frequency 10.
- $k=8$: A single bar at 8 with frequency 10.
- $k=9$: A single bar at 9 with frequency 10.
- $k=10$: A single bar at 10 with frequency 10.
- $k=11$: A single bar at 10 with frequency 10.

biosynthesis. (S)-N-methylcoclaurine 3'-hydroxylase. CYP80B1. cytochrome P450-dependent monooxygenase.

5 AAC39452.1 AF014800 *Eschscholzia californica*
DESCRIPTION: hydroxylase involved in the biosynthesis of
tetrahydrobenzylisoquinoline alkaloids in plants. (S)-N-methylcoclaurine
3'-hydroxylase. CYP80B1. cytochrome P-450-dependent monooxygenase;
CYP80B1v1.

10

AAC39453.1 AF014801 *Eschscholzia californica*
DESCRIPTION: hydroxylase involved in the biosynthesis of
tetrahydrobenzylisoquinoline alkaloids in plants. (S)-N-methylcoclaurine
15 3'-hydroxylase. CYP80B1. cytochrome P-450-dependent monooxygenase;
CYP80B1v2.

AAA32913.1 M32885 *Persea americana*
20 DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).

AAA19701.1 L24438 *Thlaspi arvense*
25 DESCRIPTION: cytochrome P450.

CAA50648.1 X71657 *Solanum melongena*
DESCRIPTION: P450 hydroxylase.

30

AAG34695.1 AF313492 *Matthiola incana*
DESCRIPTION: putative cytochrome P450.

35 AAG44132.1 AF218296 *Pisum sativum*
DESCRIPTION: cytochrome P450. P450 isolog.

BAA12159.1 D83968 *Glycine max*
40 DESCRIPTION: Cytochrome P-450 (CYP93A1).

AAC48987.1 U09610 *Berberis stolonifera*
DESCRIPTION: cytochrome P-450 CYP80.

45

AAD56282.1 AF155332 *Petunia x hybrida*
DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

5 AAC32274.1 AF081575 *Petunia x hybrida*
DESCRIPTION: flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.

10 AAB17562.1 U72654 *Eustoma grandiflorum*
DESCRIPTION: flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.

15 BAA84916.1 AB032833 *Cicer arietinum*
DESCRIPTION: cytochrome P450. CYP76D1.

AAB94588.1 AF022459 *Glycine max*
DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.

20 BAB40324.1 AB037245 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-2.

25 BAB40323.1 AB037244 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-1.

30 CAA50155.1 X70824 *Solanum melongena*
DESCRIPTION: flavonoid hydroxylase (P450). CYP75.

35 AAC39318.1 AF029858 *Sorghum bicolor*
DESCRIPTION: second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p-hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.

40 CAB56503.1 AJ238612 *Catharanthus roseus*
DESCRIPTION: cytochrome P450.

45 CAA71514.1 Y10490 *Glycine max*
DESCRIPTION: putative cytochrome P450.

BAA84071.1 AB028151 *Antirrhinum majus*
DESCRIPTION: flavone synthase II. cytochrome P450. AFNS2.

5

CAA70575.1 Y09423 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A5.

10 CAA70576.1 Y09424 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A6.

15 CAA71513.1 Y10489 *Glycine max*
DESCRIPTION: putative cytochrome P450.

20 BAA84072.1 AB028152 *Torenia hybrida*
DESCRIPTION: flavone synthase II. cytochrome P450. TFNS5.

CAA71516.1 Y10492 *Glycine max*
DESCRIPTION: putative cytochrome P450.

25 BAA13076.1 D86351 *Glycine max*
DESCRIPTION: cytochrome P-450 (CYP93A2).

30 CAA71517.1 Y10493 *Glycine max*
DESCRIPTION: putative cytochrome P450.

132

35 CAB55396.1 AL117264 *Oryza sativa*
DESCRIPTION: zwh12.1. similar to Arabidopsis putative
UDP-galactase-4-epimerase (AC007060); Method: conceptual translation with
partial peptide sequencing.

40 133

AAG43835.1 AF213455 *Zea mays*
DESCRIPTION: protein phosphatase type-2C. pp2c-1. PP2C-1.

45

AAG13599.1 AC051633 *Oryza sativa*

DESCRIPTION: putative protein phosphatase-2C. OSJNBb0015I11.26.

AAG46118.1 AC073166 *Oryza sativa*

5 DESCRIPTION: putative protein phosphatase-2C. OSJNBb0064P21.12. tRNA-Lys.

BAB12036.1 AP002820 *Oryza sativa*

10 DESCRIPTION: putative protein phosphatase. P0702D12.18.

AAC36698.1 AF075580 *Mesembryanthemum crystallinum*

15 DESCRIPTION: protein phosphatase-2C. PP2C.

CAC10359.1 AJ277087 *Nicotiana tabacum*

20 DESCRIPTION: protein phosphatase 2C. PP2C2.

CAB90633.1 AJ277743 *Fagus sylvatica*

25 DESCRIPTION: protein phpsphatase 2C (PP2C). pp2C1. ABA-induced protein.

CAC10358.1 AJ277086 *Nicotiana tabacum*

30 DESCRIPTION: protein phosphatase 2C. PP2C1.

CAA72341.1 Y11607 *Medicago sativa*

35 DESCRIPTION: protein phosphatase 2C. MP2C.

AAC36697.1 AF075579 *Mesembryanthemum crystallinum*

40 DESCRIPTION: protein phosphatase-2C. PP2C.

CAB61839.1 AJ242803 *Sporobolus stapfianus*

45 DESCRIPTION: putative serine/threonine phosphatase type 2c.

AAC36700.1 AF075582 *Mesembryanthemum crystallinum*

50 DESCRIPTION: protein phosphatase-2C. PP2C.

AAD17804.1 AF092431 *Lotus japonicus*

55 DESCRIPTION: nodule-enhanced protein phosphatase type 2C. NPP2C1.

- 5 AAD17805.1 AF092432 *Lotus japonicus*
DESCRIPTION: protein phosphatase type 2C. PP2C2.
- 10 CAC09575.1 AJ298987 *Fagus sylvatica*
DESCRIPTION: protein phosphatase 2C (PP2C). pp2Cf1.
- 15 AAC36699.1 AF075581 *Mesembryanthemum crystallinum*
DESCRIPTION: protein phosphatase-2C. PP2C.
- 20 CAB90634.1 AJ277744 *Fagus sylvatica*
DESCRIPTION: protein phosphatase 2C (PP2C). pp2C2. ABA and calcium induced protein.
- 25 AAC26828.1 AF075603 *Oryza sativa*
DESCRIPTION: kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases. kinase associated protein phosphatase. kapp. type 2C protein phosphatase.
- 30 AAC35951.1 AF079355 *Mesembryanthemum crystallinum*
DESCRIPTION: protein phosphatase-2c. PP2C.
- 35 AAK20060.1 AC025783 *Oryza sativa*
DESCRIPTION: putative protein phosphatase 2C. OSJNBa0001O14.1.
- 40 AAB93832.1 U81960 *Zea mays*
DESCRIPTION: kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases; type 2C protein phosphatase. kinase associated protein phosphatase. KAPP.
- 45 CAC09576.1 AJ298988 *Fagus sylvatica*
DESCRIPTION: protein phosphatase 2C (PP2C). pp2Cf2.

AAD26116.1 AF106954 *Brassica napus*

5 DESCRIPTION: galactinol synthase. GS. UDP-D-galactose:myo-inositol-D-galactosyltransferase.

CAB51130.1 AJ243815 *Pisum sativum*

10 DESCRIPTION: role in alpha galactoside synthesis. putative galactinol synthase.

CAB51533.1 AJ237693 *Ajuga reptans*

15 DESCRIPTION: galactosyl transfer from UDP-galactose to myo-inositol to form galactinol. galactinol synthase, isoform GolS-1. GolS.

CAB51534.1 AJ237694 *Ajuga reptans*

20 DESCRIPTION: galactosyl transfer from UDP-galactose to myo-inositol. galactinol synthase, isoform GolS-2. GolS.

AAD55726.1 AF178569 *Vitis riparia*

25 DESCRIPTION: galactinol synthase. WSI76. water stress induced protein.

135

AAB57734.1 U64818 *Lycopersicon esculentum*

30 DESCRIPTION: fructokinase. Frk2.

AAB51108.1 U62329 *Lycopersicon esculentum*

35 DESCRIPTION: fructokinase. FK.

AAA80675.1 U37838 *Beta vulgaris*

DESCRIPTION: fructokinase.

40 CAA78283.1 Z12823 *Solanum tuberosum*

DESCRIPTION: fructokinase.

AAB57733.1 U64817 *Lycopersicon esculentum*

45 DESCRIPTION: fructokinase. Frk1.

BAA94601.1 AB033504 *Populus euramericana*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. peaco-1.

5

AAA33697.1 L21978 *Petunia x hybrida*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACO3.

10

AAC48977.1 U07953 *Pelargonium x hortorum*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase.

15

CAA54449.1 X77232 *Prunus persica*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. PAO1.

20

AAF36483.1 AF129073 *Prunus persica*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACO1.

25

AAC33524.1 AF026793 *Prunus armeniaca*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACC oxidase.

30

AAB70884.1 U67861 *Pelargonium x hortorum*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. GACO3.

35

BAA90550.1 AB031027 *Prunus mume*

DESCRIPTION: ACC oxidase. PM-ACO1. 1-aminocyclopropane-1-carboxylic acid oxidase.

40

AAA99792.1 U54565 *Nicotiana glutinosa*

DESCRIPTION: oxidation of 1-aminocyclopropane-1-carboxylic acid. 1-aminocyclopropane-1-carboxylic acid oxidase. NGACO1. ACC oxidase.

45

AAB05171.1 U62764 *Nicotiana glutinosa*

DESCRIPTION: oxidation of 1-aminocyclopropane-1-carboxylic acid. ACC
oxidase. NGACO3.

5 AAC37381.1 L21976 Petunia x hybrida

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACO1.

CAA71738.1 Y10749 Betula pendula

10 DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACO.

CAA86468.1 Z46349 Nicotiana tabacum

15 DESCRIPTION: 1-aminocyclopropane-1-carboxylate deaminase.

BAA83466.1 AB012857 Nicotiana tabacum

DESCRIPTION: ACC oxidase.

20

AAC98808.1 U68215 Carica papaya

DESCRIPTION: ACC oxidase. fruit specific; ripening related.

25 BAA06526.1 D31727 Cucumis melo

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase.

CAA64797.1 X95551 Cucumis melo

30 DESCRIPTION: ACC oxidase.

CAA58232.1 X83229 Nicotiana tabacum

35 DESCRIPTION: ethylene forming enzyme. 1-aminocyclopropane-1-carboxylate
oxidase.

BAA34924.1 AB013101 Lycopersicon esculentum

40 DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. LE-ACO4. ACC
oxidase.

AAF64528.1 AF254125 Carica papaya

45 DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACC oxidase.

AAA33698.1 L21979 *Petunia x hybrida*
DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACO4.

5 CAA41212.1 X58273 *Lycopersicon esculentum*
DESCRIPTION: conversion of ACC to ethylene.
1-Aminocyclopropane-1-carboxylic acid oxidase. LEACO1.

10 BAA21541.1 AB003514 *Actinidia deliciosa*
DESCRIPTION: 1-aminocyclopropane-1-carboxylic acid oxidase.

AAB71421.1 L29405 *Helianthus annuus*
15 DESCRIPTION: 1-aminocyclopropapne-1-carboxylic acid oxidase. ACC
oxidase.

AAA99793.1 U54566 *Nicotiana glutinosa*
20 DESCRIPTION: oxidation of 1-aminocyclopropane-1-carboxylic acid.
1-aminocyclopropane-1-carboxylic acid oxidase. NGACO2. ACC oxidase.

AAF36484.1 AF129074 *Prunus persica*
25 DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase. ACO2.

CAA64799.1 X95553 *Cucumis melo*
DESCRIPTION: ACC oxidase.

30

CAA90904.1 Z54199 *Lycopersicon esculentum*
DESCRIPTION: catalyses the final step in ethylene biosynthesis.
1-aminocyclopropane-1-carboxylic acid oxidase. ACO3.

35

CAA68538.1 Y00478 *Lycopersicon esculentum*
DESCRIPTION: conversion of ACC to ethylene.
1-aminocyclopropane-1-carboxylate oxidase. LEACO2.

40

CAB97173.1 AJ297435 *Mangifera indica*
DESCRIPTION: ethene biosynthesis. putative
1-aminocyclopropane-1-carboxylic acid oxidase. aco1.

45

CAA82646.1 Z29529 *Nicotiana tabacum*

DESCRIPTION: oxidation of 1-aminocyclopropane-1-carboxylic acid. ethylene forming enzyme (EFE).

5

AAC12934.1 AF053354 *Phaseolus vulgaris*

DESCRIPTION: 1-aminocyclopropane-1-carboxylic acid oxidase. ACO1. ACC oxidase.

10

AAB70883.1 U19856 *Pelargonium x hortorum*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase.

15

AAC67233.1 AF033582 *Cucumis sativus*

DESCRIPTION: ACC oxidase 2. Cs-ACO2.

20

AAB02051.1 L76283 *Carica papaya*

DESCRIPTION: formation of ethylene. 1-aminocyclopropane-1-carboxylate oxidase. putative.

25

BAA33377.1 AB006806 *Cucumis sativus*

DESCRIPTION: ACC oxidase. CS-ACO1.

30

BAA33378.1 AB006807 *Cucumis sativus*

DESCRIPTION: ACC oxidase. CS-ACO2.

CAA71140.1 Y10034 *Rumex palustris*

DESCRIPTION: 1-aminocyclopropane-1-carboxylic acid oxidase.

35

AAA33644.1 M98357 *Pisum sativum*

DESCRIPTION: convert ACC to ethylene. 1-aminocyclopropane-1-carboxylate oxidase.

40

AAC48921.1 U06046 *Vigna radiata*

DESCRIPTION: 1-aminocyclopropane-1-carboxylate oxidase homolog.

45

AAK07883.1 AF315316 *Vigna radiata*

DESCRIPTION: ACC oxidase. ACO.

AAA33273.1 L35152 *Dianthus caryophyllus*
 DESCRIPTION: amino-cyclopropane carboxylic acid oxidase.
 5

CAA74328.1 Y14005 *Malus x domestica*
 DESCRIPTION: Converts ACC into ethylene in apple fruit. ACC oxidase.
 10 139

AAB65777.1 U97522 *Vitis vinifera*
 DESCRIPTION: class IV endochitinase. VvChi4B.
 15

AAB65776.1 U97521 *Vitis vinifera*
 DESCRIPTION: class IV endochitinase. VvChi4A.
 20

CAC17793.1 AJ301671 *Nicotiana sylvestris*
 DESCRIPTION: hydrolysis of chitin. endochitinase. chnb. class I
 chitinase.
 25

AAA34070.1 M15173 *Nicotiana tabacum*
 DESCRIPTION: endochitinase precursor (EC 3.2.1.14).
 30

CAA30142.1 X07130 *Solanum tuberosum*
 DESCRIPTION: endochitinase.
 35

CAA53626.1 X76041 *Triticum aestivum*
 DESCRIPTION: endochitinase. CHI.
 140

AAB94587.1 AF022458 *Glycine max*
 DESCRIPTION: CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
 40

BAA92894.1 AB006790 *Petunia x hybrida*
 DESCRIPTION: cytochrome P450. IMT-2.
 45

AAD56282.1 AF155332 *Petunia x hybrida*

DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

- 5 AAG44132.1 AF218296 *Pisum sativum*
DESCRIPTION: cytochrome P450. P450 isolog.
- 10 CAA65580.1 X96784 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515.
- 15 AAA32913.1 M32885 *Persea americana*
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).
- 20 CAA64635.1 X95342 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450. hsr515. hypersensitivity-related gene.
- 25 CAA70575.1 Y09423 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A5.
- 30 BAB40323.1 AB037244 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-1.
- 35 BAB40324.1 AB037245 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-2.
- 40 CAA50312.1 X70981 *Solanum melongena*
DESCRIPTION: P450 hydroxylase. CYPEG2.
- 45 CAA50155.1 X70824 *Solanum melongena*
DESCRIPTION: flavonoid hydroxylase (P450). CYP75.
- 50 AAB17562.1 U72654 *Eustoma grandiflorum*
DESCRIPTION: flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
- 55 BAA84071.1 AB028151 *Antirrhinum majus*
DESCRIPTION: flavone synthase II. cytochrome P450. AFNS2.

- AAC32274.1 AF081575 *Petunia x hybrida*
DESCRIPTION: flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.
- 5 AAG34695.1 AF313492 *Matthiola incana*
DESCRIPTION: putative cytochrome P450.
- 10 AAB94588.1 AF022459 *Glycine max*
DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
- 15 AAD37433.1 AF150881 *Lycopersicon esculentum x Lycopersicon peruvianum*
DESCRIPTION: catalyzes the hydroxylation of ferulic acid to
5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome
P450-dependent monooxygenase; F5H; FAH1.
- 20 CAA71517.1 Y10493 *Glycine max*
DESCRIPTION: putative cytochrome P450.
- 25 BAA13414.1 D87520 *Glycyrrhiza echinata*
DESCRIPTION: putative trans-cinnamic acid 4-hydroxylase. cytochrome P450
(CYP73A14). CYP Ge-1.
- 30 AAA19701.1 L24438 *Thlaspi arvense*
DESCRIPTION: cytochrome P450.
- 35 CAA50645.1 X71654 *Solanum melongena*
DESCRIPTION: P450 hydroxylase.
- 40 BAA03635.1 D14990 *Solanum melongena*
DESCRIPTION: Cytochrome P-450EG4.
- 45 AAC05148.1 AF049067 *Pinus radiata*
DESCRIPTION: cytochrome P450. PRE74.

- CAA70576.1 Y09424 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A6.
5
- AAG10196.1 AF286647 *Gossypium arboreum*
DESCRIPTION: cinnamate-4-hydroxylase. LP89. P450.
10
- AAB94584.1 AF022157 *Glycine max*
DESCRIPTION: capable of catalyzing the metabolism of phenylurea
herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
15
- CAA50648.1 X71657 *Solanum melongena*
DESCRIPTION: P450 hydroxylase.
20
- CAB43505.1 AJ239051 *Cicer arietinum*
DESCRIPTION: cytochrome P450. cyp81E2.
141

- AAB97167.1 AF030882 *Zea mays*
DESCRIPTION: SU1 isoamylase. sugary1. starch debranching enzyme.
25
- AAA91298.1 U18908 *Zea mays*
DESCRIPTION: Su1p. Sugary1. similar to *Pseudomonas* sp. isoamylase,
Swiss-Prot Accession Number P26501.
30
- AAD33889.1 AF142589 *Hordeum vulgare*
DESCRIPTION: isoamylase 1.
35
- BAA29041.1 AB015615 *Oryza sativa*
DESCRIPTION: isoamylase.
40
- AAD33891.1 AF142591 *Solanum tuberosum*
DESCRIPTION: isoamylase 1.
45
- AAD33890.1 AF142590 *Triticum aestivum*

DESCRIPTION: isoamylase 1.

5 AAD53260.1 AF142588 Hordeum vulgare
DESCRIPTION: isoamylase 1.

145

10 AAG35777.1 AF273844 Brassica oleracea var. alboglabra
DESCRIPTION: thioredoxin-h-like protein 1. THL1.

15 AAB53694.1 U59379 Brassica napus
DESCRIPTION: thioredoxin-h-like-1. THL-1. thioredoxin-h homolog.

20 CAA61908.1 X89759 Brassica oleracea
DESCRIPTION: pollen coat protein. bopcl7.

BAA25681.1 AB010434 Brassica rapa
DESCRIPTION: Thioredoxin. PEC-2.

25 BAB20886.1 AB053294 Oryza sativa
DESCRIPTION: thioredoxin h. RTRXH2.

30 AAB53695.1 U59380 Brassica napus
DESCRIPTION: thioredoxin-h-like-2. THL-2. Description: thioredoxin-h
homolog.

35 AAF88067.1 AF286593 Triticum aestivum
DESCRIPTION: thioredoxin H. similar to wheat thioredoxin H.

40 CAA94534.1 Z70677 Ricinus communis
DESCRIPTION: thioredoxin.

CAA05081.1 AJ001903 Triticum turgidum subsp. durum
DESCRIPTION: thioredoxin H.

45 CAA49540.1 X69915 Triticum aestivum

DESCRIPTION: unnamed protein product.

5 BAA13524.1 D87984 Fagopyrum esculentum
DESCRIPTION: thioredoxin.

10 CAA41415.1 X58527 Nicotiana tabacum
DESCRIPTION: thioredoxin.

CAA77847.1 Z11803 Nicotiana tabacum
DESCRIPTION: THIOREDOXIN.

15 AAC32111.1 AF051206 Picea mariana
DESCRIPTION: probable thioredoxin H. Sb09. similar to Nicotiana tabacum
thioredoxin H1 encoded by GenBank Accession Number X58527.

20 BAA05546.1 D26547 Oryza sativa
DESCRIPTION: rice thioredoxin h.

25 BAA04864.1 D21836 Oryza sativa
DESCRIPTION: thioredoxin h. encoding rice phloem sap 13kD protein-1.

30 AAB51522.1 U92541 Oryza sativa
DESCRIPTION: thioredoxin h.

35 AAD49232.1 AF159387 Lolium perenne
DESCRIPTION: thioredoxin-like protein. Trx.

AAD56954.1 AF186240 Secale cereale
DESCRIPTION: thioredoxin-like protein. Trx.

40 AAD49231.1 AF159386 Secale cereale
DESCRIPTION: thioredoxin-like protein. Trx.

45 AAD49230.1 AF159385 Hordeum bulbosum
DESCRIPTION: thioredoxin-like protein. Trx.

- 5 AAD49234.1 AF159389 Phalaris coerulescens
DESCRIPTION: thioredoxin-like protein. Trx.
- 10 AAD49233.1 AF159388 Phalaris coerulescens
DESCRIPTION: thioredoxin-like protein. Trx.
- 15 BAB39913.1 AP002912 Oryza sativa
DESCRIPTION: thioredoxin-like protein. P0028E10.17. contains EST
C72705(E2091).
- 20 CAA55399.1 X78822 Chlamydomonas reinhardtii
DESCRIPTION: thioredoxin h. Trx.
- 25 CAA56850.1 X80887 Chlamydomonas reinhardtii
DESCRIPTION: thioredoxin h. Trx h.
- 30 AAD33596.1 AF133127 Hevea brasiliensis
DESCRIPTION: thioredoxin h.
- 35 CAA35826.1 X51462 Spinacia oleracea
DESCRIPTION: thioredoxin M precursor (AA -67 to 114).
- 40 CAA35827.1 X51463 Spinacia oleracea
DESCRIPTION: thioredoxin M precursor (AA -67 to 114).
- 45 CAA45098.1 X63537 Pisum sativum
DESCRIPTION: thioredoxin F. isoform.
- 50 AAC49357.1 U35830 Pisum sativum
DESCRIPTION: thioredoxin f.
- 55 AAC19392.1 AF069314 Mesembryanthemum crystallinum
DESCRIPTION: thioredoxin F precursor.

AAC04671.1 AF018174 Brassica napus
DESCRIPTION: thioredoxin-f. TRXF.

5

AAB47556.1 U87141 Mesembryanthemum crystallinum
DESCRIPTION: thioredoxin h.

10 CAA53900.1 X76269 Pisum sativum
DESCRIPTION: thioredoxin m.

15 AAC49358.1 U35831 Pisum sativum
DESCRIPTION: thioredoxin m. chloroplastic.

20 CAA33082.1 X14959 Spinacia oleracea
DESCRIPTION: pre-thioredoxin f (AA -77 to 113).

CAA06736.1 AJ005841 Oryza sativa
DESCRIPTION: thioredoxin M.

25

CAA55398.1 X78821 Chlamydomonas reinhardtii
DESCRIPTION: thioredoxin m. Trx.

30 CAA56851.1 X80888 Chlamydomonas reinhardtii
DESCRIPTION: thioredoxin m. Trx m.

35 CAA44209.1 X62335 Chlamydomonas reinhardtii
DESCRIPTION: thioredoxin Ch2. Trx.

40 AAA92464.1 L40957 Zea mays
DESCRIPTION: regulation of activities of photosynthetic enzymes.
thioredoxin M. putative.

45 CAA06735.1 AJ005840 Triticum aestivum
DESCRIPTION: thioredoxin M.

AAB52409.1 U76831 Brassica napus
DESCRIPTION: thioredoxin-m.

5 AAD45358.1 AF160870 Brassica napus
DESCRIPTION: thioredoxin-m precursor.

10 CAA71103.1 Y09987 Solanum tuberosum
DESCRIPTION: CDSP32 protein (Chloroplast Drought-induced Stress Protein
of 32kDa).

15 AAA32662.1 M82973 Medicago sativa
DESCRIPTION: putative endomembrane protein; putative.

20 CAA77575.1 Z11499 Medicago sativa
DESCRIPTION: protein disulfide isomerase.
148

25 AAA33376.1 L36129 Helianthus annuus
DESCRIPTION: NADPH thioredoxin reductase.
150

30 AAA92013.1 U49454 Prunus persica
DESCRIPTION: beta-1,3-glucanase. Gns1.

35 CAA54952.1 X77990 Brassica rapa
DESCRIPTION: beta-1,3-glucanase. bgl.

AAF33405.1 AF230109 Populus x canescens
DESCRIPTION: beta-1,3 glucanase. BGLUC.

40 AAA33946.1 M37753 Glycine max
DESCRIPTION: beta-1,3-endoglucanase (EC 3.2.1.39).

45 CAA03908.1 AJ000081 Citrus sinensis
DESCRIPTION: glucan hydrolase. beta-1,3-glucanase. gns1.

CAB91554.1 AJ277900 *Vitis vinifera*
DESCRIPTION: beta 1-3 glucanase. gl.

5

AAB03501.1 U41323 *Glycine max*
DESCRIPTION: beta-1,3-glucanase. SGN1.

10 AAA34078.1 M63634 *Nicotiana plumbaginifolia*
DESCRIPTION: regulator of beta(1,3)-glucanase. beta(1,3)-glucanase
regulator.

15 CAA30261.1 X07280 *Nicotiana plumbaginifolia*
DESCRIPTION: beta-glucanase.

20 AAA51643.1 M23120 *Nicotiana plumbaginifolia*
DESCRIPTION: beta-glucanase precursor.

25 AAA87456.1 U22147 *Hevea brasiliensis*
DESCRIPTION: beta-1,3-glucanase. HGN1. hydrolytic enzyme.

CAB38443.1 AJ133470 *Hevea brasiliensis*
DESCRIPTION: beta-1,3-glucanase. hgn1.

30

AAA03618.1 M80608 *Lycopersicon esculentum*
DESCRIPTION: beta-1,3-glucanase.

35 AAA18928.1 U01901 *Solanum tuberosum*
DESCRIPTION: catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in
1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan
glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic,
40 class I). glub2. plant defense gene; induced expression in response to
infection, elicitor, ethylene, wounding.

AAC19114.1 AF067863 *Solanum tuberosum*
DESCRIPTION: 1,3-beta-glucan glucanohydrolase. glucanase.

45

CAA92278.1 Z68154 *Gossypium hirsutum*
DESCRIPTION: 1,3-beta-glucanase.

5 AAG24921.1 AF311749 *Hevea brasiliensis*
DESCRIPTION: beta-1,3-glucanase.

10 AAA63539.1 M60402 *Nicotiana tabacum*
DESCRIPTION: glucan beta-1,3-glucanase. glucanase GLA.

15 AAA63540.1 M60403 *Nicotiana tabacum*
DESCRIPTION: glucan-1,3-beta-glucosidase. glucanase GLB.

20 AAA88794.1 U01900 *Solanum tuberosum*
DESCRIPTION: catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in
1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan
glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic,
class I). gluB1. plant defense gene; induced expression in response to
infection, elicitor, ethylene, wounding.

25 AAA63541.1 M59442 *Nicotiana tabacum*
DESCRIPTION: basic beta-1,3-glucanase. glucanase.

30 AAB82772.2 AF001523 *Musa acuminata*
DESCRIPTION: beta-1, 3-glucanase. similar to beta-1, 3-glucanase.

35 CAA37289.1 X53129 *Phaseolus vulgaris*
DESCRIPTION: 1,3,-beta-D-glucanase.

40 AAF08679.1 AF004838 *Musa acuminata*
DESCRIPTION: beta-1,3-glucanase.

AAD33881.1 AF141654 *Nicotiana tabacum*
DESCRIPTION: beta-1,3-glucanase. GGL4.

45 AAD33880.1 AF141653 *Nicotiana tabacum*
DESCRIPTION: beta-1,3-glucanase. GGL1.

AAA33648.1 L02212 Pisum sativum
 DESCRIPTION: beta-1,3-glucan hydrolysis. beta-1,3-glucanase. putative.

5

AAA34082.1 M20620 Nicotiana tabacum
 DESCRIPTION: prepro-beta-1,3-glucanase precursor.

10

AAA19111.1 U01902 Solanum tuberosum
 DESCRIPTION: catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in
 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan
 glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic,
 15 class I). gluB3. plant defense gene; induced expression in response to
 infection, elicitor, ethylene, wounding.

CAA57255.1 X81560 Nicotiana tabacum
 DESCRIPTION: (1-)-beta-glucanase. Sp41a.

20

AAA34053.1 M60464 Nicotiana tabacum
 DESCRIPTION: beta-1,3-glucanase.

25

AAA63542.1 M59443 Nicotiana tabacum
 DESCRIPTION: acidic beta-1,3-glucanase. glucanase.

30

AAB24398.1 S51479 Pisum sativum
 DESCRIPTION: beta-1,3-glucanase. beta-1,3-glucanase. This sequence comes
 from Fig. 1B.

35

AAB41551.1 U27179 Medicago sativa subsp. sativa
 DESCRIPTION: acidic glucanase.

40

AAD10384.1 U72253 Oryza sativa
 DESCRIPTION: beta-1,3-glucanase precursor. Gns7.

AAA03617.1 M80604 Lycopersicon esculentum
 DESCRIPTION: beta-1,3-glucanase.

45

BAA19102.1 AB000408 *Populus kitakamiensis*
DESCRIPTION: o-methyltransferase. caffeoyl-CoA 3-O-methyltransferase.

5

AAC28973.1 U20736 *Medicago sativa* subsp. *sativa*
DESCRIPTION: synthesis of feruloyl-CoA from caffeoyl-CoA and
S-adenosyl-L-methionine. S-adenosyl-L-methionine:trans-caffeoyl-CoA
3-O-methyltransferase. CCOMT.

10

CAA12198.1 AJ224894 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: methylates lignin precursors. caffeoyl-CoA
3-O-methyltransferase.

15

CAA11496.1 AJ223621 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: caffeoyl CoA 3-O-methyltransferase. CCoAOMT1.

20

AAB80931.1 AF022775 *Nicotiana tabacum*
DESCRIPTION: caffeoyl-CoA 3-O-methyltransferase 5. CCoAOMT-5.
implicated
in lignification and defense reaction against pathogens.

25

CAA83943.1 Z33878 *Petroselinum crispum*
DESCRIPTION: caffeoyl-CoA 3-O-methyltransferase.

30

AAA33851.1 M69184 *Petroselinum crispum*
DESCRIPTION: caffeoyl-CoA 3-O-methyltransferase. CCoAMT.

35

CAA90894.1 Z54183 *Petroselinum crispum*
DESCRIPTION: trans-caffeoyl-CoA 3-O-methyltransferase. CCoAOMT.

40

CAA90969.1 Z54233 *Vitis vinifera*
DESCRIPTION: plant defense and lignification. caffeoyl-CoA
O-methyltransferase.

45

AAA59389.1 U13151 *Zinnia elegans*
DESCRIPTION: S-adenosyl-L-methionine:trans-caffeoyl-CoA

3-O-methyltransferase. CCoAOMT.

- 5 CAB05369.1 Z82982 *Nicotiana tabacum*
DESCRIPTION: methylation of caffeoyl-CoA in lignin biosynthesis.
caffeoyl-CoA O-methyltransferase 5. CCoAOMT-5.
- 10 AAA80651.1 U27116 *Populus tremuloides*
DESCRIPTION: caffeoyl-CoA 3-O-methyltransferase. S-adenyosyl-methionine
caffeoyl-CoA 3-O-methyltransferase; similar to Swiss-Prot Accession Number
P28034; similar to proteins encoded by GenBank accession Numbers U20736,
U13151, and L22203; Mr = 27.9 kDa and pI = 5.16.
- 15 AAC08395.1 AF053553 *Mesembryanthemum crystallinum*
DESCRIPTION: caffeoyl-CoA O-methyltransferase.
- 20 CAA12200.1 AJ224896 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: methylates lignin precursors. caffeoyl-CoA
3-O-methyltransferase.
- 25 CAA12199.1 AJ224895 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: methylates lignin precursors. caffeoyl-CoA
3-O-methyltransferase.
- 30 CAA11495.1 AJ223620 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: caffeoyl CoA 3-O-methyltransferase. CCoAOMT2.
- 35 AAD50443.1 AF168780 *Eucalyptus globulus*
DESCRIPTION: caffeoyl-CoA O-methyltransferase. CCoAOMT2.
- 40 AAF44689.1 AF240466 *Populus tomentosa*
DESCRIPTION: caffeoyl-CoA O-methyltransferase. CCoAOMT.
- 45 AAC49913.1 U38612 *Nicotiana tabacum*
DESCRIPTION: methylation of caffeoyl-CoA in feruloyl-coA in
phenylpropanoid pathway. caffeoyl-coenzymeA O-methyltransferase.
CCoAOMT-1.

CAA72911.1 Y12228 Eucalyptus gunnii

DESCRIPTION: caffeoyl-CoA O-methyltransferase. COOAMT.

5

AAC49916.1 U62736 Nicotiana tabacum

DESCRIPTION: methylation of caffeoyl-CoA in feruloyl-CoA in phenylpropanoid pathway (lignin biosynthesis). caffeoyl-CoA O-methyltransferase 4. CCoAOMT-4.

10

BAA78733.1 AB023482 Oryza sativa

DESCRIPTION: ESTs AU058067(E20733), AAU058070(E20873) correspond to a

15

region of the predicted gene.; Similar to Populus tremuloides caffeoyl-CoA 3-O-methyltransferase mRNA, complete cds.(U27116).

CAA91228.1 Z56282 Nicotiana tabacum

20

DESCRIPTION: plant defense and lignification. caffeoyl-CoA O-methyltransferase. NTCCOAOMT.

AAC49914.1 U62734 Nicotiana tabacum

25

DESCRIPTION: methylation of caffeoyl-CoA in feruloyl-CoA in phenylpropanoid pathway (lignin biosynthesis). caffeoyl-CoA O-methyltransferase 2. CCoAOMT-2.

30

AAC26191.1 AF046122 Eucalyptus globulus

DESCRIPTION: catalyses the methylation of caffeoyl CoA in lignin biosynthesis. caffeoyl-CoA 3-O-methyltransferase. CCOMT. S-adenosyl-L-methionine:caffeoyl-CoA 3-O-methyltransferase.

35

AAC49915.1 U62735 Nicotiana tabacum

DESCRIPTION: methylation of caffeoyl-CoA in feruloyl-CoA in phenylpropanoid pathway (lignin biosynthesis). caffeoyl-CoA O-methyltransferase 3. CCoAOMT-3.

40

AAD02050.1 AF036095 Pinus taeda

DESCRIPTION: caffeoyl-CoA O-methyltransferase. CCoAOMT. lignin pathway

45

O-methyltransferase.

AAK16714.1 AF327458 *Populus alba* x *Populus glandulosa*
DESCRIPTION: caffeoyl-CoA 3-O-methyltransferase. CCoAOMT.

5

CAB45150.1 AJ242981 *Zea mays*
DESCRIPTION: lignin synthesis. Caffeoyl CoA O-methyltransferase.
ccoAOMT.

10

CAB45149.1 AJ242980 *Zea mays*
DESCRIPTION: lignin synthesis. Caffeoyl CoA O-methyltransferase.
ccoAOMT.

15

AAB61680.1 L22203 *Stellaria longipes*
DESCRIPTION: S-adenosyl-L-methionine:trans-caffeoyl-CoA
3-O-methyltransferase. 26.7-kDa; pI=5.3.

20

BAA88234.1 AB035144 *Citrus natsudaoidai*
DESCRIPTION: Methylation of caffeoyl-coA in feruloyl-coA in
phenylpropanoid pathway. caffeoyl-CoA 3-O-methyltransferase. CCoAMT.

25

BAA81776.1 AP000364 *Oryza sativa*
DESCRIPTION: ESTs C98431(E0144),C71728(E0144) correspond to a region
of
the predicted gene.; Similar to *Medicago sativa* S-adenosyl-L-methionine.
(U20736).

30

BAA81774.1 AP000364 *Oryza sativa*
DESCRIPTION: ESTs AU030740(E60171),AU030739(E60171) correspond to
a
region of the predicted gene.; Similar to *Populus tremuloides* caffeoyl-CoA
3-O-methyltransferase. (U27116).

35

BAA81777.1 AP000364 *Oryza sativa*
DESCRIPTION: Similar to *Petroselinum crispum* caffeoyl-CoA
3-O-methyltransferase. (S49342).

40

CAA10217.1 AJ130841 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: methylates lignin precursors. caffeoyl-CoA

45

3-O-methyltransferase.

- CAA04769.1 AJ001447 *Fragaria vesca*
5 DESCRIPTION: caffeoyl-CoA 3-O-methyltransferase. putative.
- AAD50441.1 AF168778 *Eucalyptus globulus*
10 DESCRIPTION: caffeoyl-CoA O-methyltransferase. CCoAOMT1.
- AAD50442.1 AF168779 *Eucalyptus globulus*
DESCRIPTION: caffeoyl-CoA O-methyltransferase. CCoAOMT2.
- 15 AAC15067.1 AF060180 *Nicotiana tabacum*
DESCRIPTION: plant lignification and defense. caffeoyl-coenzyme A trunc2.
truncated caffeoyl-coenzyme A.
- 20 152

AAK11255.1 AF329729 *Nicotiana tabacum*
DESCRIPTION: regulator of gene silencing. rgs-CaM; calmodulin-related
protein.
- 25 AAD10245.1 AF030033 *Phaseolus vulgaris*
DESCRIPTION: calmodulin. CaM. EF-hand protein; calcium-dependent
protein;
30 functions in calcium signal transduction pathways.
- CAA62150.1 X90560 *Physcomitrella patens*
35 DESCRIPTION: Calmodulin. CaM.
- BAA94696.1 AB041711 *Chara corallina*
DESCRIPTION: calmodulin. cccam1.
- 40 BAA96536.1 AB044286 *Chara corallina*
DESCRIPTION: calmodulin. ccam.
- 45 BAA94697.1 AB041712 *Chara corallina*
DESCRIPTION: calmodulin. cccam2.

- BAA87825.1 AP000815 *Oryza sativa*
 DESCRIPTION: ESTs AU030013(E50493),AU081341(E50493) correspond to
 5 a region of the predicted gene. Similar to *O.sativa* gene encoding
 calmodulin. (Z12828).
- 10 CAA61980.1 X89890 *Bidens pilosa*
 DESCRIPTION: Calmodulin.
- 15 AAA19571.1 U10150 *Brassica napus*
 DESCRIPTION: calcium binding. calmodulin. bcm1.
- 20 AAA87347.1 M88307 *Brassica juncea*
 DESCRIPTION: calmodulin.
- 25 CAA74111.1 Y13784 *Mougeotia scalaris*
 DESCRIPTION: Calmodulin.
- AAA92677.1 U13736 *Pisum sativum*
 DESCRIPTION: binds calcium. calmodulin-like protein.
- 30 AAA34015.1 L01433 *Glycine max*
 DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-4.
 putative.
- 35 AAA33083.1 M20729 *Chlamydomonas reinhardtii*
 DESCRIPTION: calmodulin.
- 40 AAK25753.1 AF334833 *Castanea sativa*
 DESCRIPTION: calmodulin. CAM2.
- 45 AAF73157.1 AF150059 *Brassica napus*
 DESCRIPTION: calmodulin. CaM1. involved in seed germination.

[illegible]

DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-2.
putative.

5 AAA34013.1 L01430 Glycine max
DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-1.
putative.

10 AAB36130.1 S81594 Vigna radiata
DESCRIPTION: auxin-regulated calmodulin. auxin-regulated calmodulin,
arCaM. This sequence comes from Fig. 1; arCaM.

15 AAA33901.1 L18913 Oryza sativa
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.
putative.

20 AAA92681.1 U13882 Pisum sativum
DESCRIPTION: calcium-binding protein. calmodulin.

25 AAA33706.1 M80836 Petunia x hybrida
DESCRIPTION: calmodulin. CAM81.

30 AAA33705.1 M80831 Petunia x hybrida
DESCRIPTION: calmodulin-related protein. CAM53.

CAA78287.1 Z12827 Oryza sativa
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

35 CAA46150.1 X65016 Oryza sativa
DESCRIPTION: calmodulin. cam.

40 CAA36644.1 X52398 Medicago sativa
DESCRIPTION: calmodulin (AA 1-149).

45 CAA43143.1 X60738 Malus x domestica
DESCRIPTION: Calmodulin. CaM.

CAA78301.1 Z12839 *Lilium longiflorum*
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

5

AAA33397.1 L18912 *Lilium longiflorum*
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.
putative.

10

AAB68399.1 U79736 *Helianthus annuus*
DESCRIPTION: calmodulin. HaCaM.

15

CAA42423.1 X59751 *Daucus carota*
DESCRIPTION: calmodulin. Ccam-1.

20

AAA32938.1 M27303 *Hordeum vulgare*
DESCRIPTION: calmodulin.

25

BAA88540.1 AP000969 *Oryza sativa*
DESCRIPTION: ESTs AU081349(E61253), D41425(S3918) correspond to a
region
of the predicted gene. Similar to calmodulin. (AF042840).

30

AAG27432.1 AF295637 *Elaeis guineensis*
DESCRIPTION: calmodulin.

35

AAG11418.1 AF292108 *Prunus avium*
DESCRIPTION: calmodulin.

40

AAC36059.1 AF042840 *Oryza sativa*
DESCRIPTION: calmodulin. CaM1.

CAA40474.1 X57187 *Phaseolus vulgaris*
DESCRIPTION: chitinase. Chi4.

45

AAB65776.1 U97521 *Vitis vinifera*

DESCRIPTION: class IV endochitinase. VvChi4A.

CAA61281.1 X88803 Vigna unguiculata
5 DESCRIPTION: chitinase class 4. CHI4.

AAB65777.1 U97522 Vitis vinifera
10 DESCRIPTION: class IV endochitinase. VvChi4B.

BAA22966.1 D45182 Chenopodium amaranticolor
DESCRIPTION: chitinase.

15 BAA22968.1 D45184 . Chenopodium amaranticolor
DESCRIPTION: chitinase.

20 BAA22965.1 D45181 Chenopodium amaranticolor
DESCRIPTION: chitinase.

CAA43708.1 X61488 Brassica napus
25 DESCRIPTION: chitinase.

BAA22967.1 D45183 Chenopodium amaranticolor
30 DESCRIPTION: chitinase.

CAA53544.1 X75945 Beta vulgaris
DESCRIPTION: chitinase. Ch4.

35 AAC49435.1 U52845 Daucus carota
DESCRIPTION: class IV chitinase EP3-1/H5. EP3.

40 AAB08468.1 U52846 Daucus carota
DESCRIPTION: class IV chitinase EP3-2/H1. EP3.

AAB08470.1 U52848 Daucus carota
45 DESCRIPTION: class IV chitinase EP3B/E6. EP3.

- AAB08469.1 U52847 *Daucus carota*
DESCRIPTION: class IV chitinase EP3-3/E7. EP3.
- 5
AAA33445.1 M84165 *Zea mays*
DESCRIPTION: chitinase B. seed chitinase.
- 10
AAA33444.1 M84164 *Zea mays*
DESCRIPTION: chitinase A. seed chitinase.
- 15
AAA32916.1 L25826 *Beta vulgaris*
DESCRIPTION: chitinase. SP2.
- 20
AAD28733.1 AF112966 *Triticum aestivum*
DESCRIPTION: chitinase IV precursor. Cht4.
- 25
BAB21377.1 AB054811 *Oryza sativa*
DESCRIPTION: PR-3 class IV chitinase. Cht4. Catalytic domain.
- 30
BAB21374.1 AB054687 *Oryza sativa*
DESCRIPTION: PR-3 class IV chitinase. Cht4. catalytic domain.
- 35
BAA19793.1 AB003194 *Oryza sativa*
DESCRIPTION: chitinase IIb.
- 40
AAA85364.1 L42467 *Picea glauca*
DESCRIPTION: chitinase. chi.
- 45
AAB01665.1 U21848 *Brassica napus*
DESCRIPTION: chitinase class IV. LSC222.
- AAC35981.1 AF090336 *Citrus sinensis*
DESCRIPTION: chitin hydrolase. chitinase CHI1. chi1.
- AAD28730.1 AF112963 *Triticum aestivum*

DESCRIPTION: chitinase II precursor. Cht2.

5 AAF04454.1 AF000966 Poa pratensis
DESCRIPTION: chitinase. Chi2.

10 CAC17793.1 AJ301671 Nicotiana sylvestris
DESCRIPTION: hydrolysis of chitin. endochitinase. chnb. class I
chitinase.

15 AAF04453.1 AF000964 Poa pratensis
DESCRIPTION: chitinase. Chi1.

20 CAA34812.1 X16938 Nicotiana tabacum
DESCRIPTION: chitinase precursor.

CAA34813.1 X16939 Nicotiana tabacum
DESCRIPTION: chitinase precursor (AA -23 to 306).

25 CAA45822.1 X64519 Nicotiana tabacum
DESCRIPTION: chitinase B class I. CHN200.

30 CAA35945.1 X51599 Nicotiana tabacum
DESCRIPTION: chitinase. CHN50.

35 AAB23374.1 S44869 Nicotiana tabacum
DESCRIPTION: basic chitinase. basic chitinase. This sequence comes from
Fig. 1.

40 AAA34070.1 M15173 Nicotiana tabacum
DESCRIPTION: endochitinase precursor (EC 3.2.1.14).

CAA30142.1 X07130 Solanum tuberosum
DESCRIPTION: endochitinase.

45 CAA33517.1 X15494 Solanum tuberosum

DESCRIPTION: pre-chitinase (AA -26 to 302).

- 5 AAG53609.1 AF280437 *Secale cereale*
DESCRIPTION: 31.7 kDa class I endochitinase-antifreeze protein precursor.
cht9.
- 10 CAB01591.1 Z78202 *Persea americana*
DESCRIPTION: hydrolysis of the 1,4-beta-linkages of chitin.
endochitinase. chl1.
- 15 CAA53626.1 X76041 *Triticum aestivum*
DESCRIPTION: endochitinase. CHI.
- 20 CAA78845.1 Z15140 *Lycopersicon esculentum*
DESCRIPTION: chitinase. Encodes 30 kD basic intracellular chitinase.
- 25 AAC16010.1 AF061805 *Elaeagnus umbellata*
DESCRIPTION: acidic chitinase.
- 30 AAA32640.1 M94106 *Allium sativum*
DESCRIPTION: chitinase. chitinase.
- 35 AAA32641.1 M94105 *Allium sativum*
DESCRIPTION: chitinase. chitinase.
- 40 AAA56787.1 L34211 *Hordeum vulgare*
DESCRIPTION: hydrolysis of chitin. chitinase. CHI33.
- 45 AAA17409.1 U02607 *Solanum tuberosum*
DESCRIPTION: catalyzes the random hydrolysis of
1,4-beta-(2-acetamido-2-deoxy-D-glucoside) linkages in chitin; plant
defense gene. chitinase. chtB3. induced expression in response to
infection, elicitor, ethylene, wounding; preproprotein; gene product
subunit is monomer.
- AAA18332.1 U02605 *Solanum tuberosum*

DESCRIPTION: catalyzes the random hydrolysis of
1,4-beta-(2-acetamido-2-deoxy-D-glucoside) linkages in chitin; plant
defense gene. chitinase. chtB1. induced expression in response to
infection, elicitor, ethylene, wounding; preproprotein; gene product
subunit is a monomer.

CAA45821.1 X64518 *Nicotiana tabacum*
DESCRIPTION: chitinase C class I. CHN14.

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AAB35812.1 S80554 *Arabidopsis*
DESCRIPTION: chalcone synthase. chalcone synthase, CHS. This sequence
comes from Fig. 5; CHS.

AAF23570.1 AF112095 *Arabidopsis halleri*
DESCRIPTION: chalcone synthase. CHS.

20

AAF23568.1 AF112093 *Arabidopsis griffithiana*
DESCRIPTION: chalcone synthase. CHS.

25

AAG43351.1 AF144533 *Arabidopsis korshinskyi*
DESCRIPTION: chalcone synthase. chs.

30 AAF23581.1 AF112106 *Capsella rubella*
DESCRIPTION: chalcone synthase. CHS.

35 AAF23569.1 AF112094 *Halimolobos perplexa* var. *perplexa*
DESCRIPTION: chalcone synthase. CHS.

AAG43349.1 AF144531 *Arabidopsis himalaica*
DESCRIPTION: chalcone synthase. chs.

40

AAF23575.1 AF112100 *Arabidopsis lyrata* subsp. *lyrata*
DESCRIPTION: chalcone synthase. CHS.

45

AAF23567.1 AF112092 *Arabidopsis griffithiana*

DESCRIPTION: chalcone synthase. CHS.

5 AAF23578.1 AF112103 *Arabidopsis lyrata* subsp. *petraea*
DESCRIPTION: chalcone synthase. CHS.

10 AAF23576.1 AF112101 *Arabis parishii*
DESCRIPTION: chalcone synthase. CHS.

AAF23574.1 AF112099 *Arabis lyallii*
DESCRIPTION: chalcone synthase. CHS.

15 AAF23566.1 AF112091 *Arabis glabra*
DESCRIPTION: chalcone synthase. CHS.

20 AAF23565.1 AF112090 *Arabis fendleri*
DESCRIPTION: chalcone synthase. CHS.

25 AAF23563.1 AF112088 *Arabis drummondii*
DESCRIPTION: chalcone synthase. CHS.

30 AAF23564.1 AF112089 *Arabis drummondii*
DESCRIPTION: chalcone synthase. CHS.

AAF23579.1 AF112104 *Arabidopsis lyrata* subsp. *petraea*
DESCRIPTION: chalcone synthase. CHS.

35 AAF23573.1 AF112098 *Arabis lignifera*
DESCRIPTION: chalcone synthase. CHS.

40 AAF23560.1 AF112085 *Cardamine amara*
DESCRIPTION: chalcone synthase. CHS.

45 AAG43348.1 AF144530 *Rorippa amphibia*
DESCRIPTION: chalcone synthase. chs.

AAG43356.1 AF144538 *Cardamine penzesii*
DESCRIPTION: chalcone synthase. chs.

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AAG43359.1 AF144541 *Sisymbrium irio*
DESCRIPTION: chalcone synthase. chs.

10 AAG43352.1 AF144534 *Lepidium campestre*
DESCRIPTION: chalcone synthase. chs.

15 CAA32495.1 X14314 *Sinapis alba*
DESCRIPTION: chalcone synthase (AA 1-395).

20 AAG43357.1 AF144539 *Cardamine rivularis*
DESCRIPTION: chalcone synthase. chs.

AAF23583.1 AF112108 *Barbarea vulgaris*
DESCRIPTION: chalcone synthase. CHS.

25 AAC31914.1 AF076336 *Brassica napus*
DESCRIPTION: chalcone synthase B2. CHSB2.

30 AAC31912.1 AF076334 *Brassica napus*
DESCRIPTION: chalcone synthase A2. CHSA2.

35 AAF23577.1 AF112102 *Arabis pauciflora*
DESCRIPTION: chalcone synthase. CHS.

40 AAG43350.1 AF144532 *Cochlearia danica*
DESCRIPTION: chalcone synthase. chs.

CAA34460.1 X16437 *Sinapis alba*
DESCRIPTION: chalcone synthase.

45 CAA35600.1 X17577 *Matthiola incana*

DESCRIPTION: chalcone synthase (AA 1-394).

5 AAG43358.1 AF144540 Cardamine pratensis
DESCRIPTION: chalcone synthase. chs.

10 AAG43353.1 AF144535 Thlaspi arvense
DESCRIPTION: chalcone synthase. chs.

AAC31913.1 AF076335 Brassica napus
DESCRIPTION: chalcone synthase B1. CHSB1.

15 AAF23571.1 AF112096 Arabis hirsuta
DESCRIPTION: chalcone synthase. CHS.

20 AAF23582.1 AF112107 Arabis turrita
DESCRIPTION: chalcone synthase. CHS.

25 AAG43406.1 AF174529 Aubrieta deltoidea
DESCRIPTION: chalcone synthase. chs.

30 AAG43355.1 AF144537 Alliaria petiolata
DESCRIPTION: chalcone synthase. chs.

AAF23580.1 AF112105 Arabis procurrens
DESCRIPTION: chalcone synthase. CHS.

35 AAF23572.1 AF112097 Arabis jacquinii
DESCRIPTION: chalcone synthase. CHS.

40 AAF23562.1 AF112087 Arabis blepharophylla
DESCRIPTION: chalcone synthase. CHS.

45 AAF23584.1 AF112109 Aubrieta deltoidea
DESCRIPTION: chalcone synthase. CHS.

AAG43354.1 AF144536 *Microthlaspi perfoliatum*
DESCRIPTION: chalcone synthase. chs.

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AAF23557.1 AF112082 *Aethionema grandiflora*
DESCRIPTION: chalcone synthase. CHS.

10 AAF23558.1 AF112083 *Arabis alpina*
DESCRIPTION: chalcone synthase. CHS.

15 AAF23559.1 AF112084 *Arabis alpina*
DESCRIPTION: chalcone synthase. CHS.

20 AAB87072.1 AF031922 *Raphanus sativus*
DESCRIPTION: chalcone synthase. CHS.

AAG43360.1 AF144542 *Ionopsidium abulense*
DESCRIPTION: chalcone synthase. chs.

25

AAC31911.1 AF076333 *Brassica napus*
DESCRIPTION: chalcone synthase A1. CHSA1.

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AAD10327.1 U63534 *Fragaria x ananassa*
DESCRIPTION: catalyzes the reduction of cinnamylaldehydes leading to
monolignols. cinnamyl alcohol dehydrogenase. CAD. involved with lignin
biosynthesis.

35

AAK28509.1 AF320110 *Fragaria x ananassa*
DESCRIPTION: cinnamyl alcohol dehydrogenase.

40

AAB38503.1 U79770 *Mesembryanthemum crystallinum*
DESCRIPTION: cinnamyl-alcohol dehydrogenase Eli3.

45 CAA48028.1 X67817 *Petroselinum crispum*
DESCRIPTION: Eli3.

[illegible]

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CAA05097.1 AJ001926 *Picea abies*
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad8.

5 CAA05096.1 AJ001925 *Picea abies*
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad7.

10 AAC31166.1 AF060491 *Pinus radiata*
DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.

15 CAA86073.1 Z37992 *Pinus taeda*
DESCRIPTION: cinnamyl alcohol dehydrogenase.

CAA44216.1 X62343 *Nicotiana tabacum*
DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD14.

20 CAA44217.1 X62344 *Nicotiana tabacum*
DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD19.

25 BAA03099.1 D13991 *Aralia cordata*
DESCRIPTION: cinnamyl alcohol dehydrogenase. cadac1.

30 CAA79625.1 Z19573 *Medicago sativa*
DESCRIPTION: lignin biosynthesis. cinnamyl alcohol dehydrogenase.

35 AAF43140.1 AF217957 *Populus tremuloides*
DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.

AAC35845.1 AF083332 *Medicago sativa*
DESCRIPTION: cinnamyl-alcohol dehydrogenase. MsaCad2.

40 CAC07423.1 AJ295837 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: lignin monomer biosynthesis. cinnamyl alcohol dehydrogenase.
cad.

45 CAA79622.1 Z19568 *Populus deltoides*

DESCRIPTION: lignin biosynthesis. cinnamyl alcohol dehydrogenase.

AAC07987.1 AF038561 Eucalyptus globulus

- 5 DESCRIPTION: catalyses the reduction of cinnamaldehydes to the corresponding cinnamyl alcohols as the last step in the production of lignin monomers. cinnamyl alcohol dehydrogenase. CAD.

10 AAG15553.1 AF294793 Eucalyptus saligna

DESCRIPTION: cinnamyl alcohol dehydrogenase. cad. CAD.

AAK00679.1 AF229407 Brassica napus

- 15 DESCRIPTION: Eli3 product. ELI3-BN-2. protein identity based on similarity to Arabidopsis sequence; intron/exon junctions deduced from alignments to DNA or mRNA sequences already present in the GenBank database.

20

CAA46585.1 X65631 Eucalyptus gunnii

DESCRIPTION: cinnamyl-alcohol dehydrogenase. cad.

25 CAA53211.1 X75480 Eucalyptus gunnii

DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD.

AAK00681.1 AF229409 Brassica napus

- 30 DESCRIPTION: Eli3 product. ELI3-BN-4. protein identity based on similarity to Arabidopsis sequence; intron/exon junctions deduced from alignments to DNA or mRNA sequences already present in the GenBank database.

35

AAB70908.1 AF010290 Lolium perenne

DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.

40 AAK00682.1 AF229410 Brassica oleracea

DESCRIPTION: Eli3 product. ELI3-BO-1. protein identity based on similarity to Arabidopsis sequence; intron/exon junctions deduced from alignments to DNA or mRNA sequences already present in the GenBank database.

45

CAA74070.1 Y13733 Zea mays
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad.

5 CAA06687.1 AJ005702 Zea mays
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad.

10 AAK00678.1 AF229406 Brassica napus
DESCRIPTION: Eli3 product. ELI3-BN-1. protein identity based on
similarity to Arabidopsis sequence; intron/exon junctions deduced from
alignments to DNA or mRNA sequences already present in the GenBank
database.

15 CAA13177.1 AJ231135 Saccharum officinarum
DESCRIPTION: lignin biosynthesis. cinnamyl alcohol dehydrogenase. cad.

20 AAK00684.1 AF229412 Brassica rapa
DESCRIPTION: Eli3 product. ELI3-BR-2. protein identity based on
similarity to Arabidopsis sequence; intron/exon junctions deduced from
alignments to DNA or mRNA sequences already present in the GenBank
database.

25 AAK00680.1 AF229408 Brassica napus
DESCRIPTION: Eli3 product. ELI3-BN-3. protein identity based on
similarity to Arabidopsis sequence; intron/exon junctions deduced from
30 alignments to DNA or mRNA sequences already present in the GenBank
database.

35 AAK00683.1 AF229411 Brassica rapa
DESCRIPTION: Eli3 product. ELI3-BR-1. protein identity based on
similarity to Arabidopsis sequence; intron/exon junctions deduced from
alignments to DNA or mRNA sequences already present in the GenBank
database.

40 BAA19487.1 D86590 Zinnia elegans
DESCRIPTION: cinnamyl alcohol dehydrogenase. ZCAD1.

45 BAA04046.1 D16624 Eucalyptus botryoides
DESCRIPTION: cinnamyl alcohol dehydrogenase. Cad1:Eb:1.

AAD18000.1 AF109157 Eucalyptus globulus
 DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.
 5

AAF23409.1 AF207552 Brassica napus
 DESCRIPTION: cinnamyl alcohol dehydrogenase. CADa-1.
 10

AAF23412.1 AF207555 Brassica rapa
 DESCRIPTION: cinnamyl alcohol dehydrogenase. CADa.
 15

AAF23411.1 AF207554 Brassica oleracea
 DESCRIPTION: cinnamyl alcohol dehydrogenase. CADa.
 20

AAF23410.1 AF207553 Brassica napus
 DESCRIPTION: cinnamyl alcohol dehydrogenase. CADa-2.
 25

AAF23416.1 AF207559 Brassica rapa
 DESCRIPTION: cinnamyl alcohol dehydrogenase. CADb.
 30

AAF23415.1 AF207558 Brassica oleracea
 DESCRIPTION: cinnamyl alcohol dehydrogenase. CADb.
 35

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 BAA87853.1 AP000816 Oryza sativa
 DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
 predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
 (AF001308).
 40

BAA78764.1 AB023482 Oryza sativa
 DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region
 of
 the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein
 tyrosine-serine-threonine kinase.(D12522).
 45

AAF43496.1 AF131222 Lophopyrum elongatum
 DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by

salt stress, osmotic stress, and ABA treatment.

5 AAK11674.1 AF339747 *Lophopyrum elongatum*
DESCRIPTION: protein kinase. ESI47.

10 BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A*Arabidopsis thaliana*.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

15 AAG16628.1 AY007545 *Brassica napus*
DESCRIPTION: protein serine/threonine kinase BNK1.

20 AAC27894.1 AF023164 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. ltk1.

BAA94509.1 AB041503 *Populus nigra*
DESCRIPTION: protein kinase 1. PnPK1.

25 BAA94510.1 AB041504 *Populus nigra*
DESCRIPTION: protein kinase 2. PnPK2.

30 BAB03429.1 AP002817 *Oryza sativa*
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted
gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12;
putative protein kinase (AC006587).

35 BAB07999.1 AP002525 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST
C22619(S11214).

40 BAB39409.1 AP002901 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).

45 AAC27895.1 AF023165 *Zea mays*
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 2. ltk2.

- BAB21241.1 AP002953 *Oryza sativa*
 DESCRIPTION: Putative Pto kinase interactor 1. P0426D06.21. contains ESTs
 5 AU108280(E0721),D48017(S13927).
- AAG59657.1 AC084319 *Oryza sativa*
 DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.
 10
- AAF91337.1 AF249318 *Glycine max*
 DESCRIPTION: Pti1 kinase-like protein. Pti1b. protein kinase.
 15
- AAF91336.1 AF249317 *Glycine max*
 DESCRIPTION: Pti1 kinase-like protein. Pti1a. protein kinase.
 20
- CAB51834.1 00069 *Oryza sativa*
 DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.
 25
- BAA87852.1 AP000816 *Oryza sativa*
 DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).
 30
- BAA92221.1 AP001278 *Oryza sativa*
 DESCRIPTION: Similar to Arabidopsis thaliana chromosome II BAC F12L6
 35 genomic sequence, putative protein kinase. (AC004218).
- AAK00425.1 AC069324 *Oryza sativa*
 DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
 40
- AAB09771.1 U67422 *Zea mays*
 DESCRIPTION: CRINKLY4 precursor. cr4. receptor kinase homolog.
 45
- BAB18321.1 AP002865 *Oryza sativa*
 DESCRIPTION: putative receptor protein kinase. P0034C11.11.
- BAB40081.1 AP003074 *Oryza sativa*
 DESCRIPTION: putative receptor protein kinase. OSJNBa0004G10.30.

- 5 AAC61805.1 U28007 *Lycopersicon esculentum*
DESCRIPTION: serine/threonine protein kinase. Pto kinase interactor 1.
Pti1. Pti1 kinase.
- 10 BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).
- 15 AAD38286.1 AC007789 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0049B20.13.
- 20 BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).
- 25 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- 30 AAG03090.1 AC073405 *Oryza sativa*
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis
receptor-like kinase (AC007504).
- 35 BAB18292.1 AP002860 *Oryza sativa*
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.
- 40 AAF34428.1 AF172282 *Oryza sativa*
DESCRIPTION: receptor-like protein kinase. DUPR11.18.
- 45 AAG25966.1 AF302082 *Nicotiana tabacum*
DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase;
transcript abundance decreases rapidly after cytokinin treatment.
- AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.

DESCRIPTION: Similar to Arabidopsis thaliana wak4 gene; wall-associated kinase 4. (AJ009695).

- 5 AAC36318.1 AF053127 Malus x domestica
DESCRIPTION: leucine-rich receptor-like protein kinase. LRPKml.

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- 10 AAA86687.1 U15777 Lupinus albus
DESCRIPTION: farnesyl pyrophosphate synthase. fps1.

- 15 AAA87729.1 U20771 Lupinus albus
DESCRIPTION: farnesyl pyrophosphate synthase. fps1.

- 20 CAA72793.1 Y12072 Gossypium arboreum
DESCRIPTION: farnesyl pyrophosphate synthase. fps1.

- 25 BAB40665.1 AB053486 Humulus lupulus
DESCRIPTION: farnesyl pyrophosphate synthase. fpps.

- BAB40666.1 AB053487 Humulus lupulus
DESCRIPTION: farnesyl pyrophosphate synthase. fpps.

- 30 CAA57893.1 X82543 Parthenium argentatum
DESCRIPTION: farnesyl diphosphate synthase. fps2.

- 35 AAC78557.1 AF019892 Helianthus annuus
DESCRIPTION: farnesyl pyrophosphate synthase. FPS.

- 40 CAA57892.1 X82542 Parthenium argentatum
DESCRIPTION: farnesyl diphosphate synthase. fps1.

- AAC49452.1 U36376 Artemisia annua
DESCRIPTION: farnesyl diphosphate synthase. fps1.

- 45 CAA59170.1 X84695 Capsicum annuum

DESCRIPTION: dimethylallyltransferase. Fps, farnesyl pyrophosphate synthase gene.

- 5 AAC73051.1 AF048747 *Lycopersicon esculentum*
DESCRIPTION: synthesis of farnesyl pyrophosphate. farnesyl pyrophosphate synthase. FPS1. prenyl transferase; farnesyl diphosphate synthetase.
- 10 AAD17204.1 AF112881 *Artemisia annua*
DESCRIPTION: farnesyl diphosphate synthase.
- 15 BAA19856.1 D85317 *Oryza sativa*
DESCRIPTION: farnesyl pyrophosphate synthase. dimethylallyltransferase; geranyltranstransferase.
- 20 BAA36276.1 AB021747 *Oryza sativa*
DESCRIPTION: farnesyl diphosphate synthase. FPPS1.
- 25 AAD32648.1 AF136602 *Artemisia annua*
DESCRIPTION: farnesyl diphosphate synthase. fps2.
- 30 AAB39276.1 L39789 *Zea mays*
DESCRIPTION: farnesyl pyrophosphate synthetase. fps. putative.
- 35 AAD27558.1 AF111710 *Oryza sativa* subsp. *indica*
DESCRIPTION: putative farnesyl pyrophosphate synthase. similar to *Oryza sativa* EST clones E10230_1A, C52647_1A, 232.
- 40 BAA36347.1 AB021979 *Oryza sativa*
DESCRIPTION: farnesyl diphosphate synthase. FPPS2.
- 45 AAD37789.1 AF149257 *Artemisia annua*
DESCRIPTION: farnesyl diphosphate synthase. FPP synthase.
- BAB20822.1 AB045713 *Taraxacum japonicum*
DESCRIPTION: putative FPP synthase. TJFPPS.

BAB16688.1 AB041627 *Eucommia ulmoides*
DESCRIPTION: FPP synthase 2. EUFPPS2. putative.

5

BAB21061.1 AB046212 *Sonchus oleraceus*
DESCRIPTION: putative FPP synthase. SoFPPS.

10 AAD45122.1 AF164026 *Xanthoceras sorbifolium*
DESCRIPTION: synthesis of farnesyl pyrophosphate. farnesyl pyrophosphate
synthase. FPS. prenyl transferase; farnesyl diphosphate synthetase.

15 AAB93951.1 U97330 *Nicotiana tabacum*
DESCRIPTION: farnesylpyrophosphate synthase. FPPS.

20 BAB16687.1 AB041626 *Eucommia ulmoides*
DESCRIPTION: FPP synthase 1. EUFPPS1. putative.

25 BAB39479.1 AB049086 *Youngia japonica*
DESCRIPTION: putative FPP synthase 1. YjFPPS1.

AAB93984.1 AF005201 *Parthenium argentatum*
DESCRIPTION: farnesyl pyrophosphate synthase. FPS3.

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BAB03615.1 AP002522 *Oryza sativa*
DESCRIPTION: putative gamma-glutamyltransferase. P0009G03.15. contains
ESTs AU056150(S20332),AU056151(S20332).

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BAB03616.1 AP002522 *Oryza sativa*
DESCRIPTION: putative gamma-glutamyltransferase. P0009G03.16. contains
EST AU056150(S20332).

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CAB96145.1 AJ250951 *Mesembryanthemum crystallinum*
DESCRIPTION: phospholipid hydroperoxide glutathione peroxidase-like
protein. gpxmc1.

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- CAA42780.1 X60219 *Nicotiana sylvestris*
DESCRIPTION: homologous to animal glutathione peroxidases.
- 5 BAB16430.1 AB041518 *Nicotiana tabacum*
DESCRIPTION: glutathione peroxidase Nt-SubC08. Nt-SubC08.
- 10 CAA75054.1 Y14762 *Lycopersicon esculentum*
DESCRIPTION: glutathione peroxidase. GPXle-1.
- 15 AAB94892.1 AF037051 *Gossypium hirsutum*
DESCRIPTION: glutathione peroxidase.
- 20 CAB59893.1 AJ238697 *Hordeum vulgare*
DESCRIPTION: GPX12Hv, glutathione peroxidase-like protein.
- 25 BAA22194.1 D63425 *Spinacia oleracea*
DESCRIPTION: phospholipid hydroperoxide glutathione peroxidase-like protein. similar to mammalian phospholipid hydroperoxide glutathione peroxidases.
- 30 CAB59895.1 AJ238745 *Hordeum vulgare*
DESCRIPTION: glutathione peroxidase-like protein GPX54Hv.
- 35 AAC78466.1 AF053311 *Zantedeschia aethiopica*
DESCRIPTION: glutathione peroxidase. gpx.
- CAA04142.1 AJ000508 *Pisum sativum*
DESCRIPTION: phospholipid glutathione peroxidase. plastid-localised.
- 40 CAA75009.1 Y14707 *Helianthus annuus*
DESCRIPTION: glutathione peroxidase. GPxha-2.
- 45 CAB59894.1 AJ238744 *Hordeum vulgare*
DESCRIPTION: glutathione peroxidase-like protein GPX15Hv.

- CAA74775.1 Y14429 Helianthus annuus
DESCRIPTION: glutathione peroxidase. GPxha-1.
- 5 CAC17628.1 AJ270955 Oryza sativa
DESCRIPTION: putative role in antioxidative systems. putative
phospholipid hydroperoxide glutathione peroxidase. riPHGPX.
- 10 BAA83594.1 AB009083 Chlamydomonas sp. W80
DESCRIPTION: glutathione peroxidase.
- 15 AAB66330.1 AF014927 Chlamydomonas reinhardtii
DESCRIPTION: glutathione peroxidase homolog. gpxh.
- 20 CAA75055.1 Y14763 Lycopersicon esculentum
DESCRIPTION: glutathione peroxidase. GPXle-2.
- 25 CAA09194.1 AJ010455 Triticum aestivum
DESCRIPTION: glutathione peroxidase. PHGPX6.
- CAB66331.1 AJ279689 Betula pendula
DESCRIPTION: glutathione peroxidase. gpx.
- 30 163

AAF67753.1 AF255651 Brassica rapa subsp. pekinensis
DESCRIPTION: conversion of oxidized glutathione to reduced glutathione.
cytosolic glutathione reductase. GR1.
- 35 AAC49980.2 AF008441 Brassica rapa
DESCRIPTION: glutathione reductase. BcGR1. cytosolic.
- 40 BAA11214.1 D78136 Oryza sativa
DESCRIPTION: Glutathione Reductase. putative.
- 45 CAA66924.1 X98274 Pisum sativum
DESCRIPTION: glutathione reductase. cytosolic.

- 5 BAA36283.1 D85751 *Oryza sativa*
DESCRIPTION: glutathione reductase.
- 10 BAA37092.1 AB009592 *Oryza sativa*
DESCRIPTION: conversion of oxidized glutathione to reduced glutathione.
cytosolic glutathione reductase. RGRC2. Amino Acids 1-496.
- 15 BAA07108.1 D37870 *Spinacia oleracea*
DESCRIPTION: Glutathione Reductase precursor. Chloroplastic glutathione
reductase.
- 20 CAC13956.1 AJ400816 *Mesembryanthemum crystallinum*
DESCRIPTION: reduction of glutathione. glutathione reductase. gr1.
- 25 CAB66332.1 AJ279690 *Betula pendula*
DESCRIPTION: glutathione reductase. gr.
- 30 CAA53925.1 X76293 *Nicotiana tabacum*
DESCRIPTION: glutathione reductase (NADPH). gor.
- 35 CAA42921.1 X60373 *Pisum sativum*
DESCRIPTION: glutathione reductase (NADPH). Protein sequence is in
conflict with the conceptual translation.
- 40 AAK27157.1 AF349449 *Brassica juncea*
DESCRIPTION: glutathione reductase. GR2.
- 45 AAD28177.1 AF109694 *Brassica juncea*
DESCRIPTION: glutathione reductase. GR1.
- CAA62482.1 X90996 *Pisum sativum*
DESCRIPTION: glutathione reductase (NADPH). gr. alpha II subunit.
- AAF26175.1 AF105199 *Glycine max*

DESCRIPTION: glutathione reductase. GR-5.

AAB70837.1 AF019907 *Vitis vinifera*

5 DESCRIPTION: glutathione reductase (NADPH). GOR. VvGR1.

AAA33962.1 L11632 *Glycine max*

10 DESCRIPTION: glutathione reductase. GR.

CAA54043.1 X76533 *Nicotiana tabacum*

DESCRIPTION: glutathione reductase (NADPH). gor.

CAA06835.1 AJ006055 *Zea mays*

DESCRIPTION: NADPH-dependent reduction of glutathione disulphide.
glutathione reductase. gor1.

CAA53993.1 X76455 *Nicotiana tabacum*

DESCRIPTION: glutathione reductase. gor.

AAB30526.1 S70187 *Glycine max*

DESCRIPTION: ferric leghemoglobin reductase. ferric leghemoglobin
reductase, FLbR. Method: conceptual translation with partial peptide
sequencing; This sequence comes from Fig. 3; FLbR.

AAC26053.1 AF074940 *Glycine max*

DESCRIPTION: ferric leghemoglobin reductase-2 precursor. FLbR
homolog;FLbR-2.

AAD53185.1 AF181096 *Vigna unguiculata*

DESCRIPTION: ferric leghemoglobin reductase. flbr.

AAA60979.1 U06461 *Pisum sativum*

DESCRIPTION: catalyzes the conversion of monodehydroascorbate to
ascorbate, oxidizing NADH in the process, binds to flavin as a single
subunit. monodehydroascorbate reductase.

BAA05408.1 D26392 *Cucumis sativus*

DESCRIPTION: monodehydroascorbate reductase.

5 AAC41654.1 L41345 Lycopersicon esculentum
DESCRIPTION: ascorbate free radical reductase. AFRR.

10 AAD53522.1 AF158602 Zantedeschia aethiopica
DESCRIPTION: monodehydroascorbate reductase. MDAR. putative.

AAD28178.1 AF109695 Brassica juncea
DESCRIPTION: monodehydroascorbate reductase. MDAR1.

15 BAA77214.1 D85764 Oryza sativa
DESCRIPTION: cytosolic monodehydroascorbate reductase.

164
20 -----
CAA04391.1 AJ000923 Carica papaya
DESCRIPTION: glutathione transferase. PGST1.

25 AAC18566.1 AF048978 Glycine max
DESCRIPTION: 2,4-D inducible glutathione S-transferase. GSTa.

30 AAG34800.1 AF243365 Glycine max
DESCRIPTION: glutathione S-transferase GST 10.

35 AAF22647.1 AF193439 Lycopersicon esculentum
DESCRIPTION: glutathione S-transferase/oxidase. BI-GST/GPX.

CAA71784.1 Y10820 Glycine max
DESCRIPTION: glutathione transferase.

40 AAG34799.1 AF243364 Glycine max
DESCRIPTION: glutathione S-transferase GST 9.

45 AAG16760.1 AY007562 Lycopersicon esculentum
DESCRIPTION: putative glutathione S-transferase T5.

[illegible]

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5 AAG16758.1 AY007560 Lycopersicon esculentum
DESCRIPTION: putative glutathione S-transferase T3.

AAG34798.1 AF243363 Glycine max
DESCRIPTION: glutathione S-transferase GST 8.

10 AAG34842.1 AF244699 Zea mays
DESCRIPTION: glutathione S-transferase GST 34.

15 AAG34807.1 AF243372 Glycine max
DESCRIPTION: glutathione S-transferase GST 17.

20 AAG34809.1 AF243374 Glycine max
DESCRIPTION: glutathione S-transferase GST 19.

25 AAG34839.1 AF244696 Zea mays
DESCRIPTION: glutathione S-transferase GST 31.

AAG34804.1 AF243369 Glycine max
DESCRIPTION: glutathione S-transferase GST 14.

30 AAG34844.1 AF244701 Zea mays
DESCRIPTION: glutathione S-transferase GST 36.

35 AAG34831.1 AF244688 Zea mays
DESCRIPTION: glutathione S-transferase GST 23.

40 AAG34797.1 AF243362 Glycine max
DESCRIPTION: glutathione S-transferase GST 7.

45 AAG34832.1 AF244689 Zea mays
DESCRIPTION: glutathione S-transferase GST 24.

AAG32471.1 AF309378 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTU4.

5 AAG34796.1 AF243361 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 6.

10 AAG34810.1 AF243375 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 20.

15 AAG34835.1 AF244692 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 27.

20 AAC32139.1 AF051238 *Picea mariana*
DESCRIPTION: probable glutathione S-transferase. Sb52. similar to
Nicotiana tabacum probable glutathione S-transferase encoded by GenBank
Accession Number X56266.

165

25 CAA71878.1 Y10984 *Brassica juncea*
DESCRIPTION: ATP-dependent addition of glycine to gamma-
glutamylcysteine.
glutathione synthetase. gshII.

30 AAB71231.1 AF017984 *Lycopersicon esculentum*
DESCRIPTION: glutathione synthetase. GSH2.

35 AAF98157.1 AF258320 *Phaseolus vulgaris*
DESCRIPTION: homoglutathione synthetase. hgshs.

40 AAF98156.1 AF258319 *Pisum sativum*
DESCRIPTION: putative homoglutathione synthetase. hgshs.

45 CAB91078.1 AJ272035 *Glycine max*
DESCRIPTION: homoglutathione synthetase. hGS. putatively predicted to be
targetted to the chloroplast.

AAF98121.1 AF231137 Pisum sativum
DESCRIPTION: glutathione synthetase precursor. gshs. putative
mitochondrial protein.

5

AAD29848.1 AF075699 Medicago truncatula
DESCRIPTION: putative glutathione synthetase. GSHS1.

10

AAD29849.1 AF075700 Medicago truncatula
DESCRIPTION: putative glutathione synthetase. GSHS2.

166

15

BAA83711.1 AB014484 Nicotiana tabacum
DESCRIPTION: heat shock factor. NtHSF2.

20

AAF37579.1 AF235958 Medicago sativa
DESCRIPTION: heat shock transcription factor. HSFA4-6. MsHSFA4-6.

25

CAA58117.1 X82943 Zea mays
DESCRIPTION: heat shock factor. hsfb.

30

CAA47868.1 X67599 Lycopersicon esculentum
DESCRIPTION: heat stress transcription factor 8. hsf8.

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CAA47869.1 X67600 Lycopersicon peruvianum
DESCRIPTION: heat shock transcription factor 8. hsf8.

CAA47870.1 X67601 Lycopersicon peruvianum
DESCRIPTION: heat stress transcription factor HSF30. hsf30.

40

AAF74563.1 AF208544 Lycopersicon peruvianum
DESCRIPTION: heat stress transcription factor A3. HSFA3.

45

CAA87080.1 Z46956 Glycine max
DESCRIPTION: heat shock transcription factor 5. HSF.

CAA87076.1 Z46952 Glycine max
DESCRIPTION: heat shock transcription factor 21. HSF.

5 CAA39034.1 X55347 Lycopersicon peruvianum
DESCRIPTION: heat stress transcription factor. Lp-HSF24.

10 BAA83710.1 AB014483 Nicotiana tabacum
DESCRIPTION: heat shock factor. NtHSF1.

15 CAA87077.1 Z46953 Glycine max
DESCRIPTION: heat shock transcription factor 34. HSF. corresponds to
longest open reading frame; preceded by four short open reading frames in
the 5' leader sequence.

20 BAB19067.1 AP002744 Oryza sativa
DESCRIPTION: putative heat shock factor protein 1 (HSF 1). P0006C01.9.

25 CAA09301.1 AJ010644 Pisum sativum
DESCRIPTION: heat shock transcription factor (HSFA). hsfA.

30 CAA87079.1 Z46955 Glycine max
DESCRIPTION: heat shock transcription factor 31. HSF.

CAA87075.1 Z46951 Glycine max
DESCRIPTION: heat shock transcription factor 29. HSF.

35 CAA09300.1 AJ010643 Pisum sativum
DESCRIPTION: heat shock transcription factor (HSFA). hsfA.

168

40 BAA83710.1 AB014483 Nicotiana tabacum
DESCRIPTION: heat shock factor. NtHSF1.

45 CAA39034.1 X55347 Lycopersicon peruvianum
DESCRIPTION: heat stress transcription factor. Lp-HSF24.

CAA87077.1 Z46953 Glycine max
DESCRIPTION: heat shock transcription factor 34. HSF. corresponds to
longest open reading frame; preceeded by four short open reading frames in
the 5' leader sequence.

CAA87080.1 Z46956 Glycine max
DESCRIPTION: heat shock transcription factor 5. HSF.

CAA47869.1 X67600 Lycopersicon peruvianum
DESCRIPTION: heat shock transcription factor 8. hsf8.

CAA47868.1 X67599 Lycopersicon esculentum
DESCRIPTION: heat stress transcription factor 8. hsf8.

BAA83711.1 AB014484 Nicotiana tabacum
DESCRIPTION: heat shock factor. NtHSF2.

CAA58117.1 X82943 Zea mays
DESCRIPTION: heat shock factor. hsfb.

CAA87075.1 Z46951 Glycine max
DESCRIPTION: heat shock transcription factor 29. HSF.

CAA87076.1 Z46952 Glycine max
DESCRIPTION: heat shock transcription factor 21. HSF.

CAA47870.1 X67601 Lycopersicon peruvianum
DESCRIPTION: heat stress transcription factor HSF30. hsf30.

AAF74563.1 AF208544 Lycopersicon peruvianum
DESCRIPTION: heat stress transcription factor A3. HSFA3.

AAF37579.1 AF235958 Medicago sativa
DESCRIPTION: heat shock transcription factor. HSFA4-6. MsHSFA4-6.

CAA87079.1 Z46955 Glycine max
DESCRIPTION: heat shock transcription factor 31. HSF.

5

BAB19067.1 AP002744 Oryza sativa
DESCRIPTION: putative heat shock factor protein 1 (HSF 1). P0006C01.9.

10

CAA09301.1 AJ010644 Pisum sativum
DESCRIPTION: heat shock transcription factor (HSFA). hsfA.

15

CAA09300.1 AJ010643 Pisum sativum
DESCRIPTION: heat shock transcription factor (HSFA). hsfA.

169

20

AAB72109.1 AF022217 Brassica rapa
DESCRIPTION: low molecular weight heat-shock protein. BcHSP17.6. 17.6
kDa; cytosolic class I.

25

CAB93512.1 AJ243565 Brassica oleracea
DESCRIPTION: putative class I small heat shock protein. HSP17.7-a
protein. hsp17.7-a.

30

CAA37847.1 X53851 Daucus carota
DESCRIPTION: heat shock protein.

35

AAD49336.1 AF166277 Nicotiana tabacum
DESCRIPTION: low molecular weight heat-shock protein. LHS-1. TLHS-1.

40

BAA33062.1 AB017273 Cuscuta japonica
DESCRIPTION: low-molecular-weight heat shock protein. CJHSP17.

45

CAB36910.1 AJ000691 Quercus suber
DESCRIPTION: stress protein chaperone. heat shock protein 17.4. hsp17.
CAA08908.1 AJ009880 Castanea sativa
DESCRIPTION: molecular chaperone. cytosolic class I small heat-shock

protein HSF17.5. hsp17.5.

5 AAA33975.1 M11395 Glycine max
DESCRIPTION: small heat shock protein.

10 CAA25578.1 X01104 Glycine max
DESCRIPTION: heat shock protein 6871 (aa 1-153).

AAB03893.1 M11318 Glycine max
DESCRIPTION: 17.5 kd heat shock protein Gmhsp17.6L.

15 CAA41547.1 X58711 Medicago sativa
DESCRIPTION: heat shock protein.

20 AAB63310.1 U46544 Helianthus annuus
DESCRIPTION: 18.6 kDa heat-shock protein. Class I low-molecular-weight
heat-shock protein.

25 CAB08441.1 Z95153 Helianthus annuus
DESCRIPTION: 17.6 kD class I small heat-shock protein HSP17.6. Ha
hsp17.6.

30 CAA42222.1 X59701 Helianthus annuus
DESCRIPTION: 17.6 kDa heat shock protein.

35 CAA37848.1 X53852 Daucus carota
DESCRIPTION: heat shock protein.

40 AAC39360.1 U63631 Fragaria x ananassa
DESCRIPTION: LMW heat shock protein.

AAA33672.1 M33899 Pisum sativum
DESCRIPTION: 18.1 kDa heat shock protein (hsp18.1).

45 AAB63311.1 U46545 Helianthus annuus

DESCRIPTION: 17.7 kDa heat shock protein. Class I low-molecular-weight heat-shock protein.

- 5 AAA33974.1 M11317 Glycine max
DESCRIPTION: 17.6 kd heat shock protein Gmhsp17.6L.
- 10 CAA63903.1 X94193 Pennisetum glaucum
DESCRIPTION: heat shock protein 17.9. hsp17.9.
- 15 AAA61632.1 U08601 Papaver somniferum
DESCRIPTION: low molecular weight heat-shock protein.
- CAB55634.2 AJ237596 Helianthus annuus
DESCRIPTION: 17.9 kDa heat-shock protein. hsp17.9.
- 20 AAC78392.1 U83669 Oryza sativa
DESCRIPTION: low molecular mass heat shock protein Oshsp17.3.
OSHSP17.3.
class I LMMHSP.
- 25 AAA33910.1 M80939 Oryza sativa
DESCRIPTION: 16.9 kDa heat shock protein.
- 30 BAA02160.1 D12635 Oryza sativa
DESCRIPTION: 'low molecular weight heat shock protein'.
- 35 CAA43210.1 X60820 Oryza sativa
DESCRIPTION: 16.9 KD low molecular weight heat shock protein.
- 40 CAA37864.1 X53870 Chenopodium rubrum
DESCRIPTION: heat-shock protein.
- 45 AAA33909.1 M80938 Oryza sativa
DESCRIPTION: 16.9 kDa heat shock protein.

AAC78393.1 U83670 Oryza sativa
DESCRIPTION: low molecular mass heat shock protein Oshsp18.0.
OSHSP18.0.
class I LMMHSP.

5

AAB39856.1 U81385 Oryza sativa
DESCRIPTION: heat shock protein. Oshsp16.9C. class I, low molecular mass.

10

AAD30454.1 AF123257 Lycopersicon esculentum
DESCRIPTION: 17.6 kD class I small heat shock protein. HSP17.6.

15 AAA33671.1 M33900 Pisum sativum
DESCRIPTION: 17.9 kDa heat shock protein (hsp17.9).

20 AAC78394.1 U83671 Oryza sativa
DESCRIPTION: low molecular mass heat shock protein Oshsp17.7.
OSHSP17.7.
class I LMMHSP.

25 CAB93514.1 AJ243567 Brassica oleracea
DESCRIPTION: Putative class I small heat shock protein. HSP17.x protein.
hsp17.x.

30 CAA63901.1 X94191 Pennisetum glaucum
DESCRIPTION: heat shock protein 17.0. hsp17.0.

35 CAA63902.1 X94192 Pennisetum glaucum
DESCRIPTION: heat shock protein 16.9. hsp16.9.

40 AAD30452.1 AF123255 Lycopersicon esculentum
DESCRIPTION: 17.7 kD class I small heat shock protein. HSP17.7.

45 CAA46641.1 X65725 Zea mays
DESCRIPTION: heat shock protein 17.2. Zmhs17.2. Class I low molecular
weight heat shock protein.

CAA39603.1 X56138 *Lycopersicon esculentum*
DESCRIPTION: small heat shock protein (class I).

5 CAA63570.1 X92983 *Pseudotsuga menziesii*
DESCRIPTION: low molecular weight heat-shock protein.

10 AAD30453.1 AF123256 *Lycopersicon esculentum*
DESCRIPTION: 17.8 kD class I small heat shock protein. HSP17.8.

15 CAA63571.1 X92984 *Pseudotsuga menziesii*
DESCRIPTION: low molecular weight heat-shock protein.

CAA31785.1 X13431 *Triticum aestivum*
DESCRIPTION: put. heat shock protein (AA 1 -151).

20 CAA53286.1 X75616 *Oryza sativa*
DESCRIPTION: heat shock protein 17.8.

170
25 -----
AAC14577.1 U72396 *Lycopersicon esculentum*
DESCRIPTION: class II small heat shock protein Le-HSP17.6. heat
treatment/chilling tolerance related protein from tomato fruit.

30 AAA33670.1 M33901 *Pisum sativum*
DESCRIPTION: 17.7 kDa heat shock protein (hsp17.7).

35 CAA82653.1 Z29554 *Helianthus annuus*
DESCRIPTION: 17.9 kDa heat-shock protein.

40 AAD41409.1 AF159562 *Prunus dulcis*
DESCRIPTION: cytosolic class II low molecular weight heat shock protein.
hsp17.5.

45 CAA65020.1 X95716 *Petroselinum crispum*
DESCRIPTION: small heat shock protein. cytoplasmic class II HSP.

AAC36312.1 AF090115 *Lycopersicon esculentum*
DESCRIPTION: cytosolic class II small heat shock protein HCT2. HSP17.4.

5

AAB01561.1 L47717 *Picea glauca*
DESCRIPTION: heat shock protein 17.0. EMB27.

10

AAB39336.1 M99430 *Ipomoea nil*
DESCRIPTION: small heat shock protein.

15

AAB01562.1 L47740 *Picea glauca*
DESCRIPTION: class II cytoplasmic small molecular weight heat shock protein 17.1. EMB29, SMW HSP17.1.

20

CAA67206.1 X98617 *Medicago sativa*
DESCRIPTION: 17kD heat shock protein.

25

BAA99529.1 AP002484 *Oryza sativa*
DESCRIPTION: putative heat shock protein, 18K - maize. P0489A01.20.
contains ESTs C99035(E4351),AU093460(E3974).

30

CAA41218.1 X58279 *Triticum aestivum*
DESCRIPTION: heat shock protein 17.3. Tahsp17.3.

35

CAA67726.1 X99346 *Picea abies*
DESCRIPTION: small heat shock protein.

40

CAA38012.1 X54075 *Zea mays*
DESCRIPTION: 18kDa heat shock protein.

45

CAA38013.1 X54076 *Zea mays*
DESCRIPTION: 18kDa heat shock protein.

AAB26481.1 S59777 *Zea mays*
DESCRIPTION: HSP18. HSP18. 18 kda heat shock protein; This sequence comes

from Fig. 2B.

- 5 AAB39335.1 M99429 *Ipomoea nil*
DESCRIPTION: small heat shock protein.
- 10 AAD09184.1 AF089845 *Funaria hygrometrica*
DESCRIPTION: cytosolic II small heat shock protein HSP16.4II. HSP16.4II.
- 15 BAA04841.1 D21817 *Lilium longiflorum*
DESCRIPTION: small heat shock protein. LIM11.
- AAD09185.1 AF089846 *Funaria hygrometrica*
DESCRIPTION: cytosolic II small heat shock protein HSP18.3II. HSP18.3II.
- 20 BAA04842.1 D21818 *Lilium longiflorum*
DESCRIPTION: small heat shock protein. LIM12.
- 25 CAA63570.1 X92983 *Pseudotsuga menziesii*
DESCRIPTION: low molecular weight heat-shock protein.
- 30 CAA63571.1 X92984 *Pseudotsuga menziesii*
DESCRIPTION: low molecular weight heat-shock protein.
- AAC39360.1 U63631 *Fragaria x ananassa*
DESCRIPTION: LMW heat shock protein.
- 35 AAD09178.1 AF087640 *Funaria hygrometrica*
DESCRIPTION: cytosolic I small heat shock protein HSP17.2IA. HSP17.2IA.
- 40 AAD09182.1 AF089843 *Funaria hygrometrica*
DESCRIPTION: cytosolic I small heat shock protein HSP17.2IC. HSP17.2IC.
- 45 BAA04840.1 D21816 *Lilium longiflorum*
DESCRIPTION: small heat shock protein. LIM10.

CAB93514.1 AJ243567 *Brassica oleracea*
 DESCRIPTION: Putative class I small heat shock protein. HSP17.x protein.
 hsp17.x.

5

AAD30452.1 AF123255 *Lycopersicon esculentum*
 DESCRIPTION: 17.7 kD class I small heat shock protein. HSP17.7.

10

AAB63311.1 U46545 *Helianthus annuus*
 DESCRIPTION: 17.7 kDa heat shock protein. Class I low-molecular-weight
 heat-shock protein.

15

CAA31785.1 X13431 *Triticum aestivum*
 DESCRIPTION: put. heat shock protein (AA 1 -151).

20

CAA63901.1 X94191 *Pennisetum glaucum*
 DESCRIPTION: heat shock protein 17.0. hsp17.0.

25

AAA33672.1 M33899 *Pisum sativum*
 DESCRIPTION: 18.1 kDa heat shock protein (hsp18.1).

30

CAA41547.1 X58711 *Medicago sativa*
 DESCRIPTION: heat shock protein.

35

CAA46641.1 X65725 *Zea mays*
 DESCRIPTION: heat shock protein 17.2. Zmhsp 17.2. Class I low molecular
 weight heat shock protein.

40

AAB39856.1 U81385 *Oryza sativa*
 DESCRIPTION: heat shock protein. Oshsp16.9C. class I, low molecular mass.

45

AAC78394.1 U83671 *Oryza sativa*
 DESCRIPTION: low molecular mass heat shock protein Oshsp17.7.
 OSHSP17.7.
 class I LMMHSP.

AAC78392.1 U83669 *Oryza sativa*
DESCRIPTION: low molecular mass heat shock protein Oshsp17.3.
OSHSP17.3.
class I LMMHSP.

5

CAA39603.1 X56138 *Lycopersicon esculentum*
DESCRIPTION: small heat shock protein (class I).

10

AAA33910.1 M80939 *Oryza sativa*
DESCRIPTION: 16.9 kDa heat shock protein.

15 AAA33909.1 M80938 *Oryza sativa*
DESCRIPTION: 16.9 kDa heat shock protein.

20 CAA43210.1 X60820 *Oryza sativa*
DESCRIPTION: 16.9 KD low molecular weight heat shock protein.

25 AAD30453.1 AF123256 *Lycopersicon esculentum*
DESCRIPTION: 17.8 kD class I small heat shock protein. HSP17.8.

AAA34294.1 L14444 *Triticum aestivum*
DESCRIPTION: heat shock protein 16.9C. hsp16.9C.

30

CAA69172.1 Y07844 *Hordeum vulgare*
DESCRIPTION: 17 kDa class I small heat shock protein. hsp17. putative.

35 AAD30454.1 AF123257 *Lycopersicon esculentum*
DESCRIPTION: 17.6 kD class I small heat shock protein. HSP17.6.

171

40 CAA82653.1 Z29554 *Helianthus annuus*
DESCRIPTION: 17.9 kDa heat-shock protein.

45 AAC14577.1 U72396 *Lycopersicon esculentum*
DESCRIPTION: class II small heat shock protein Le-HSP17.6. heat
treatment/chilling tolerance related protein from tomato fruit.

- CAA65020.1 X95716 *Petroselinum crispum*
DESCRIPTION: small heat shock protein. cytoplasmic class II HSP.
- 5
- AAB39336.1 M99430 *Ipomoea nil*
DESCRIPTION: small heat shock protein.
- 10
- AAA33670.1 M33901 *Pisum sativum*
DESCRIPTION: 17.7 kDa heat shock protein (hsp17.7).
- 15
- AAD41409.1 AF159562 *Prunus dulcis*
DESCRIPTION: cytosolic class II low molecular weight heat shock protein.
hsp17.5.
- 20
- CAA67206.1 X98617 *Medicago sativa*
DESCRIPTION: 17kD heat shock protein.
- 25
- BAA99529.1 AP002484 *Oryza sativa*
DESCRIPTION: putative heat shock protein, 18K - maize. P0489A01.20.
contains ESTs C99035(E4351),AU093460(E3974).
- 30
- AAC36312.1 AF090115 *Lycopersicon esculentum*
DESCRIPTION: cytosolic class II small heat shock protein HCT2. HSP17.4.
- 35
- CAA38012.1 X54075 *Zea mays*
DESCRIPTION: 18kDa heat shock protein.
- 40
- CAA38013.1 X54076 *Zea mays*
DESCRIPTION: 18kDa heat shock protein.
- 45
- CAA41218.1 X58279 *Triticum aestivum*
DESCRIPTION: heat shock protein 17.3. Tahsp17.3.
- AAB26481.1 S59777 *Zea mays*

DESCRIPTION: HSP18. HSP18. 18 kda heat shock protein; This sequence comes from Fig. 2B.

5

AAB01561.1 L47717 *Picea glauca*
DESCRIPTION: heat shock protein 17.0. EMB27.

10

AAB39335.1 M99429 *Ipomoea nil*
DESCRIPTION: small heat shock protein.

15

AAB01562.1 L47740 *Picea glauca*
DESCRIPTION: class II cytoplasmic small molecular weight heat shock protein 17.1. EMB29, SMW HSP17.1.

20

CAA67726.1 X99346 *Picea abies*
DESCRIPTION: small heat shock protein.

25

AAD09184.1 AF089845 *Funaria hygrometrica*
DESCRIPTION: cytosolic II small heat shock protein HSP16.4II. HSP16.4II.

30

BAA04841.1 D21817 *Lilium longiflorum*
DESCRIPTION: small heat shock protein. LIM11.

35

BAA04842.1 D21818 *Lilium longiflorum*
DESCRIPTION: small heat shock protein. LIM12.

40

AAD09185.1 AF089846 *Funaria hygrometrica*
DESCRIPTION: cytosolic II small heat shock protein HSP18.3II. HSP18.3II.

45

BAA04840.1 D21816 *Lilium longiflorum*
DESCRIPTION: small heat shock protein. LIM10.

CAA63570.1 X92983 *Pseudotsuga menziesii*
DESCRIPTION: low molecular weight heat-shock protein.

CAA63571.1 X92984 *Pseudotsuga menziesii*
DESCRIPTION: low molecular weight heat-shock protein.

5 AAD30452.1 AF123255 *Lycopersicon esculentum*
DESCRIPTION: 17.7 kD class I small heat shock protein. HSP17.7.

10 AAD09178.1 AF087640 *Funaria hygrometrica*
DESCRIPTION: cytosolic I small heat shock protein HSP17.2IA. HSP17.2IA.

15 AAB63311.1 U46545 *Helianthus annuus*
DESCRIPTION: 17.7 kDa heat shock protein. Class I low-molecular-weight
heat-shock protein.

20 CAA39603.1 X56138 *Lycopersicon esculentum*
DESCRIPTION: small heat shock protein (class I).

25 AAC39360.1 U63631 *Fragaria x ananassa*
DESCRIPTION: LMW heat shock protein.

AAA33672.1 M33899 *Pisum sativum*
DESCRIPTION: 18.1 kDa heat shock protein (hsp18.1).

30 AAD30453.1 AF123256 *Lycopersicon esculentum*
DESCRIPTION: 17.8 kD class I small heat shock protein. HSP17.8.

35 AAD30454.1 AF123257 *Lycopersicon esculentum*
DESCRIPTION: 17.6 kD class I small heat shock protein. HSP17.6.

40 CAA41547.1 X58711 *Medicago sativa*
DESCRIPTION: heat shock protein.

CAA31785.1 X13431 *Triticum aestivum*
DESCRIPTION: put. heat shock protein (AA 1 -151).

45 AAB39856.1 U81385 *Oryza sativa*

DESCRIPTION: heat shock protein. Oshsp16.9C. class I, low molecular mass.

CAA41546.1 X58710 Medicago sativa
5 DESCRIPTION: heat shock protein.

CAB93514.1 AJ243567 Brassica oleracea
10 DESCRIPTION: Putative class I small heat shock protein. HSP17.x protein.
hsp17.x.

CAA63901.1 X94191 Pennisetum glaucum
15 DESCRIPTION: heat shock protein 17.0. hsp17.0.

AAA33910.1 M80939 Oryza sativa
20 DESCRIPTION: 16.9 kDa heat shock protein.

AAA33909.1 M80938 Oryza sativa
DESCRIPTION: 16.9 kDa heat shock protein.

CAA43210.1 X60820 Oryza sativa
25 DESCRIPTION: 16.9 KD low molecular weight heat shock protein.

AAB03097.1 U21723 Glycine max
30 DESCRIPTION: Hsp22.3. Gmhsp22.3. low molecular weight heat shock
protein.

AAC78394.1 U83671 Oryza sativa
35 DESCRIPTION: low molecular mass heat shock protein Oshsp17.7.
OSHSP17.7.
class I LMMHSP.

AAC78392.1 U83669 Oryza sativa
40 DESCRIPTION: low molecular mass heat shock protein Oshsp17.3.
OSHSP17.3.
class I LMMHSP.

AAD09182.1 AF089843 Funaria hygrometrica
45

DESCRIPTION: cytosolic I small heat shock protein HSP17.2IC. HSP17.2IC.

173

5 AAD30456.1 AF123259 Lycopersicon esculentum
DESCRIPTION: heat shock protein 90. HSP90.

10 AAF31705.1 AF221856 Euphorbia esula
DESCRIPTION: heat-shock protein 80.

15 AAC32131.1 AF051230 Picea mariana
DESCRIPTION: heat shock protein. Sb40. similar to Oryza sativa heat shock
protein 82 encoded by GenBank Accession Number Z11920.

20 AAF64453.1 AF239931 Euphorbia esula
DESCRIPTION: putative heat-shock protein 90. GRP94; similar to
endoplasmic reticulum precursor; contains the endoplasmic reticulum
targeting sequence KDEL at the 3'-tail.

25 CAA78738.1 Z15018 Oryza sativa
DESCRIPTION: heat shock protein. heat shock protein hsp82. hsp82.

174

30 AAG43546.1 AF211528 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 4. ACRE4. similar to
Nicotiana glutinosa Ntr truncated N resistance protein encoded by GenBank
Accession Number U15605.

35 AAA50763.1 U15605 Nicotiana glutinosa
DESCRIPTION: virus resistance. N.

40 CAA08797.1 AJ009719 Solanum tuberosum
DESCRIPTION: disease resistance. NL25. nl25.

45 CAA08798.1 AJ009720 Solanum tuberosum
DESCRIPTION: disease resistance. NL27. nl27.

AAG09951.1 AF175388 Glycine max
DESCRIPTION: resistance protein LM6.

5 AAG09954.1 AF175399 Glycine max
DESCRIPTION: resistance protein MG13.

10 AAD25974.1 AF093647 Linum usitatissimum
DESCRIPTION: flax rust resistance protein. L.

15 AAD25966.1 AF093639 Linum usitatissimum
DESCRIPTION: flax rust resistance protein. L.

AAD25969.1 AF093642 Linum usitatissimum
DESCRIPTION: flax rust resistance protein. L.

20 AAD25965.1 AF093638 Linum usitatissimum
DESCRIPTION: flax rust resistance protein. L.

25 AAD25968.1 AF093641 Linum usitatissimum
DESCRIPTION: flax rust resistance protein. L.

30 AAA91021.1 U27081 Linum usitatissimum
DESCRIPTION: rust resistance. L6tr. L6. The shorter of two alternate protein products of The L6 gene that results from retention of intron 3 in the mRNA; truncated L6 gene product.

35 AAA91022.1 U27081 Linum usitatissimum
DESCRIPTION: rust resistance. L6. L6. The longer of two alternate proteins encoded by the L6 gene.

40 AAD25967.1 AF093640 Linum usitatissimum
DESCRIPTION: flax rust resistance protein. L.

45 AAK28803.1 AF310958 Linum usitatissimum
DESCRIPTION: resistance-like protein P1-A. p1-A.

AAK28808.1 AF310961 *Linum usitatissimum*
DESCRIPTION: resistance-like protein P3-A. p3-A.

5

AAK28805.1 AF310960 *Linum usitatissimum*
DESCRIPTION: resistance-like protein P2-A. p2-A.

10 AAD25976.1 AF093649 *Linum usitatissimum*
DESCRIPTION: flax rust resistance protein. L.

15 AAD25973.1 AF093646 *Linum usitatissimum*
DESCRIPTION: flax rust resistance protein. L.

20 AAD25972.1 AF093645 *Linum usitatissimum*
DESCRIPTION: flax rust resistance protein. L.

AAD25971.1 AF093644 *Linum usitatissimum*
DESCRIPTION: flax rust resistance protein. L.

25 AAD25970.1 AF093643 *Linum usitatissimum*
DESCRIPTION: flax rust resistance protein. L.

30 AAD25975.1 AF093648 *Linum usitatissimum*
DESCRIPTION: flax rust resistance protein. L.

35 AAG48132.1 AF322632 *Glycine max*
DESCRIPTION: putative resistance protein. L20a.

40 AAG01052.1 AF175395 *Glycine max*
DESCRIPTION: resistance protein MG23.

CAC35330.1 AJ310155 *Linum usitatissimum*
DESCRIPTION: N1-D protein. N1-D. N locus resistance gene homolog:
TIR-NBS-LRR protein.

45

CAC35333.1 AJ310158 *Linum usitatissimum*
DESCRIPTION: N2-C protein. N2-C. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

5

AAG48133.1 AF322633 *Glycine max*
DESCRIPTION: putative resistance protein. L33.

10 AAF61452.1 AF139523 *Tagetes erecta*
DESCRIPTION: disease-resistance protein NRSA1.

CAC35334.1 AJ310159 *Linum usitatissimum*
15 DESCRIPTION: N2-D protein. N2-D. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

CAC35337.1 AJ310162 *Linum usitatissimum*
20 DESCRIPTION: Nbi-C protein. Nbi-C. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

CAC35339.1 AJ310164 *Linum usitatissimum*
25 DESCRIPTION: Nho-C protein. Nho-C. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

CAC35326.1 AJ310151 *Linum usitatissimum*
30 DESCRIPTION: Ngc-C protein. Ngc-C. N rust resistance gene homolog:
TIR-NBS-LRR protein.

AAG01051.1 AF175394 *Glycine max*
35 DESCRIPTION: resistance protein LM12.

CAC35338.1 AJ310163 *Linum usitatissimum*
40 DESCRIPTION: Nbi-D protein. Nbi-D. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

CAC35329.1 AJ310154 *Linum usitatissimum*
45 DESCRIPTION: N1-C protein. N1-C. N locus resistance gene homolog:
TIR-NBS-LRR protein.

AAK28804.1 AF310959 *Linum usitatissimum*
DESCRIPTION: resistance-like protein P1-B. p1-B.

5

AAK28809.1 AF310962 *Linum usitatissimum*
DESCRIPTION: resistance-like protein P3-B. p3-B.

10 CAC35332.1 AJ310157 *Linum usitatissimum*
DESCRIPTION: N2-B protein. N2-B. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

15 CAC35328.1 AJ310153 *Linum usitatissimum*
DESCRIPTION: N1-B protein. N1-B. N locus resistance gene homolog:
TIR-NBS-LRR protein.

20 CAC35325.1 AJ310150 *Linum usitatissimum*
DESCRIPTION: Ngc-B protein. Ngc-B. N rust resistance gene homolog:
TIR-NBS-LRR protein.

25 CAC35336.1 AJ310161 *Linum usitatissimum*
DESCRIPTION: Nbi-B protein. Nbi-B. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

30 CAC35321.1 AJ310150 *Linum usitatissimum*
DESCRIPTION: Ngc-D protein. Ngc-D. N rust resistance gene: TIR-NBS-LRR
protein.

35 CAC35331.1 AJ310156 *Linum usitatissimum*
DESCRIPTION: N2-A protein. N2-A. N locus rust resistance gene homolog:
TIR-NBS-LRR protein.

40 CAC35323.1 AJ310150 *Linum usitatissimum*
DESCRIPTION: Ngc-A protein. Ngc-A. N rust resistance gene homolog:
TIR-NBS-LRR protein.

45 AAB47618.1 U73916 *Linum usitatissimum*
DESCRIPTION: rust resistance protein M. nucleotide-binding site,

leucine-rich repeat class of plant disease resistance protein.

5 AAG01053.1 AF175396 Glycine max
DESCRIPTION: resistance protein MG55.

10 CAC35327.1 AJ310152 Linum usitatissimum
DESCRIPTION: N1-A protein. N1-A. N locus resistance gene homolog:
TIR-NBS-LRR protein.

15 AAK28811.1 AF310966 Linum usitatissimum
DESCRIPTION: resistance-like protein P-B. p-B.
175

20 CAB52796.1 AJ245861 Solanum tuberosum
DESCRIPTION: respiratory chain. putative internal rotenone-insensitive
NADH dehydrogenase. nda1.

25 CAB52797.1 AJ245862 Solanum tuberosum
DESCRIPTION: respiratory chain. putative external rotenone-insensitive
NADH dehydrogenase. ndb1.
176

30 BAA05648.1 D26601 Nicotiana tabacum
DESCRIPTION: protein kinase.

35 CAA08997.1 AJ010093 Brassica napus
DESCRIPTION: MAP3K beta 1 protein kinase. MAP3K beta 1.

40 CAA08995.1 AJ010091 Brassica napus
DESCRIPTION: MAP3K alpha 1 protein kinase. MAP3K alpha 1.

AAF34436.1 AF172282 Oryza sativa
DESCRIPTION: similar to mitogen-activated protein kinases. DUPR11.32.

45 CAB54520.1 AJ238845 Brassica napus
DESCRIPTION: putative role in cell cycle control. MAP3K epsilon 1 protein

kinase. MAP3Kε1.

CAA08758.1 AJ009609 Brassica napus
5 DESCRIPTION: BnMAP4K alpha2.

CAA08757.1 AJ009608 Brassica napus
10 DESCRIPTION: BnMAP4K alpha1.

AAC83393.1 U83625 Zea mays
15 DESCRIPTION: protein kinase ZmMEK1. mitogen-activated; ERK-activating
protein kinase (MEK) homolog.

AAG53979.1 AF325168 Nicotiana tabacum
20 DESCRIPTION: mitogen-activated protein kinase 2. MEK2. upstream kinase
for SIPK and WIPK, two tobacco MAP kinases.

AAG40578.1 AF216314 Oryza sativa
25 DESCRIPTION: MAP kinase kinase 1. protein kinase; MEK1.

CAA04261.2 AJ000728 Lycopersicon esculentum
DESCRIPTION: MAP kinase kinase. mek1.

30 AAF67262.1 AF165186 Nicotiana tabacum
DESCRIPTION: MAP kinase kinase.

AAG45491.1 AY013245 Oryza sativa
35 DESCRIPTION: 36I5.3. putative serine/threonine kinase.

BAB32405.1 AB055514 Nicotiana tabacum
40 DESCRIPTION: NQK1 MAPKK. nqk1.

AAG49001.1 AY013246 Hordeum vulgare
DESCRIPTION: putative serine/threonine kinase. 635P2.3.

45 AAF19403.1 AF203481 Lycopersicon esculentum

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AAF19402.1 AF203480 *Lycopersicon esculentum*

10

DESCRIPTION: protein kinase. MAP kinase. mek1.

BAA06731.1 D31964 *Nicotiana tabacum*

20

DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.

AAF19401.1 AF203479 Glycine max

30

DESCRIPTION: ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to Arabidopsis thaliana negative

regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.

40

DESCRIPTION: putative protein kinase.

DESCRIPTION: protein kinase.

45

- 5 AAD23582.1 AF128443 *Glycine max*
DESCRIPTION: probably involved in plant stress responses possibly
regulates gene expression. SNF-1-like serine/threonine protein kinase.
expressed in nodules, roots and leaves.
- 10 CAA06334.1 AJ005077 *Lycopersicon esculentum*
DESCRIPTION: protein kinase. TCTR2 protein. TCTR2.
- 15 AAD10057.1 AF110519 *Lycopersicon esculentum*
DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase
homolog; ethylene and fruit ripening inducible CTR1-like protein kinase;
TCTR1v.
- 20 CAB89082.1 AJ277534 *Asparagus officinalis*
DESCRIPTION: S6 ribosomal protein kinase. pk1. putative.
- 25 AAC78558.1 AF030879 *Solanum tuberosum*
DESCRIPTION: protein kinase CPK1.
- 30 AAD10056.1 AF110518 *Lycopersicon esculentum*
DESCRIPTION: ethylene-inducible CTR1-like protein kinase. protein kinase
homolog; ethylene and fruit ripening inducible CTR1-like protein kinase;
TCTR1.
- 35 AAK18832.1 AC082645 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBb0033N16.9.
- 40 AAG31142.1 AF305912 *Hordeum vulgare*
DESCRIPTION: EDR1. EDR1. MAP kinase kinase kinase; similar to
Arabidopsis thaliana EDR1.
- 45 AAC24961.1 AF009337 *Tradescantia virginiana*
DESCRIPTION: CDPK-related protein kinase. CRK1.
- 50 BAB21278.1 AP002844 *Oryza sativa*
DESCRIPTION: putative MAP kinase. P0410E03.9.

- AAA61682.1 L27484 Zea mays
DESCRIPTION: calcium-dependent protein kinase. CDPK.
- 5
- CAA56313.1 X79992 Avena sativa
DESCRIPTION: putative pp70 ribosomal protein S6 kinase. Aspk11.
- 10
- AAD31900.1 AF145482 Mesembryanthemum crystallinum
DESCRIPTION: putative serine/threonine protein kinase.
- 15
- AAC25423.1 AF072908 Nicotiana tabacum
DESCRIPTION: calcium-dependent protein kinase. CDPK1.
- 20
- CAA71142.1 Y10036 Cucumis sativus
DESCRIPTION: SNF1-related protein kinase.
- 25
- BAA83689.1 AB011968 Oryza sativa
DESCRIPTION: OsPK7. OsPK7. protein kinase.
- 30
- CAA46554.1 X65604 Hordeum vulgare
DESCRIPTION: protein kinase. BKIN12.
- 35
- CAA46556.1 X65606 Hordeum vulgare
DESCRIPTION: protein kinase. BKIN12.
- 40
- CAA65500.1 X96723 Medicago sativa
DESCRIPTION: protein kinase. CDPK.
- 45
- AAF05112.1 AF158091 Mesembryanthemum crystallinum
DESCRIPTION: day/night regulation of carbon fixation by crassulacean acid metabolism pathway. phosphoenolpyruvate carboxylase-kinase. SNIK. protein kinase; salt/night induced kinase; phosphorylase; member of Ca²⁺/Cam protein kinase family; lacks both CAM domain and autoinhibitory domain; Ser/Thr kinase.

AAD17800.1 AF090835 *Mesembryanthemum crystallinum*
DESCRIPTION: Ca²⁺-dependent protein kinase. CPK1. serine/threonine
protein kinase.

5

CAA07813.1 AJ007990 *Hordeum vulgare*
DESCRIPTION: SnRK1-type protein kinase. kin12a.

177

10

BAB16335.1 AP002818 *Oryza sativa*
DESCRIPTION: putative NAM protein. P0436E04.18. contains ESTs
E10793(C19698),E10793(C99379).

15

BAA84803.1 AP000559 *Oryza sativa*
DESCRIPTION: Similar to NAM like protein (AC005310).

20

BAB19365.1 AP002542 *Oryza sativa*
DESCRIPTION: putative NAM (no apical meristem) protein. P0679C08.4.

25

BAB16328.1 AP002818 *Oryza sativa*
DESCRIPTION: putative NAM protein. P0436E04.11. contains ESTs
R4069(AU032425),R4069(AU082730).

30

CAA63102.2 X92205 *Petunia x hybrida*
DESCRIPTION: apical meristem formation. NAM.

35

CAA63101.1 X92204 *Petunia x hybrida*
DESCRIPTION: apical meristem formation. NAM.

40

AAK13151.1 AC078829 *Oryza sativa*
DESCRIPTION: putative NAM (no apical meristem) protein.
OSJNBa0026O12.6.

45

BAB03447.1 AP002817 *Oryza sativa*
DESCRIPTION: ESTs C96615(C10106),C26336(C12127),D21959(C10106)
correspond
to a region of the predicted gene. Similar to *Arabidopsis thaliana* DNA
chromosome 4, BAC clone T6K21; NAM (no apical meristem) - like protein

(AL021889).

- 5 BAA92400.1 AP001366 *Oryza sativa*
DESCRIPTION: ESTs C96615(C10106),C26336(C12127),D21959(C10106)
correspond
to a region of the predicted gene. Similar to NAM (AL021889).

178

10

- BAA25434.1 AB000708 *Raphanus sativus*
DESCRIPTION: SAUR.

- 15 AAG14454.1 AF283706 *Tulipa gesneriana*
DESCRIPTION: auxin-induced protein TGSAUR12. SAUR12. small auxin
upregulated RNA.

- 20 AAG14455.1 AF283707 *Tulipa gesneriana*
DESCRIPTION: auxin-induced protein TGSAUR21. SAUR21. small auxin
upregulated RNA.

- 25 AAG14456.1 AF283708 *Tulipa gesneriana*
DESCRIPTION: auxin-induced protein TGSAUR22. SAUR22. small auxin
upregulated RNA.

179

30

- BAA78738.1 AB023482 *Oryza sativa*
DESCRIPTION: EST AU055776(S20048) corresponds to a region of the
predicted gene.; Similar to *Arabidopsis thaliana* AP2 domain containing
protein RAP2.10 mRNA, partial cds.(AF003103).

35

- CAB96899.1 AJ251249 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

40

- CAB96900.1 AJ251250 *Catharanthus roseus*
DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.

- 45 AAF76898.1 AF274033 *Atriplex hortensis*
DESCRIPTION: apetala2 domain-containing protein.

CAC12822.1 AJ299252 *Nicotiana tabacum*
 DESCRIPTION: AP2 domain-containing transcription factor. ap2.
 5

AAC14323.1 AF058827 *Nicotiana tabacum*
 DESCRIPTION: TSI1. Tsi1. contains putative AP2 DNA-binding domain;
 similar to Pti6.
 10

BAA97123.1 AB016265 *Nicotiana sylvestris*
 DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
 basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
 element binding factor. nserf3.
 15

CAB93940.1 AJ238740 *Catharanthus roseus*
 DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
 protein. orca2.
 20

AAC24587.1 AF071893 *Prunus armeniaca*
 DESCRIPTION: AP2 domain containing protein. AP2DCP.
 25

BAB03248.1 AB037183 *Oryza sativa*
 DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive
 element binding factor3. osERF3.
 30

BAB16083.1 AB036883 *Oryza sativa*
 DESCRIPTION: transcriptional repressor. osERF3. osERF3. ERF protein
 family ERF3 associated repression domain.
 35

BAA76734.1 AB024575 *Nicotiana tabacum*
 DESCRIPTION: ethylene responsive element binding factor.
 40

CAB93939.1 AJ238739 *Catharanthus roseus*
 DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
 protein. orca1.
 45

AAG43545.1 AF211527 *Nicotiana tabacum*

DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.

- 5 AAG43548.1 AF211530 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
- 10 AAG43549.1 AF211531 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
- 15 AAF23899.1 AF193803 *Oryza sativa*
DESCRIPTION: transcription factor EREBP1. EREBP/AP2-like transcription factor.
- 20 AAK31271.1 AC079890 *Oryza sativa*
DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.
- 25 AAF63205.1 AF245119 *Mesembryanthemum crystallinum*
DESCRIPTION: AP2-related transcription factor. CDBP. stress induced transcription factor.
- 30 BAA07321.1 D38123 *Nicotiana tabacum*
DESCRIPTION: ERF1. ethylene-responsive transcription factor.
- 35 BAA97122.1 AB016264 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.
- 40 BAA97124.1 AB016266 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
- 45 BAA94514.2 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 4, BAC clone

F9D16; putative Ap2 domain protein (AL035394).

- 5 AAC62619.1 AF057373 *Nicotiana tabacum*
DESCRIPTION: transcription factor. ethylene response element binding protein 1. EREBP1.
- 10 AAK01088.1 AF298230 *Hordeum vulgare*
DESCRIPTION: CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
- 15 BAA99376.1 AP002526 *Oryza sativa*
DESCRIPTION: ESTs AU093391(E60370),AU091593(C60458), AU093392(E60370) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana BAC F21J9; AP2 domain protein. (AC000103).
- 20
- AAK01089.1 AF298231 *Hordeum vulgare*
DESCRIPTION: CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.
- 25
- AAG59618.1 AF239616 *Hordeum vulgare*
DESCRIPTION: CRT/DRE-binding factor. CBF.
- 30 181

CAB71134.1 AJ271667 *Cicer arietinum*
DESCRIPTION: putative proteasome regulatory subunit.
- 35 185

BAA85440.1 AP000616 *Oryza sativa*
DESCRIPTION: ESTs AU055729(S20023),AU055730(S20023) correspond to a region of the predicted gene.; similar to Medicago nodulin N21-like protein (AC004218).
- 40
- CAB53493.1 AJ245900 *Oryza sativa*
DESCRIPTION: CAA303720.1 protein. q3037.20. Similar to Medicago nodulin N21 (MtN21).
- 45

BAB17350.1 AP002747 Oryza sativa
DESCRIPTION: putative nodulin. P0698G03.34. contains ESTs
D39891(S1543),D41717(S4395),AU033037(S1543).

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186

BAA02724.1 D13506 Glycine max
DESCRIPTION: early nodulin.

10

BAA33816.1 AB018378 Glycine max
DESCRIPTION: early nodulin. GmENOD93.

15

BAA83560.1 AP000399 Oryza sativa
DESCRIPTION: EST AU077941(C12908) corresponds to a region of the
predicted gene. Similar to OsENOD93a gene for early nodulin (AB018375).

20

BAA33815.1 AB018377 Oryza sativa
DESCRIPTION: early nodulin. OsENOD93b.

25

BAA83566.1 AP000399 Oryza sativa
DESCRIPTION: ESTs C98280(C1391),D15843(C1391) correspond to a region
of
the predicted gene. Similar to OsENOD93a gene for early nodulin
(AB018375).

30

BAA83568.1 AP000399 Oryza sativa
DESCRIPTION: EST AU077972(C53511) corresponds to a region of the
predicted gene. Similar to OsENOD93a gene for early nodulin (AB018375).

35

BAA83565.1 AP000399 Oryza sativa
DESCRIPTION: ESTs C98096(C0688),C98097(C0688) correspond to a region
of
the predicted gene. Similar to OsENOD93a gene for early nodulin
(AB018375).

40

AAD30134.1 AF140229 Oryza sativa
DESCRIPTION: early nodulin.

45

BAA33814.1 AB018376 *Oryza sativa*
DESCRIPTION: early nodulin. OsENOD93a.

5

BAA33813.1 AB018375 *Oryza sativa*
DESCRIPTION: early nodulin. OsENOD93a.

10 BAA83567.1 AP000399 *Oryza sativa*
DESCRIPTION: EST C97982(C0324) corresponds to a region of the predicted
gene. Similar to OsENOD93a gene for early nodulin (AB018375).

15 BAA83559.1 AP000399 *Oryza sativa*
DESCRIPTION: EST C97982(C0324) corresponds to a region of the predicted
gene. Similar to OsENOD93a gene for early nodulin (AB018375).

20 BAA83557.1 AP000399 *Oryza sativa*
DESCRIPTION: Similar to OsENOD93a gene for early nodulin (AB018375).

188

25 AAA33811.1 L02830 *Solanum tuberosum*
DESCRIPTION: calcium-binding protein.

30 AAG43547.1 AF211529 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 31. ACRE31. similar to
Solanum tuberosum CAST calcium binding protein encoded by GenBank
Accession Number L02830.

35 CAB63264.1 AJ251808 *Lotus japonicus*
DESCRIPTION: calcium-binding protein. cbp1.

40 AAA34015.1 L01433 *Glycine max*
DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-4.
putative.

45 AAA92677.1 U13736 *Pisum sativum*
DESCRIPTION: binds calcium. calmodulin-like protein.

AAF31152.1 AF078680 Olea europaea
DESCRIPTION: calcium-binding protein. PCA23. Pca23.

5

AAA33948.1 L19359 Glycine max
DESCRIPTION: calcium-binding regulatory protein. calmodulin. SCaM-5.
putative.

10

AAD10245.1 AF030033 Phaseolus vulgaris
DESCRIPTION: calmodulin. CaM. EF-hand protein; calcium-dependent
protein;
functions in calcium signal transduction pathways.

15

AAF31151.1 AF078679 Olea europaea
DESCRIPTION: calcium-binding protein. PCA18. Pca18.

20

AAA19571.1 U10150 Brassica napus
DESCRIPTION: calcium binding. calmodulin. bcm1.

25

AAC49587.1 U49105 Triticum aestivum
DESCRIPTION: calmodulin TaCaM4-1. calcium-binding protein.

30

AAC49586.1 U49104 Triticum aestivum
DESCRIPTION: calmodulin TaCaM3-3. calcium-binding protein.

35

AAC49585.1 U49103 Triticum aestivum
DESCRIPTION: calmodulin TaCaM3-2. calcium-binding protein.

40

AAC49584.1 U48693 Triticum aestivum
DESCRIPTION: calmodulin TaCaM3-1. calcium-binding protein.

45

AAC49580.1 U48689 Triticum aestivum
DESCRIPTION: calmodulin TaCaM1-3. calcium-binding protein.

45

AAC49579.1 U48688 Triticum aestivum
DESCRIPTION: calmodulin TaCaM1-2. calcium binding protein.

AAA92681.1 U13882 Pisum sativum
DESCRIPTION: calcium-binding protein. calmodulin.

5 CAA78288.1 Z12828 Oryza sativa
DESCRIPTION: calcium binding protein, signal transduction. calmodulin.

190

10 AAF72197.1 AF263737 Euphorbia esula
DESCRIPTION: glutathione S-transferase. theta class GST.

AAG34815.1 AF243380 Glycine max
15 DESCRIPTION: glutathione S-transferase GST 25.

AAG34825.1 AF244682 Zea mays
20 DESCRIPTION: glutathione S-transferase GST 17.

AAG32474.1 AF309381 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTZ1.
25

AAG34826.1 AF244683 Zea mays
DESCRIPTION: glutathione S-transferase GST 18.

30 AAA33277.1 M64268 Dianthus caryophyllus
DESCRIPTION: glutathione transferase. CARSR8.

CAA41279.1 X58390 Dianthus caryophyllus
35 DESCRIPTION: glutathione s-transferase. CARSR8.

AAD09190.1 AF109714 Triticum aestivum
DESCRIPTION: glutathione S-transferase. GST.
40

AAB60886.1 AF002211 Triticum aestivum
DESCRIPTION: glutathione-S-transferase.

45 AAA51450.1 L05916 Dianthus caryophyllus

DESCRIPTION: glutathione s-transferase. GST2.

5 AAC50036.1 U42463 Coccomyxa sp. PA
DESCRIPTION: glutathione S-transferase. GST.

10 AAG34801.1 AF243366 Glycine max
DESCRIPTION: glutathione S-transferase GST 11.

AAG32469.1 AF309376 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTU6.

15 AAG34850.1 AF244707 Zea mays
DESCRIPTION: glutathione S-transferase GST 42.

20 AAG34807.1 AF243372 Glycine max
DESCRIPTION: glutathione S-transferase GST 17.

25 CAB38119.1 AJ010296 Zea mays
DESCRIPTION: Glutathione transferase III(b). gst3b.

30 AAF23357.1 AF109194 Hordeum vulgare
DESCRIPTION: glutathione-S-transferase.

AAG34849.1 AF244706 Zea mays
DESCRIPTION: glutathione S-transferase GST 41.

35 CAB38118.1 AJ010295 Zea mays
DESCRIPTION: Glutathione transferase III(a). gst3a.

40 AAG32475.1 AF309382 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTF5.

45 AAB65163.1 AF002692 Solanum commersonii
DESCRIPTION: glutathione S-transferase, class-phi. GST1. low temperature induced.

AAD10129.1 AF004358 *Aegilops tauschii*
DESCRIPTION: chloroacetamide herbicide metabolism. glutathione
S-transferase TSI-1. GST isozyme.

5

AAG41204.1 AF321437 *Suaeda maritima*
DESCRIPTION: glutathione transferase.

10

AAG34810.1 AF243375 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 20.

15

AAG34804.1 AF243369 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 14.

20

AAG34814.1 AF243379 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 24.

25

AAG32472.1 AF309379 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTU3.

AAG32471.1 AF309378 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTU4.

30

CAA09187.1 AJ010448 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST1a.

35

AAG34835.1 AF244692 *Zea mays*
DESCRIPTION: glutathione S-transferase GST 27.

40

AAF64449.1 AF239927 *Euphorbia esula*
DESCRIPTION: glutathione S-transferase. theta class GST.

45

AAG16758.1 AY007560 *Lycopersicon esculentum*
DESCRIPTION: putative glutathione S-transferase T3.

[illegible]

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- 708 -

from *Arabidopsis thaliana* encoded by GenBank Accession Number AC000132.

195

- 5 AAK13154.1 AC078829 *Oryza sativa*
DESCRIPTION: putative casein kinase. OSJNBa0026O12.5.
- 10 BAA92986.1 AP001550 *Oryza sativa*
DESCRIPTION: ESTs D41826(S4655),C22685(S4655) correspond to a region of
the predicted gene.; Similar to *Arabidopsis thaliana* chromosome 4, BAC
clone F16A16; protein kinase-like protein (AL035353).
- 15 AAF19807.1 AF180356 *Brassica oleracea*
DESCRIPTION: casein kinase I-like protein. CK1b. strong similarity to
Arabidopsis thaliana casein kinase 1.
- 20 AAD20819.1 AF107592 *Dendrobium grex Madame Thong-In*
DESCRIPTION: putative casein kinase I. otg16.
- 25 AAF19403.1 AF203481 *Lycopersicon esculentum*
DESCRIPTION: phosphoenolpyruvate carboxylase kinase. protein kinase;
member of Ca²⁺/CaM kinase family; lacks the autoinhibitory region and EF
hands.
- 30 AAF19402.1 AF203480 *Lycopersicon esculentum*
DESCRIPTION: phosphoenolpyruvate carboxylase kinase. protein kinase;
member of Ca²⁺/CaM kinase family; lacks the autoinhibitory region and EF
hands.
- 35 BAA05648.1 D26601 *Nicotiana tabacum*
DESCRIPTION: protein kinase.
- 40 AAF23901.2 AF194414 *Oryza sativa*
DESCRIPTION: calcium-dependent protein kinase. CDPK5. OsCDPK5.
- 45 AAC04324.1 U73937 *Nicotiana tabacum*
DESCRIPTION: ethylene signal transduction. PK12 protein kinase. PK12.

component of the LAMMER family of protein kinases; dual-specificity protein kinase.

- 5 AAF23900.1 AF194413 *Oryza sativa*
DESCRIPTION: calcium-dependent protein kinase. CDPK1. OsCDPK1.
- 10 BAA34675.1 AB011670 *Triticum aestivum*
DESCRIPTION: wpk4 protein kinase. wpk4.
- 15 BAA13440.1 D87707 *Ipomoea batatas*
DESCRIPTION: calcium dependent protein kinase. CDPK.
- 20 AAD17800.1 AF090835 *Mesembryanthemum crystallinum*
DESCRIPTION: Ca²⁺-dependent protein kinase. CPK1. serine/threonine protein kinase.
- 25 CAA57157.1 X81394 *Oryza sativa*
DESCRIPTION: calcium-dependent protein kinase. OSCPK2.
- 30 AAD23582.1 AF128443 *Glycine max*
DESCRIPTION: probably involved in plant stress responses possibly regulates gene expression. SNF-1-like serine/threonine protein kinase. expressed in nodules, roots and leaves.
- 35 CAA39936.1 X56599 *Daucus carota*
DESCRIPTION: calcium- dependent protein kinase. DcPK431.
- 40 BAA12715.1 D85039 *Zea mays*
DESCRIPTION: calcium-dependent protein kinase.
- 45 CAA58750.1 X83869 *Daucus carota*
DESCRIPTION: CDPK-related protein kinase. CRK (or PK421).
- AAB80693.1 U69174 *Glycine max*
DESCRIPTION: calmodulin-like domain protein kinase isoenzyme gamma. CDPK

gamma.

- 5 AAF21062.1 AF216527 *Dunaliella tertiolecta*
DESCRIPTION: calcium-dependent protein kinase. CPK1; CDPK.
- 10 CAA74646.1 Y14274 *Sorghum bicolor*
DESCRIPTION: putative serine/threonine protein kinase. SNFL3.
- 15 AAD28192.2 AF115406 *Solanum tuberosum*
DESCRIPTION: calcium-dependent protein kinase. CDPK; catalytic domain.
- 20 BAA05649.1 D26602 *Nicotiana tabacum*
DESCRIPTION: protein kinase.
- 25 AAA69507.1 U28376 *Zea mays*
DESCRIPTION: calcium-dependent protein kinase. MZECDPK2.
- 30 AAB05457.1 U55768 *Oryza sativa*
DESCRIPTION: SNF1-related protein kinase. RSk1. Ser/Thr protein kinase homolog.
- 35 AAG36872.1 AF239819 *Zea mays*
DESCRIPTION: protein kinase CK2 catalytic subunit CK2 alpha-3.
- 40 CAA89202.1 Z49233 *Chlamydomonas eugametos*
DESCRIPTION: calcium-stimulated protein kinase.
- 45 CAA72362.1 Y11649 *Zea mays*
DESCRIPTION: protein kinase CK2, alpha subunit.
- CAA72290.1 Y11526 *Zea mays*
DESCRIPTION: casein kinase II alpha subunit. CK2.
- CAA43659.1 X61387 *Zea mays*
DESCRIPTION: casein kinase II alpha subunit. ZMACK2.

- CAA65244.1 X95997 *Solanum tuberosum*
DESCRIPTION: SNF1-related protein kinase. PKIN1.
5
- AAF76187.1 AF271237 *Zea mays*
DESCRIPTION: casein kinase II alpha subunit.
10
- BAB21591.1 AB036788 *Oryza sativa*
DESCRIPTION: casein kinase II alpha subunit. OSCKA2.
15
- BAB21589.1 AB036786 *Oryza sativa*
DESCRIPTION: casein kinase II alpha subunit. OSCKA2.
20
- CAB89082.1 AJ277534 *Asparagus officinalis*
DESCRIPTION: S6 ribosomal protein kinase. pk1. putative.
25
- AAF06970.1 AF162662 *Kalanchoe fedtschenkoi*
DESCRIPTION: phosphoenolpyruvate carboxylase kinase. calcium-independent
protein kinase.
30
- AAF06969.1 AF162661 *Kalanchoe fedtschenkoi*
DESCRIPTION: phosphoenolpyruvate carboxylase kinase. calcium-independent
protein kinase.
35
- CAA41172.1 X58194 *Oryza sativa*
DESCRIPTION: cdc2+/CDC28-related protein kinase.
40
- CAA65500.1 X96723 *Medicago sativa*
DESCRIPTION: protein kinase. CDPK.
45
- BAA12691.1 D84507 *Zea mays*
DESCRIPTION: CDPK-related protein kinase. Does not require calcium for
its activity (by similarity).
- AAB47181.1 S82324 *Zea mays*

DESCRIPTION: /gene="calcium/calmodulin-dependent
protein kinase. This sequence comes from Fig. 1.

- 5 CAA07481.1 AJ007366 Zea mays
DESCRIPTION: calcium-dependent protein kinase.
- 10 BAA99439.1 AP002743 Oryza sativa
DESCRIPTION: putative protein kinase. P0710E05.26. contains ESTs
C22394(C30013),C22393(C30013).
- 15 BAB12687.1 AP002746 Oryza sativa
DESCRIPTION: putative protein kinase. P0671B11.2. contains ESTs
C22394(C30013),C22393(C30013).
- 20 AAF40430.1 AF234652 Mesembryanthemum crystallinum
DESCRIPTION: protein kinase MK5.
- 25 BAB21081.1 AP002819 Oryza sativa
DESCRIPTION: putative calcium-dependent protein kinase. P0501G01.10.
196

- 30 AAF37267.1 AF220406 Vitis riparia
DESCRIPTION: 26S proteasome regulatory ATPase subunit S10b. Rev136-3.
197

- 35 BAA08104.1 D45074 Panicum miliaceum
DESCRIPTION: 2-oxoglutarate/malate translocator. mitochondrial
2-oxoglutarate/malate translocator.
- 40 BAA08103.1 D45073 Panicum miliaceum
DESCRIPTION: 2-oxoglutarate/malate translocator. mitochondrial
2-oxoglutarate/malate translocator.
- 45 BAA08105.1 D45075 Panicum miliaceum
DESCRIPTION: 2-oxoglutarate/malate translocator. mitochondrial
2-oxoglutarate/malate translocator.

- CAA72107.1 Y11220 Solanum tuberosum
DESCRIPTION: mitochondrial uncoupling protein.
- 5 CAC12820.1 AJ299250 Nicotiana tabacum
DESCRIPTION: mitochondrial 2-oxoglutarate/malate carrier protein. momcl.
- 10 AAB71744.1 U75346 Chlamydomonas reinhardtii
DESCRIPTION: envelope protein. LIP-36G2. low CO2 inducible carrier protein LIP-36 with a molecular weight of 36 kDa.
- 15 AAB71743.1 U75345 Chlamydomonas reinhardtii
DESCRIPTION: envelope protein. LIP-36G1. low CO2 inducible carrier protein LIP-36 with a molecular weight of 36 kDa.
- 20 CAA07568.1 AJ007580 Ribes nigrum
DESCRIPTION: Mitochondrial carrier protein. prib7.
- 25 BAB40117.1 AP003311 Oryza sativa
DESCRIPTION: putative peroxisomal Ca-dependent solute carrier protein. P0024G09.9.
- 30 BAB16462.1 AP002483 Oryza sativa
DESCRIPTION: putative peroxisomal Ca-dependent solute carrier protein. P0019D06.21.
- 35 CAA56325.1 X80023 Triticum turgidum
DESCRIPTION: ATP/ADP carrier protein.
- 40 CAA46311.1 X65194 Chlamydomonas reinhardtii
DESCRIPTION: mitochondrial ADP/ATP translocator protein. CRANT.
- CAA67107.1 X98474 Solanum tuberosum
DESCRIPTION: mitochondrial energy transfer protein. brittle1.
- 45 CAC27140.1 AJ132535 Picea abies

[illegible]

CAA69726.1 Y08499 Betula pendula
5 DESCRIPTION: mitochondrial phosphate translocator.

BAA31583.1 AB016064 Zea mays
DESCRIPTION: mitochondrial phosphate transporter.

CAB61741.1 AJ275306 *Cicer arietinum*
DESCRIPTION: mitochondrial phosphate transporter.

15 AAG45489.1 AY013245 Oryza sativa
DESCRIPTION: 36I5.1. putative mitochondrial carrier protein.

20 BAA31584.1 AB016065 Oryza sativa
DESCRIPTION: mitochondrial phosphate transporter.

25 BAA92520.1 AP001383 *Oryza sativa*
DESCRIPTION: ESTs AU068633(C30614),AU068634(C30614) correspond to
a region of the predicted gene. Similar to *Bos taurus* mitochondrial solute
carrier protein. (AF049236).

30 199

BAA03455.1 D14605 *Daucus carota*
DESCRIPTION: AX110P, AX110.

35 204

AAD21872.1 AF078082 *Phaseolus vulgaris*
DESCRIPTION: receptor-like protein kinase homolog RK20-1.

40 AAC23542.1 U20948 Ipomoea trifida
DESCRIPTION: receptor protein kinase. IRK1.

45 CAA73133.1 Y12530 Brassica oleracea
DESCRIPTION: serine /threonine kinase. ARLK.

- CAA67145.1 X98520 Brassica oleracea
DESCRIPTION: receptor-like kinase. SFR2.
5
- CAB41879.1 Y18260 Brassica oleracea
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.
10
- BAA92836.1 AB032473 Brassica oleracea
DESCRIPTION: S18 S-locus receptor kinase. SRK18.
15
- CAA74662.1 Y14286 Brassica oleracea
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
20
- AAB93834.1 U82481 Zea mays
DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
25
- CAB41878.1 Y18259 Brassica oleracea
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.
30
- CAA73134.1 Y12531 Brassica oleracea
DESCRIPTION: serine/threonine kinase. BRLK.
35
- CAA74661.1 Y14285 Brassica oleracea
DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
40
- BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.
45
- AAA33000.1 M76647 Brassica oleracea
DESCRIPTION: receptor protein kinase. SKR6.
50
- AAA62232.1 U00443 Brassica napus

DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like domain.

- 5 CAB89179.1 AJ245479 Brassica napus subsp. napus
DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.
- 10 AAA33008.1 M97667 Brassica napus
DESCRIPTION: serine/threonine kinase receptor.
- 15 BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).
- 20 BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.
- 25 AAK02023.1 AC074283 Oryza sativa
DESCRIPTION: Putative protein kinase-like. OSJNBa0087H07.5.
- 30 CAA79355.1 Z18921 Brassica oleracea
DESCRIPTION: S-receptor kinase-like protein.
- 35 BAA92837.1 AB032474 Brassica oleracea
DESCRIPTION: S60 S-locus receptor kinase. SRK60.
- 40 BAB21001.1 AB054061 Brassica rapa
DESCRIPTION: S locus receptor kinase. SRK22.
- 45 BAA07577.2 D38564 Brassica rapa
DESCRIPTION: receptor protein kinase SRK12.
- 45 BAA07576.1 D38563 Brassica rapa
DESCRIPTION: receptor protein kinase SRK8.
- 45 AAD52097.1 AF088885 Nicotiana tabacum
DESCRIPTION: receptor-like kinase CHRK1. Chrk1.

- 5 BAB18292.1 AP002860 *Oryza sativa*
DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.
- 10 BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).
- 15 BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).
- 20 BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A*Arabidopsis thaliana*.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
- 25 BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).
- 30 AAA33915.1 L27821 *Oryza sativa*
DESCRIPTION: receptor type serine/threonine kinase. protein kinase.
- 35 CAB51836.1 AJ243961 *Oryza sativa*
DESCRIPTION: Putitive Ser/Thr protein kinase. 11332.7.
- 40 CAA97692.1 Z73295 *Catharanthus roseus*
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation
predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
- 45 AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.
- BAA94529.2 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase

(AJ010166).

5 BAA94510.1 AB041504 Populus nigra
DESCRIPTION: protein kinase 2. PnPK2.

10 BAA92954.1 AP001551 Oryza sativa
DESCRIPTION: Similar to Oryza sativa protein kinase (OSPK10) mRNA.
(L27821).

15 BAA94509.1 AB041503 Populus nigra
DESCRIPTION: protein kinase 1. PnPK1.

211

20 AAG13478.1 AC026758 Oryza sativa
DESCRIPTION: putative trehalose-6-phosphate phosphatase.
OSJNBa0015J15.3.

212

25 AAC27894.1 AF023164 Zea mays
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. ltk1.

30 AAC27895.1 AF023165 Zea mays
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 2. ltk2.

35 AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.

AAC61805.1 U28007 Lycopersicon esculentum
DESCRIPTION: serine/threonine protein kinase. Pto kinase interactor 1.
Pti1. Pti1 kinase.

40 BAB21241.1 AP002953 Oryza sativa
DESCRIPTION: Putative Pto kinase interactor 1. P0426D06.21. contains ESTs
AU108280(E0721),D48017(S13927).

45 AAF91336.1 AF249317 Glycine max

DESCRIPTION: Pti1 kinase-like protein. Pti1a. protein kinase.

- 5 AAF91337.1 AF249318 Glycine max
DESCRIPTION: Pti1 kinase-like protein. Pti1b. protein kinase.

- 10 BAA82394.1 AP000367 Oryza sativa
DESCRIPTION: ESTs D23521(C2939),C22481(C2939) correspond to a region
of
the predicted gene.; Similar to serine/threonine protein kinase like
protein. (AL022140).

- 15 BAA87853.1 AP000816 Oryza sativa
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).

- 20 AAG16628.1 AY007545 Brassica napus
DESCRIPTION: protein serine/threonine kinase BNK1.

- 25 BAB07999.1 AP002525 Oryza sativa
DESCRIPTION: putative protein kinase. P0462H08.22. contains EST
C22619(S11214).

- 30 BAB03429.1 AP002817 Oryza sativa
DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted
gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12;
putative protein kinase (AC006587).

- 35 BAB16871.1 AP002537 Oryza sativa
DESCRIPTION: putative protein kinase APK1AArabidopsis thaliana.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

- 40 BAA94510.1 AB041504 Populus nigra
DESCRIPTION: protein kinase 2. PnPK2.

- 45 BAB39409.1 AP002901 Oryza sativa
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST

C23560(R0290).

5 BAA94509.1 AB041503 *Populus nigra*
DESCRIPTION: protein kinase 1. PnPK1.

10 BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

15 AAK11674.1 AF339747 *Lophopyrum elongatum*
DESCRIPTION: protein kinase. ESI47.

20 AAF43496.1 AF131222 *Lophopyrum elongatum*
DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by
salt stress, osmotic stress, and ABA treatment.

25 BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

30 BAA78764.1 AB023482 *Oryza sativa*
DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region
of
the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein
tyrosine-serine-threonine kinase.(D12522).

35 AAB09771.1 U67422 *Zea mays*
DESCRIPTION: CRINKLY4 precursor. cr4. receptor kinase homolog.

40 AAK00425.1 AC069324 *Oryza sativa*
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

45 AAG59657.1 AC084319 *Oryza sativa*
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.

AAF66615.1 AF142596 *Nicotiana tabacum*

DESCRIPTION: LRR receptor-like protein kinase.

5 AAG03090.1 AC073405 Oryza sativa
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis
receptor-like kinase (AC007504).

10 CAB51834.1 00069 Oryza sativa
DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.

15 AAG25966.1 AF302082 Nicotiana tabacum
DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase;
transcript abundance decreases rapidly after cytokinin treatment.

20 CAA97692.1 Z73295 Catharanthus roseus
DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation
predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.

25 BAA90808.1 AP001168 Oryza sativa
DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).

30 BAB40081.1 AP003074 Oryza sativa
DESCRIPTION: putative receptor protein kinase. OSJNBa0004G10.30.

BAB18321.1 AP002865 Oryza sativa
DESCRIPTION: putative receptor protein kinase. P0034C11.11.

35 AAD38286.1 AC007789 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0049B20.13.

40 CAB51480.1 Y14600 Sorghum bicolor
DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates
in mesophyll cells.

45 BAB19337.1 AP003044 Oryza sativa
DESCRIPTION: putative protein kinase. P0038C05.10. contains ESTs
AU056335(S20481),AU056336(S20481).

DESCRIPTION: lectin 3.

5 BAA36415.1 AB012634 Robinia pseudoacacia
DESCRIPTION: lectin.

10 CAA93828.1 Z69998 Phaseolus lunatus
DESCRIPTION: lectin 2.

AAC49137.1 U21959 Cladrastis kentukea
DESCRIPTION: lectin precursor.

15 AAC49150.1 U21940 Cladrastis kentukea
DESCRIPTION: storage protein precursor. lectin.

20 CAB96391.1 AJ271873 Phaseolus lunatus
DESCRIPTION: carbohydrate-binding. lectin. lb15.

25 CAB96392.1 AJ271874 Phaseolus lunatus
DESCRIPTION: carbohydrate-binding. lectin. lb16.

30 CAA76366.1 Y16754 Medicago sativa
DESCRIPTION: lectin. lec2.

BAA82556.1 AB030083 Populus nigra
DESCRIPTION: lectin-like protein kinase. PnLPK.

35 CAA93830.1 Z70000 Phaseolus lunatus
DESCRIPTION: lectin 4.

40 AAG16779.1 AF190633 Ulex europaeus
DESCRIPTION: lectin II.

45 AAC49136.1 U21958 Cladrastis kentukea
DESCRIPTION: lectin precursor.

AAB39933.1 U65009 Maackia amurensis
DESCRIPTION: lectin precursor.

5

AAB39934.1 U65010 Maackia amurensis
DESCRIPTION: lectin precursor.

10 AAA33766.1 L26237 Phaseolus lunatus
DESCRIPTION: lectin II.

15 AAA33143.1 M34270 Dolichos biflorus
DESCRIPTION: seed lectin.

20 CAA57697.1 X82216 Medicago truncatula
DESCRIPTION: lectin. lec3.

BAA36413.1 AB012632 Robinia pseudoacacia
DESCRIPTION: lectin.

25 AAA80182.1 U12783 Robinia pseudoacacia
DESCRIPTION: lectin.

30 BAA04604.1 D17757 Robinia pseudoacacia
DESCRIPTION: lectin precursor.

35 CAA68497.1 Y00440 Pisum sativum
DESCRIPTION: lectin-precursor (AA -30 to 245).

40 AAC49271.1 U24249 Robinia pseudoacacia
DESCRIPTION: lectin precursor.

AAA80181.1 U12782 Robinia pseudoacacia
DESCRIPTION: lectin.

45 BAA36416.1 AB012635 Robinia pseudoacacia

DESCRIPTION: lectin-related polypeptide.

5 AAA33676.1 M18160 Pisum sativum
DESCRIPTION: lectin.

10 CAA47011.1 X66368 Pisum sativum
DESCRIPTION: Psl lectin. psl.

15 AAA33141.1 J02721 Dolichos biflorus
DESCRIPTION: lectin subunit I precursor.

20 BAA36414.1 AB012633 Robinia pseudoacacia
DESCRIPTION: lectin.

25 BAA02049.1 D12481 Bauhinia purpurea
DESCRIPTION: lectin.

30 AAA80183.1 U12784 Robinia pseudoacacia
DESCRIPTION: lectin precursor.

35 AAC49272.1 U24250 Robinia pseudoacacia
DESCRIPTION: lectin precursor.

40 AAA82737.1 U18296 Medicago sativa
DESCRIPTION: lectin. Mslecl.

45 AAA74571.1 U22468 Arachis hypogaea
DESCRIPTION: agglutinin. galactose-binding lectin precursor. lec. lectin.

50 AAB51441.1 U63011 Sophora japonica
DESCRIPTION: lectin precursor.

55 AAA74574.1 U22471 Arachis hypogaea
DESCRIPTION: agglutinin. galactose-binding lectin precursor. lec. lectin.

AAG00508.1 AF285121 *Sophora flavescens*
DESCRIPTION: lectin.

5 AAB39932.1 U65008 *Maackia amurensis*
DESCRIPTION: lectin precursor.

215

10 -----
CAA64327.1 X94624 *Brassica napus*
DESCRIPTION: acyl-CoA synthetase.

15 CAA96523.1 Z72153 *Brassica napus*
DESCRIPTION: acyl CoA synthetase.

CAC19877.1 AJ401089 *Brassica napus*
20 DESCRIPTION: activation of free fatty acids. long chain acyl-CoA
synthetase. acs6. activity confirmed by expression in *E. coli*.

CAA06820.1 AJ006025 *Cicer arietinum*
25 DESCRIPTION: acyl-coA synthetase.

AAC39365.1 AF008183 *Populus x generosa*
DESCRIPTION: 4-coumarate:CoA ligase 2. 4CL2.
30

CAA31697.1 X13325 *Petroselinum crispum*
DESCRIPTION: 4-coumarate:CoA ligase Pc4Cl-2 (AA 1-544).

35 CAA31696.1 X13324 *Petroselinum crispum*
DESCRIPTION: 4-coumarate:CoA ligase Pc4Cl-1 (AA 1-544).

40 AAC39366.1 AF008184 *Populus x generosa*
DESCRIPTION: 4-coumarate:CoA ligase 1. 4CL1.

AAF37734.1 AF052223 *Lolium perenne*
45 DESCRIPTION: 4-coumarate--CoA ligase 4CL3.

AAF91309.1 AF239686 Rubus idaeus
DESCRIPTION: 4-coumarate:coA ligase 2. adenylate-forming enzyme; 4CL2.

5

AAF37733.1 AF052222 Lolium perenne
DESCRIPTION: 4-coumarate--CoA ligase 4CL2.

10 CAA36850.1 X52623 Oryza sativa
DESCRIPTION: 4-coumarate-CoA ligase.

15 BAA07828.1 D43773 Nicotiana tabacum
DESCRIPTION: 4-coumarate:coenzyme A ligase.

20 BAA08365.1 D49366 Lithospermum erythrorhizon
DESCRIPTION: 4-coumarate:CoA ligase.

AAB18637.1 U50845 Nicotiana tabacum
DESCRIPTION: 4-coumarate:coenzyme A ligase. 4CL1. Nt4CL-1.

25

AAD40664.1 AF150686 Solanum tuberosum
DESCRIPTION: 4-coumarate:coenzyme A ligase. 4CL-2a.

30 AAA33842.1 M62755 Solanum tuberosum
DESCRIPTION: 4-coumarate--CoA ligase. St4C1-1.

35 AAB18638.1 U50846 Nicotiana tabacum
DESCRIPTION: 4-coumarate:coenzyme A ligase. 4CL2. Nt4CL-19.

40 AAF91310.1 AF239687 Rubus idaeus
DESCRIPTION: 4-coumarate:coA ligase 1. adenylate-forming enzyme; 4CL1.

AAC24503.1 AF041049 Populus tremuloides
DESCRIPTION: 4-coumarate:CoA ligase.

45

AAF37732.1 AF052221 Lolium perenne

DESCRIPTION: 4-coumarate--CoA ligase 4CL1.

5 AAA92669.1 U12013 Pinus taeda
DESCRIPTION: 4-coumarate-CoA ligase enzyme.

10 AAB42382.1 U39404 Pinus taeda
DESCRIPTION: 4-coumarate:CoA ligase. lp4CL-2.

AAB42383.1 U39405 Pinus taeda
DESCRIPTION: 4-coumarate:CoA ligase. lp4CL-1.

15 AAF91308.1 AF239685 Rubus idaeus
DESCRIPTION: 4-coumarate:coA ligase 3. adenylate-forming enzyme; 4CL3.

20 AAC24504.1 AF041050 Populus tremuloides
DESCRIPTION: 4-coumarate:CoA ligase.

25 AAA92668.1 U12012 Pinus taeda
DESCRIPTION: 4-coumarate-CoA ligase enzyme.

30 CAC36095.1 X69955 Glycine max
DESCRIPTION: 4-coumarate:Coenzyme A ligase isoenzyme 4. 4CL4.

AAG43823.1 AF212317 Capsicum annuum
DESCRIPTION: 4-coumarate:coenzyme A ligase. 4CL.

35 AAA69580.1 L43362 Oryza sativa
DESCRIPTION: 4-coumarate:CoA ligase isoform 2. 4cl.2. putative.

40 BAA08366.2 D49367 Lithospermum erythrorhizon
DESCRIPTION: 4-coumarate:CoA ligase.

45 CAA49575.1 X69954 Glycine max
DESCRIPTION: 4-coumarate--CoA ligase.

CAB97359.1 AJ278455 *Juglans nigra*
DESCRIPTION: 4-coumarate-CoA ligase. 4CL.

5

AAF73995.2 AF144502 *Pinus armandii*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

10

AAF73994.2 AF144501 *Pinus armandii*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

15

AAF74018.2 AF144525 *Tsuga canadensis*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

20

AAF74010.2 AF144517 *Abies holophylla*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

25

AAF74020.2 AF144527 *Pseudolarix amabilis*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

30

AAF74016.2 AF144523 *Nothotsuga longibracteata*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

35

AAF74013.2 AF144520 *Abies beshanzuensis*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

40

AAF74008.2 AF144515 *Abies firma*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

45

AAF74022.2 AF144529 *Cedrus atlantica*
DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

AAF74005.2 AF144512 *Larix gmelini*

DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

AAF74021.2 AF144528 *Pseudolarix amabilis*

5 DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

AAF74003.2 AF144510 *Pseudotsuga sinensis*

10 DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

AAF74019.2 AF144526 *Tsuga canadensis*

DESCRIPTION: 4-coumarate:CoA ligase. 4CL.

15 221

AAB37246.1 U58971 *Nicotiana tabacum*

DESCRIPTION: calmodulin-binding protein. TCB60.

20 224

BAB19413.1 AP002870 *Oryza sativa*

DESCRIPTION: putative acetone-cyanohydrin lyase. P0458A05.22.

25

AAC49184.1 U40402 *Hevea brasiliensis*

DESCRIPTION: hydroxynitrile lyase. hnl.

30 CAA11219.1 AJ223281 *Manihot esculenta*

DESCRIPTION: alpha-hydroxynitrile lyase. HNL4.

CAA82334.1 Z29091 *Manihot esculenta*

35 DESCRIPTION: alpha-hydroxynitrile lyase.

225

BAB16335.1 AP002818 *Oryza sativa*

40 DESCRIPTION: putative NAM protein. P0436E04.18. contains ESTs
E10793(C19698),E10793(C99379).

AAK13151.1 AC078829 *Oryza sativa*

45 DESCRIPTION: putative NAM (no apical meristem) protein.
OSJNBa0026O12.6.

CAA63102.2 X92205 *Petunia x hybrida*
DESCRIPTION: apical meristem formation. NAM.

5

CAA63101.1 X92204 *Petunia x hybrida*
DESCRIPTION: apical meristem formation. NAM.

10

BAB16328.1 AP002818 *Oryza sativa*
DESCRIPTION: putative NAM protein. P0436E04.11. contains ESTs
R4069(AU032425),R4069(AU082730).

15

BAB19365.1 AP002542 *Oryza sativa*
DESCRIPTION: putative NAM (no apical meristem) protein. P0679C08.4.

20

BAA84803.1 AP000559 *Oryza sativa*
DESCRIPTION: Similar to NAM like protein (AC005310).

25

BAB03447.1 AP002817 *Oryza sativa*
DESCRIPTION: ESTs C96615(C10106),C26336(C12127),D21959(C10106)
correspond
to a region of the predicted gene. Similar to *Arabidopsis thaliana* DNA
chromosome 4, BAC clone T6K21; NAM (no apical meristem) - like protein
(AL021889).

30

BAA92400.1 AP001366 *Oryza sativa*
DESCRIPTION: ESTs C96615(C10106),C26336(C12127),D21959(C10106)
correspond
to a region of the predicted gene. Similar to NAM (AL021889).

35

226

BAA96221.1 AP002094 *Oryza sativa*
DESCRIPTION: ESTs C19814(E10971),AU090481(E10971) correspond to a
region
of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2,
sequence from clones T3F17, F11C10, F13A10; auxin-responsive GH3-like
protein (AC006526).

45

AAD32141.1 AF123503 *Nicotiana tabacum*
DESCRIPTION: Nt-gh3 deduced protein.

- 5 CAA42636.1 X60033 *Glycine max*
DESCRIPTION: auxin-responsive GH3 product. GH3.

227

- 10 CAA70403.1 Y09204 *Nicotiana tabacum*
DESCRIPTION: histidinol-phosphate aminotransferase. hpa.

- 15 CAC20728.1 AJ278767 *Nicotiana plumbaginifolia*
DESCRIPTION: essential for histidine biosynthesis. histidinol phosphate
aminotransferase. hpa.

229

- 20 AAF33670.1 AF079872 *Nicotiana tabacum*
DESCRIPTION: cyclic nucleotide-gated calmodulin-binding ion channel.
CBP4.

- 25 AAF33669.1 AF079871 *Nicotiana tabacum*
DESCRIPTION: cyclic nucleotide-gated calmodulin-binding ion channel.
CBP7.

- 30 AAK16188.1 AC079887 *Oryza sativa*
DESCRIPTION: putative cyclic nucleotide and calmodulin-regulated ion
channel protein. OSJNBa0040E01.13.

- 35 AAB53255.1 U65390 *Nicotiana tabacum*
DESCRIPTION: cyclic nucleotide gated channel protein. CaMB-channel
protein. channel protein homolog.

- 40 CAB54856.1 AJ132686 *Zea mays*
DESCRIPTION: potassium channel protein ZMK2. ZMK2.

- 45 AAD16278.1 AF099095 *Samanea saman*
DESCRIPTION: pulvinus inward-rectifying channel for potassium SPICK1.
similar to Arabidopsis potassium channel AKT3.

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- 734 -

DESCRIPTION: potassium channel. ZMK1.

CAA60016.1 X86021 Solanum tuberosum

5 DESCRIPTION: potassium channel. SKT1 gene. putative start codon.

CAA65254.1 X96390 Lycopersicon esculentum

10 DESCRIPTION: potassium channel. LKT1.

CAA12645.1 AJ225805 Egeria densa

15 DESCRIPTION: inward potassium channel alpha subunit. homologous to the sequences of the family of inwardly rectifying potassium channels in plants which is structurally related to the shaker family of outwardly rectifying channels in Drosophila.

AAF36832.1 AF207745 Triticum aestivum

20 DESCRIPTION: AKT1-like potassium channel. TaAKT1.

CAC10514.1 AJ299019 Samanea saman

25 DESCRIPTION: potassium release. outwardly rectifying potassium channel. spork1.

AAF81249.1 AF267753 Mesembryanthemum crystallinum

30 DESCRIPTION: putative potassium channel protein Mkt1p.

CAC05488.1 AJ271446 Populus tremula x Populus tremuloides

35 DESCRIPTION: potassium channel. outward rectifying potassium channel. ptork.

232

AAA80575.1 U13148 Pennisetum ciliare

40 DESCRIPTION: possible apospory-associated protein.

AAF34174.1 AF195243 Chlamydomonas reinhardtii

45 233

DESCRIPTION: apospory-associated protein C. APOC.

AAB97366.1 AF039531 *Oryza sativa*
DESCRIPTION: lysophospholipase homolog. LPL1.

235

5

AAC61839.1 AF025430 *Papaver somniferum*
DESCRIPTION: berberine bridge enzyme. bbe1. (S)-reticuline:oxygen
oxidoreductase (methylene bridge forming).

10

AAC39358.1 AF005655 *Eschscholzia californica*
DESCRIPTION: oxidizes the N-methyl group of (S)-reticuline to the
berberine bridge carbon C-8 of (S)-scoulerine in berberine and
benzophenanthridine alkaloid biosynthesis. berberine bridge enzyme. bbe1.
15 covalently-bound FAD-dependent oxidase; elicitor-inducible.

20

AAB20352.1 S65550 *Eschscholzia californica*
DESCRIPTION: (S)-reticuline:oxygen oxidoreductase
(methylene-bridge-forming).
/gene="(S)-reticuline:oxygen oxidoreductase. This sequence comes from Fig
2; berberine bridge enzyme.

25

AAD17487.1 AF049347 *Berberis stolonifera*
DESCRIPTION: Catalyzes the oxidative cyclization of the N-methyl group of
(S)-reticuline into the berberine bridge carbon (C-8) of (S)-scoulerine.
berberine bridge enzyme. bbe1. Covalently flavinylated oxidase of
isoquinoline alkaloid biosynthesis in plants.

30

244

35

AAD17487.1 AF049347 *Berberis stolonifera*
DESCRIPTION: Catalyzes the oxidative cyclization of the N-methyl group of
(S)-reticuline into the berberine bridge carbon (C-8) of (S)-scoulerine.
berberine bridge enzyme. bbe1. Covalently flavinylated oxidase of
isoquinoline alkaloid biosynthesis in plants.

40

AAB20352.1 S65550 *Eschscholzia californica*
DESCRIPTION: (S)-reticuline:oxygen oxidoreductase
(methylene-bridge-forming).
/gene="(S)-reticuline:oxygen oxidoreductase. This sequence comes from Fig
2; berberine bridge enzyme.

45

- AAC39358.1 AF005655 *Eschscholzia californica*
 DESCRIPTION: oxidizes the N-methyl group of (S)-reticuline to the
 berberine bridge carbon C-8 of (S)-scoulerine in berberine and
 benzophenanthridine alkaloid biosynthesis. berberine bridge enzyme. bbe1.
 5 covalently-bound FAD-dependent oxidase; elicitor-inducible.
- AAC61839.1 AF025430 *Papaver somniferum*
 DESCRIPTION: berberine bridge enzyme. bbe1. (S)-reticuline:oxygen
 10 oxidoreductase (methylene bridge forming).
- 247

- AAF37267.1 AF220406 *Vitis riparia*
 15 DESCRIPTION: 26S proteasome regulatory ATPase subunit S10b. Rev136-3.
- 248

- BAA78764.1 AB023482 *Oryza sativa*
 20 DESCRIPTION: ESTs C98382(C2985),D22444(C11129) correspond to a region
 of
 the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein
 tyrosine-serine-threonine kinase.(D12522).
- 25
 BAA94509.1 AB041503 *Populus nigra*
 DESCRIPTION: protein kinase 1. PnPK1.
- 30 AAG16628.1 AY007545 *Brassica napus*
 DESCRIPTION: protein serine/threonine kinase BNK1.
- BAB03429.1 AP002817 *Oryza sativa*
 35 DESCRIPTION: EST C22619(S11214) corresponds to a region of the predicted
 gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12;
 putative protein kinase (AC006587).
- 40 BAB07999.1 AP002525 *Oryza sativa*
 DESCRIPTION: putative protein kinase. P0462H08.22. contains EST
 C22619(S11214).
- 45 BAA94510.1 AB041504 *Populus nigra*
 DESCRIPTION: protein kinase 2. PnPK2.

AAK11674.1 AF339747 *Lophopyrum elongatum*
DESCRIPTION: protein kinase. ESI47.

5

AAF43496.1 AF131222 *Lophopyrum elongatum*
DESCRIPTION: protein serine/threonine kinase. ESI47. induced in roots by
salt stress, osmotic stress, and ABA treatment.

10

BAB16871.1 AP002537 *Oryza sativa*
DESCRIPTION: putative protein kinase APK1A*Arabidopsis thaliana*.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

15

BAA87853.1 AP000816 *Oryza sativa*
DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.
(AF001308).

20

BAB39409.1 AP002901 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).

25

BAB39873.1 AP002882 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

30

BAB21240.1 AP002953 *Oryza sativa*
DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

35

AAK21965.1 AY028699 *Brassica napus*
DESCRIPTION: receptor protein kinase PERK1.

40

AAK00425.1 AC069324 *Oryza sativa*
DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.

45

AAG03090.1 AC073405 *Oryza sativa*

DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).

5 AAG59657.1 AC084319 Oryza sativa
DESCRIPTION: putative protein kinase. OSJNBa0004B24.20.

10 AAF91336.1 AF249317 Glycine max
DESCRIPTION: Pti1 kinase-like protein. Pti1a. protein kinase.

15 AAF91337.1 AF249318 Glycine max
DESCRIPTION: Pti1 kinase-like protein. Pti1b. protein kinase.

20 BAB21241.1 AP002953 Oryza sativa
DESCRIPTION: Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721),D48017(S13927).

25 CAB51834.1 00069 Oryza sativa
DESCRIPTION: 11332.5. contains eukaryotic protein kinase domain PF.

30 AAC61805.1 U28007 Lycopersicon esculentum
DESCRIPTION: serine/threonine protein kinase. Pto kinase interactor 1. Pti1. Pti1 kinase.

35 AAG33377.1 AF290411 Oryza meyeriana
DESCRIPTION: serine/threonine protein kinase. R1.

40 AAC27894.1 AF023164 Zea mays
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 1. ltk1.

45 BAA90808.1 AP001168 Oryza sativa
DESCRIPTION: Similar to putative receptor-like protein kinase (AL035679).

AAC27895.1 AF023165 Zea mays
DESCRIPTION: leucine-rich repeat transmembrane protein kinase 2. ltk2.

AAB61708.1 U93048 *Daucus carota*

DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.

5 CAA97692.1 Z73295 *Catharanthus roseus*

DESCRIPTION: receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.

10 AAK11566.1 AF318490 *Lycopersicon hirsutum*

DESCRIPTION: Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.

15 BAB18292.1 AP002860 *Oryza sativa*

DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

CAB51480.1 Y14600 *Sorghum bicolor*

20 DESCRIPTION: putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

AAG25966.1 AF302082 *Nicotiana tabacum*

25 DESCRIPTION: cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.

AAG00510.1 AF285172 *Phaseolus vulgaris*

30 DESCRIPTION: leaf senescence-associated receptor-like protein kinase. SARK.

AAC48932.1 U13923 *Lycopersicon pimpinellifolium*

35 DESCRIPTION: Fen. putative serine/threonine protein kinase; similar to product encoded by *Lycopersicon pimpinellifolium* Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.

40 AAB47424.1 U59317 *Lycopersicon pimpinellifolium*

DESCRIPTION: serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.

45 AAF76307.1 AF220602 *Lycopersicon pimpinellifolium*

DESCRIPTION: Fen kinase.

1022290"062601

AAF66615.1 AF142596 *Nicotiana tabacum*
DESCRIPTION: LRR receptor-like protein kinase.

5

BAA92221.1 AP001278 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC F12L6
genomic sequence, putative protein kinase. (AC004218).

10

BAA87852.1 AP000816 *Oryza sativa*
DESCRIPTION: Similar to putative Ser/Thr protein kinase. (AC004218).

15

AAK11567.1 AF318491 *Lycopersicon hirsutum*
DESCRIPTION: Pto-like protein kinase F. LhirPtoF.

20

CAA73134.1 Y12531 *Brassica oleracea*
DESCRIPTION: serine/threonine kinase. BRLK.

25

BAB19337.1 AP003044 *Oryza sativa*
DESCRIPTION: putative protein kinase. P0038C05.10. contains ESTs
AU056335(S20481),AU056336(S20481).

249

30

BAA22422.1 AB001379 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP81E1.

35

BAA74465.1 AB022732 *Glycyrrhiza echinata*
DESCRIPTION: cytochrome P450. CYP Ge-31.

40

BAA93634.1 AB025016 *Lotus japonicus*
DESCRIPTION: cytochrome P450.

45

CAB43505.1 AJ239051 *Cicer arietinum*
DESCRIPTION: cytochrome P450. cyp81E2.

CAB41490.1 AJ238439 *Cicer arietinum*

DESCRIPTION: cytochrome P450 monooxygenase. cyp81E3v2.

CAA10067.1 AJ012581 Cicer arietinum
5 DESCRIPTION: cytochrome P450. cyp81E3.

CAA04117.1 AJ000478 Helianthus tuberosus
10 DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l.
chimeric sequence (from 5'-race).

CAA04116.1 AJ000477 Helianthus tuberosus
15 DESCRIPTION: fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

AAK38079.1 AF321855 Lolium rigidum
20 DESCRIPTION: putative cytochrome P450.

AAK38080.1 AF321856 Lolium rigidum
DESCRIPTION: putative cytochrome P450.

25 AAK38081.1 AF321857 Lolium rigidum
DESCRIPTION: putative cytochrome P450.

AAC34853.1 AF082028 Hemerocallis hybrid cultivar
30 DESCRIPTION: putative cyt P450-containing fatty acid hydroxylase.
senescence-associated protein 3. SA3. mRNA accumulates in senescing
petals.

35 AAB94590.1 AF022461 Glycine max
DESCRIPTION: CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.

CAB56742.1 AJ249800 Cicer arietinum
40 DESCRIPTION: cytochrome P450 monooxygenase. cyp81E5.

AAD56282.1 AF155332 Petunia x hybrida
45 DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

AAG09208.1 AF175278 Pisum sativum
DESCRIPTION: wound-inducible P450 hydroxylase. CYP82A1.

5 CAA71515.1 Y10491 Glycine max
DESCRIPTION: putative cytochrome P450.

10 CAA71516.1 Y10492 Glycine max
DESCRIPTION: putative cytochrome P450.

15 AAC49188.2 U29333 Pisum sativum
DESCRIPTION: cytochrome P450 monooxygenase. CYP82. new cytochrome
P450 family.

20 CAA71876.1 Y10982 Glycine max
DESCRIPTION: putative cytochrome P450.

25 BAA12159.1 D83968 Glycine max
DESCRIPTION: Cytochrome P-450 (CYP93A1).

30 AAC39454.1 AF014802 Eschscholzia californica
DESCRIPTION: (S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome
P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome
P-450-dependent, homologous to wound-inducible CYP82A1 of Pisum sativum
GenBank Accession Number U29333.

35 CAA65580.1 X96784 Nicotiana tabacum
DESCRIPTION: cytochrome P450. hsr515.

40 BAA13076.1 D86351 Glycine max
DESCRIPTION: cytochrome P-450 (CYP93A2).

AAA32913.1 M32885 Persea americana
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).

45 CAA71877.1 Y10983 Glycine max

DESCRIPTION: putative cytochrome P450.

5 AAG44132.1 AF218296 Pisum sativum
DESCRIPTION: cytochrome P450. P450 isolog.

10 CAA64635.1 X95342 Nicotiana tabacum
DESCRIPTION: cytochrome P450. hsr515. hypersensitivity-related gene.

AAB94587.1 AF022458 Glycine max
DESCRIPTION: CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.

15 AAD38930.1 AF135485 Glycine max
DESCRIPTION: cytochrome P450 monooxygenaseCYP93D1. CYP93E1.

20 BAA84072.1 AB028152 Torenia hybrida
DESCRIPTION: flavone synthase II. cytochrome P450. TFNS5.

25 BAA74466.1 AB022733 Glycyrrhiza echinata
DESCRIPTION: cytochrome P450. CYP Ge-51.

30 BAA22423.1 AB001380 Glycyrrhiza echinata
DESCRIPTION: cytochrome P450. CYP93B1.

BAA35080.1 AB015762 Nicotiana tabacum
DESCRIPTION: putative cytochrome P450. CYP82E1.

35 BAA92894.1 AB006790 Petunia x hybrida
DESCRIPTION: cytochrome P450. IMT-2.

40 AAC32274.1 AF081575 Petunia x hybrida
DESCRIPTION: flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.

45 CAB56743.1 AJ249801 Cicer arietinum
DESCRIPTION: cytochrome P450 monooxygenase. cyp81E4.

BAA84071.1 AB028151 Antirrhinum majus
DESCRIPTION: flavone synthase II. cytochrome P450. AFNS2.

5 250

AAD55566.1 AF110784 Volvox carteri f. nagariensis
DESCRIPTION: protein disulfide isomerase precursor. pdi.

10

AAD02069.1 AF036939 Chlamydomonas reinhardtii
DESCRIPTION: redox-regulator of 5'UTR psbA mRNA binding complex and translation. protein disulfide isomerase. localized to ER and chloroplast.

15

AAC49896.1 AF027727 Chlamydomonas reinhardtii
DESCRIPTION: involved in the redox-regulated binding of chloroplast poly(A)-binding protein to the 5'-UTR of psbA mRNA; regulates chloroplast translational activation. protein disulfide isomerase RB60. PDI.

20

AAD28260.1 AF131223 Datisca glomerata
DESCRIPTION: protein disulfide isomerase homolog. PDI.

25

AAB08519.1 L39014 Zea mays
DESCRIPTION: protein disulfide isomerase. pdi. putative.

30

AAA19660.1 U11496 Triticum aestivum
DESCRIPTION: protein disulfide isomerase. PDI.

35

CAC21230.1 AJ277379 Triticum turgidum subsp. durum
DESCRIPTION: catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.

40

CAC21228.1 AJ277377 Triticum turgidum subsp. durum
DESCRIPTION: catalyzes the formation of disulfide bonds. protein disulfide isomerase. Pdi.

45

AAA70345.1 L33251 Hordeum vulgare
DESCRIPTION: catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.

AAA70344.1 L33250 *Hordeum vulgare*
 DESCRIPTION: catalyze the formation of disulfide bonds. disulfide
 5 isomerase. PDI. putative.

AAB05641.1 U41385 *Ricinus communis*
 DESCRIPTION: protein disulphide isomerase PDI. molecular chaperone.
 10

CAA77575.1 Z11499 *Medicago sativa*
 DESCRIPTION: protein disulfide isomerase.

15 CAC21231.1 AJ277380 *Triticum turgidum* subsp. durum
 DESCRIPTION: catalyzes formation of disulfide bonds. protein disulfide
 isomerase. Pdi.

20 CAC21229.1 AJ277378 *Triticum turgidum* subsp. durum
 DESCRIPTION: catalyzes formation of disulfide bonds. protein disulfide
 isomerase. Pdi.

25 BAB18780.1 AB047268 *Cucumis sativus*
 DESCRIPTION: disulfide isomerase.

30 BAA92322.1 AB039278 *Oryza sativa*
 DESCRIPTION: protein disulfide isomerase. Pdi.

AAA70346.1 L33252 *Hordeum vulgare*
 35 DESCRIPTION: catalyze the formation of disulfide bonds. disulfide
 isomerase. PDI. putative.

CAA72092.1 Y11209 *Nicotiana tabacum*
 40 DESCRIPTION: protein disulfide-isomerase precursor. PDI.

AAG13988.1 AF298829 *Prunus avium*
 DESCRIPTION: putative protein disulfide-isomerase. PDI.
 45

251

Figure 1. The effect of the initial concentration of the monomer on the polymerization of *l*-lysine. The reaction was carried out at 40 °C in 0.1 M NaOH solution. The initial concentration of the monomer was 0.05 M. The initial concentration of the initiator was 0.001 M. The reaction time was 10 min. The reaction was carried out in a 100 mL beaker. The reaction mixture was stirred with a magnetic bar. The reaction mixture was cooled to 0 °C and the reaction was stopped by adding 10 mL of 10% trichloroacetic acid. The reaction mixture was centrifuged at 1000 rpm for 10 min. The supernatant was removed and the precipitate was washed with 10% trichloroacetic acid. The precipitate was dried at 60 °C for 24 h. The yield of the polymer was determined by gravimetry.

AAC06319.1 AF053084 Malus x domestica
DESCRIPTION: putative cinnamyl alcohol dehydrogenase. CAD.

10

15

AAD09515.1 U64917 Glycine max
DESCRIPTION: putative metal-binding protein. GMFP7. farnesylated protein.

20

BAB19757.1 AB052785 Glycine max
DESCRIPTION: nitrate transporter NRT1-2. NRT1-2.

25

BAB19756.1 AB052784 Glycine max
DESCRIPTION: nitrate transporter NRT1-1. NRT1-1.

30

BAB19760.1 AB052788 Glycine max
DESCRIPTION: nitrate transporter NRT1-5. NRT1-5.

35

AAC32034.1 AF023472 *Hordeum vulgare*
DESCRIPTION: peptide transporter. ptr1. PTR1; integral membrane protein.

AAD01600.1 AF016713 *Lycopersicon esculentum*
DESCRIPTION: LeOPT1. LeOPT1. oligopeptide transporter.

45

BAB40113.1 AP003311 *Oryza sativa*
DESCRIPTION: putative peptide transport protein. P0024G09.4. contains
ESTs D40448(S2437),C71800(E0368),AU102190(E2393),
AU055921(S20154),AU102191(E2393),AU055922(S20154),
C98524(E0368),AU097146(S2437).

- BAB16458.1 AP002483 *Oryza sativa*
 DESCRIPTION: putative peptide transport protein. P0019D06.16. contains
 ESTs D40448(S2437),C71800(E0368),AU102190(E2393),
 AU055921(S20154),AU102191(E2393),AU055922(S20154),
 5 C98524(E0368),AU097146(S2437).
- CAA93316.1 Z69370 *Cucumis sativus*
 DESCRIPTION: nitrite transporter. NiTR1.
 10
- AAK15441.1 AC037426 *Oryza sativa*
 DESCRIPTION: putative nitrate transporter. OSJNBb0014I11.9.
 15
- AAG21898.1 AC026815 *Oryza sativa*
 DESCRIPTION: putative peptide transport protein. OSJNBa0079L16.13.
 20
- CAC00544.1 AJ277084 *Nicotiana plumbaginifolia*
 DESCRIPTION: ion transport. putative low-affinity nitrate transporter.
 nrt1.1.
 25
- AAG46153.1 AC018727 *Oryza sativa*
 DESCRIPTION: putative peptide transporter. OSJNBa0056G17.8.
 30
- CAC00545.1 AJ277085 *Nicotiana plumbaginifolia*
 DESCRIPTION: ion transport. putative low-affinity nitrate transporter.
 nrt1.2.
 35
- AAG21906.1 AC026815 *Oryza sativa*
 DESCRIPTION: putative peptide transport protein. OSJNBa0079L16.9.
 40
- AAF20002.1 AF213936 *Prunus dulcis*
 DESCRIPTION: amino acid/peptide transporter. PTR2. similar to
 transporters of nitrogenous compounds.
 45
- AAF07875.1 AF140606 *Oryza sativa*
 DESCRIPTION: nitrate transporter. NRT1.

BAB16322.1 AP002318 *Oryza sativa*
DESCRIPTION: putative peptide transporter-like protein. P0436E04.4.

5 BAB19758.1 AB052786 *Glycine max*
DESCRIPTION: putative nitrate transporter NRT1-3. NRT1-3.

10 AAA80582.1 U17987 *Brassica napus*
DESCRIPTION: putative nitrate transporter. RCH2 protein.

15 CAC07206.1 AJ278966 *Brassica napus*
DESCRIPTION: Low-affinity nitrate transporter. nitrate transporter. nrt1.

20 AAG46154.1 AC018727 *Oryza sativa*
DESCRIPTION: putative peptide transporter. OSJNBa0056G17.27.

25 AAB69642.1 AF000392 *Lotus japonicus*
DESCRIPTION: peptide transporter. LjNOD65.

30 BAB19759.1 AB052787 *Glycine max*
DESCRIPTION: putative nitrate transporter NRT1-4. NRT1-4.

35 AAD16016.1 AF080545 *Nepenthes alata*
DESCRIPTION: peptide transporter. PTR1.

40 AAD42860.1 AF154930 *Prunus dulcis*
DESCRIPTION: transporter-like protein. TLP1.

45 AAG13513.1 AC068924 *Oryza sativa*
DESCRIPTION: putative peptide transporter. OSJNBa0026L12.7.

45 255

AAB01567.1 L47672 *Picea glauca*
DESCRIPTION: EMB34. embryo-abundant protein.

45 257

AAB71743.1 U75345 Chlamydomonas reinhardtii

DESCRIPTION: envelope protein. LIP-36G1. low CO2 inducible carrier protein LIP-36 with a molecular weight of 36 kDa.

5

AAB71744.1 U75346 Chlamydomonas reinhardtii

DESCRIPTION: envelope protein. LIP-36G2. low CO2 inducible carrier protein LIP-36 with a molecular weight of 36 kDa.

10

BAA92520.1 AP001383 Oryza sativa

DESCRIPTION: ESTs AU068633(C30614),AU068634(C30614) correspond to a

15

region of the predicted gene. Similar to Bos taurus mitochondrial solute carrier protein. (AF049236).

BAB16462.1 AP002483 Oryza sativa

20

DESCRIPTION: putative peroxisomal Ca-dependent solute carrier protein. P0019D06.21.

BAB40117.1 AP003311 Oryza sativa

25

DESCRIPTION: putative peroxisomal Ca-dependent solute carrier protein. P0024G09.9.

CAA07568.1 AJ007580 Ribes nigrum

30

DESCRIPTION: Mitochondrial carrier protein. prib7.

CAC27140.1 AJ132535 Picea abies

35

DESCRIPTION: ADP, ATP carrier protein precursor.

CAA56325.1 X80023 Triticum turgidum

DESCRIPTION: ATP/ADP carrier protein.

40

CAC12820.1 AJ299250 Nicotiana tabacum

DESCRIPTION: mitochondrial 2-oxoglutarate/malate carrier protein. momc1.

AAG48999.1 AY013246 Hordeum vulgare

45

DESCRIPTION: putative mitochondrial carrier protein. 635P2.1.

CAA05276.1 AJ002236 *Lycopersicon pimpinellifolium*
DESCRIPTION: resistance gene. Hcr9-9E. Hcr9-9E.

5

AAC78591.1 AF053993 *Lycopersicon esculentum*
DESCRIPTION: disease resistance protein. Cf-5.

10

AAC78596.1 AF053998 *Lycopersicon esculentum*
DESCRIPTION: Hcr2-5D. Hcr2-5D. similar to *Lycopersicon pimpinellifolium*
disease resistance protein Cf-2.2 encoded by the sequence presented in
GenBank Accession Number U42445.

15

CAA05279.1 AJ002237 *Lycopersicon esculentum*
DESCRIPTION: Hcr9-0. Hcr9-0. homologue of *Cladosporium fulvum* disease
resistance gene Cf-9.

20

AAC78593.1 AF053995 *Lycopersicon esculentum*
DESCRIPTION: Hcr2-0B. Hcr2-0B. similar to *Lycopersicon pimpinellifolium*
disease resistance protein Cf-2.2 encoded by the sequence presented in
GenBank Accession Number U42445.

25

AAA65235.1 U15936 *Lycopersicon pimpinellifolium*
DESCRIPTION: Cf-9 precursor. Cf-9. this is the ninth resistance gene to
disease caused by *Cladosporium fulvum* to be isolated.

30

CAA05274.1 AJ002236 *Lycopersicon pimpinellifolium*
DESCRIPTION: resistance gene. Cf-9. Cf-9.

35

AAC78592.1 AF053994 *Lycopersicon esculentum*
DESCRIPTION: Hcr2-0A. Hcr2-0A. similar to *Lycopersicon pimpinellifolium*
disease resistance protein Cf-2.2 encoded by the sequence presented in
GenBank Accession Number U42445.

40

AAC78595.1 AF053997 *Lycopersicon esculentum*
DESCRIPTION: Hcr2-5B. Hcr2-5B. similar to *Lycopersicon pimpinellifolium*
disease resistance protein Cf-2.2 encoded by the sequence presented in
GenBank Accession Number U42445.

45

DESCRIPTION: receptor kinase-like protein. Xa21. Xa21 disease resistance gene.

- 5 AAC80225.1 U72723 *Oryza longistaminata*
DESCRIPTION: receptor kinase-like protein. Xa21. disease resistance gene.

259

- 10 CAB52689.1 AJ132224 *Lycopersicon esculentum*
DESCRIPTION: hexose transporter. ht2.

- 15 CAA09419.1 AJ010942 *Lycopersicon esculentum*
DESCRIPTION: hexose transporter protein.

- 20 BAB19864.1 AB052885 *Oryza sativa*
DESCRIPTION: monosaccharide transporter 3. OsMST3.

- 25 AAA18534.1 L21753 *Saccharum hybrid cultivar H65-7052*
DESCRIPTION: glucose transporter. putative.

- CAA47324.1 X66856 *Nicotiana tabacum*
DESCRIPTION: monosaccharid transporter. MST1.

- 30 AAB06594.1 U38651 *Medicago truncatula*
DESCRIPTION: sugar transporter.

- 35 AAA79761.1 L08196 *Ricinus communis*
DESCRIPTION: hexose transport. sugar carrier protein. RCSTC.

- 40 CAA04511.1 AJ001061 *Vitis vinifera*
DESCRIPTION: hexose uptake. hexose transporter.

- CAA70777.1 Y09590 *Vitis vinifera*
DESCRIPTION: hexose transporter.

- 45 AAC61852.1 AF061106 *Petunia x hybrida*

DESCRIPTION: putative monosaccharide transporter 1. pmt1. similar to hexose transporter protein; PMT1.

5 AAA79857.1 L08188 Ricinus communis
DESCRIPTION: hexose transport. hexose carrier protein. HEX6.

CAB06079.1 Z83829 Picea abies
10 DESCRIPTION: monosaccharide transporter. PaMst-1. PaMst-1.

BAB19863.1 AB052884 Oryza sativa
DESCRIPTION: monosaccharide transporter 2. OsMST2.
15

BAA83554.1 AP000399 Oryza sativa
DESCRIPTION: Similar to hexose carrier protein HEX6 & RCCHCP_1
(Q07423).
20

AAK31286.1 AC079890 Oryza sativa
DESCRIPTION: putative hexose carrier protein. OSJNBb0089A17.11.
25

CAA53192.1 X75440 Chlorella kessleri
DESCRIPTION: hexose transporter like protein. HUP3.

30 CAA68813.1 Y07520 Chlorella kessleri
DESCRIPTION: H(+)/hexose cotransporter (AA 1-533).

CAA39036.1 X55349 Chlorella kessleri
35 DESCRIPTION: H(+)/hexose-cotransporter. HUP1.

BAB19862.1 AB052883 Oryza sativa
DESCRIPTION: monosaccharide transporter 1. OsMST1.
40

AAA18533.1 L21752 Saccharum hybrid cultivar H65-7052
DESCRIPTION: glucose transporter. putative.

45 CAB52688.1 AJ132223 Lycopersicon esculentum

DESCRIPTION: hexose transporter. ht1.

5 AAD55054.1 AF173655 Beta vulgaris
DESCRIPTION: glucose transporter. Gt.

10 CAB52690.1 AJ132225 Lycopersicon esculentum
DESCRIPTION: hexose transporter. ht3.

AAA33875.1 L31352 Ricinus communis
DESCRIPTION: hexose transport. hexose carrier. Hex9. putative.

15 AAK13147.1 AC083945 Oryza sativa
DESCRIPTION: Putative sugar transporter. OSJNBa0058E19.22.

20 AAB68029.1 U64903 Beta vulgaris
DESCRIPTION: BvcDNA-397. putative sugar transporter; member of major
facilitative superfamily; integral membrane protein.

25 AAB68028.1 U64902 Beta vulgaris
DESCRIPTION: BvcDNA-205. putative sugar transporter; member of major
facilitative superfamily; integral membrane protein.

30 AAG43998.1 AF215837 Apium graveolens var. dulce
DESCRIPTION: mannitol transporter. Mat1.

35 AAF74568.1 AF215854 Zea mays
DESCRIPTION: transport of hexoses across the plastid inner envelope
membrane. hexose transporter. pGlcT.

40 AAF74567.1 AF215853 Solanum tuberosum
DESCRIPTION: transport of hexoses across the plastid inner envelope
membrane. hexose transporter. pGlcT.

45 AAF74566.1 AF215852 Nicotiana tabacum
DESCRIPTION: transport of hexoses across the plastid inner envelope
membrane. hexose transporter. pGlcT.

DESCRIPTION: transport of hexoses across the plastid inner envelope membrane. hexose transporter. pGlcT.

DESCRIPTION: putative sugar transporter protein. OSJNBa0056G17.3.

DESCRIPTION: putative glucose translocator. metabolite transporter; targeted to plastid inner envelope membrane.

DESCRIPTION: putative sugar transporter. integral membrane protein. member of major facilitator superfamily.

DESCRIPTION: putative sugar transporter.

DESCRIPTION: hexose transport. hexose carrier. Hex10. putative.

DESCRIPTION: hexose carrier protein 1. HCP1.

DESCRIPTION: hexose transport protein. HEX2.

DESCRIPTION: receptor type serine/threonine kinase. protein kinase.

DESCRIPTION: receptor-like protein kinase. DUPR11.18.

BAA92954.1 AP001551 *Oryza sativa*
DESCRIPTION: Similar to *Oryza sativa* protein kinase (OSPK10) mRNA.
(L27821).

5

BAB07906.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.14.

10 BAA94516.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
(AJ010166).

15 BAA94528.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 2 BAC T20K24;
putative receptor-like protein kinase (AC002392).

20 BAA94517.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
(AJ010166).

25 BAB07905.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.13.

30 BAA94529.2 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Zea mays* S-domain receptor-like protein kinase
(AJ010166).

35 BAB07904.1 AP002835 *Oryza sativa*
DESCRIPTION: putative S-receptor kinase. P0417G05.12.

40 BAA94518.1 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 2 section 111 of
255; putative receptor-like protein kinase (AC002392).

45 CAA47962.1 X67733 *Zea mays*
DESCRIPTION: receptor-like protein kinase. PK1.

5 AAB61708.1 U93048 *Daucus carota*
 DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.

10 AAF78016.1 AF238472 *Oryza sativa*
 DESCRIPTION: receptor-like kinase. RLG15. protein kinase.

15 AAD46420.1 AF100771 *Hordeum vulgare*
 DESCRIPTION: receptor-like kinase. Hv3ARK. similar to wheat ARK1AS.

20 AAC49629.1 U51330 *Triticum aestivum*
 DESCRIPTION: rust resistance kinase Lr10. LRK10.

25 BAB17139.1 AP002867 *Oryza sativa*
 DESCRIPTION: putative receptor kinase. P0463F06.31.

BAB17331.1 AP002747 *Oryza sativa*
 DESCRIPTION: putative receptor kinase. P0698G03.12.

30 AAC01746.1 AF044489 *Oryza sativa*
 DESCRIPTION: receptor-like protein kinase. drpk1.

AAC27489.1 AF077130 *Oryza sativa*
 DESCRIPTION: receptor-like protein kinase.

35 AAC02535.1 AF044260 *Oryza sativa*
 DESCRIPTION: receptor serine/threonine kinase. protein kinase.

40 BAB39434.1 AP003338 *Oryza sativa*
 DESCRIPTION: receptor-like kinase. OJ1212_B09.1.

45 AAF78020.1 AF238476 *Oryza sativa*
 DESCRIPTION: receptor-like kinase. RLG11. protein kinase.

BAA92953.1 AP001551 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana chromosome 4 BAC clone
F10M6
; S-receptor kinase -like protein. (AL021811).

5

AAF78018.1 AF238474 Oryza sativa
DESCRIPTION: receptor-like kinase. RLG16. protein kinase.

10

AAD46917.1 AF164021 Oryza sativa
DESCRIPTION: receptor kinase.

15

BAB39438.1 AP003338 Oryza sativa
DESCRIPTION: putative receptor kinase. OJ1212_B09.7.

20

BAB39435.1 AP003338 Oryza sativa
DESCRIPTION: putative receptor kinase. OJ1212_B09.2.

25

BAB17129.1 AP002867 Oryza sativa
DESCRIPTION: putative receptor kinase. P0463F06.20.

BAB17321.1 AP002747 Oryza sativa
DESCRIPTION: putative receptor kinase. P0698G03.1.

30

AAF68398.1 AF237568 Oryza sativa
DESCRIPTION: receptor-like protein kinase. RLG2.

35

BAB39437.1 AP003338 Oryza sativa
DESCRIPTION: receptor-like kinase. OJ1212_B09.6.

AAF78019.1 AF238475 Oryza sativa
DESCRIPTION: receptor-like kinase. RLG17. protein kinase.

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261

AAD09343.1 AF026538 Hordeum vulgare
DESCRIPTION: ABA-responsive protein.

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[illegible]

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- 761 -

DESCRIPTION: zinc finger transcription factor WRKY1.

AAD55974.1 AF121353 Petroselinum crispum

5 DESCRIPTION: zinc-finger type transcription factor WRKY1. WRKY1.

CAB97004.1 AJ278507 Solanum tuberosum

10 DESCRIPTION: putative transcription factor. WRKY DNA binding protein.
WRKY1.

BAA82107.1 AB022693 Nicotiana tabacum

15 DESCRIPTION: transcription factor. NtWRKY1.

AAD32677.1 AF140554 Avena sativa

20 DESCRIPTION: DNA-binding protein WRKY1. wrky1. putative transcription
factor.

BAB16432.1 AB041520 Nicotiana tabacum

25 DESCRIPTION: WRKY transcription factor Nt-SubD48. Nt-SubD48.

AAD16138.1 AF096298 Nicotiana tabacum

30 DESCRIPTION: DNA-binding protein 1. WRKY1. transcription factor.

AAD32676.1 AF140553 Avena sativa

35 DESCRIPTION: DNA-binding protein WRKY3. wrky3. putative transcription
factor.

AAD27591.1 AF121354 Petroselinum crispum

40 DESCRIPTION: binds sequence specifically to W Boxes (TTGACC).
transcription factor. WRKY3. sequence specific DNA-binding protein.

AAF61864.1 AF193771 Nicotiana tabacum

45 DESCRIPTION: DNA-binding protein 4. WRKY4. transcription factor.

AAG35659.1 AF204926 Petroselinum crispum

DESCRIPTION: transcription factor WRKY5. WRKY5. binds to W box
(TTGACC)

elements.

AAAF61863.1 AF193770 *Nicotiana tabacum*
5 DESCRIPTION: DNA-binding protein 3. WRKY3. transcription factor.

272

BAA07395.1 D38220 *Brassica napus*
10 DESCRIPTION: nitrate reductase.

BAA07394.1 D38219 *Brassica napus*
15 DESCRIPTION: nitrate reductase.

AAG30576.1 AF314093 *Ricinus communis*
20 DESCRIPTION: nitrate reductase. NIA.

CAA32217.1 X14059 *Nicotiana tabacum*
DESCRIPTION: nitrate reductase.

AAA33713.1 L13691 *Petunia x hybrida*
25 DESCRIPTION: nitrate reductase. putative.

CAA32218.1 X14060 *Lycopersicon esculentum*
30 DESCRIPTION: nitrate reductase.

AAA33712.1 L11563 *Petunia x hybrida*
35 DESCRIPTION: nitrate reductase apoenzyme. nia.

CAA32216.1 X14058 *Nicotiana tabacum*
DESCRIPTION: nitrate reductase.

CAA56696.1 X80670 *Lotus japonicus*
40 DESCRIPTION: nitrate reductase (NADH). NIA.

AAB52786.1 U95317 *Solanum tuberosum*
45 DESCRIPTION: NADH nitrate reductase. StNR3.

10

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25

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- 764 -

AAA62316.1 U20450 Zea mays
DESCRIPTION: nitrate reductase.

5 AAD38068.1 AF153448 Zea mays
DESCRIPTION: nitrate reductase. NR1.

CAA40975.1 X57844 Hordeum vulgare
10 DESCRIPTION: nitrate reductase. cDNA is 9bp short of atg.

CAA40976.1 X57845 Hordeum vulgare
DESCRIPTION: nitrate reductase.
15

CAA42739.1 X60173 Hordeum vulgare
DESCRIPTION: nitrate reductase (NAD(P)H). nar7.

20 AAB93560.1 AF022780 Glycine max
DESCRIPTION: nitrate reductase. BCNR-A.

25 AAF17595.1 AF203033 Chlamydomonas reinhardtii
DESCRIPTION: nitrate reductase. NIT1.

CAA45497.1 X64136 Volvox carteri
30 DESCRIPTION: nitrate reductase (NADH). nitA.

AAC49460.1 U39931 Chlorella vulgaris
DESCRIPTION: nitrate reductase.
35

AAC49459.1 U39930 Chlorella vulgaris
DESCRIPTION: nitrate reductase.

40 CAA29497.1 X06134 Nicotiana tabacum
DESCRIPTION: nitrate reductase.

45 AAA18377.1 U08029 Spinacia oleracea
DESCRIPTION: reduces nitrate to nitrite with NADH. NADH:nitrate

reductase.

- 5 AAB39553.1 U64308 *Agrostemma githago*
DESCRIPTION: nitrate reductase. agnr1. NADH; similar to agnr2 product
encoded by GenBank Accession Number U64309 and to agnr3 product encoded
by
GenBank Accession Number U64310.
- 10 AAA03202.1 M27821 *Zea mays*
DESCRIPTION: NADH:nitrate reductase; (EC 1.6.6.1).
- 15 AAA33483.1 M77792 *Zea mays*
DESCRIPTION: enzyme. nitrate reductase. NAR1S.
- 20 AAB39555.1 U64310 *Agrostemma githago*
DESCRIPTION: nitrate reductase. agnr3. NADH; similar to agnr1 product
encoded by GenBank Accession Number U64308 and agnr2 product encoded by
GenBank Accession Number U64309.
- 25 AAB39554.1 U64309 *Agrostemma githago*
DESCRIPTION: nitrate reductase. agnr2. NADH; similar to agnr1 product
encoded by GenBank Accession Number U64308 and agnr3 product encoded by
GenBank Accession Number U64310.
- 30 CAA33819.1 X15820 *Oryza sativa*
DESCRIPTION: nitrate reductase apoenzyme (AA 472-916); Protein sequence
is in conflict with the conceptual translation.
- 35 CAA33817.1 X15819 *Oryza sativa*
DESCRIPTION: nitrate reductase apoenzyme.
- 40 AAA33998.1 L23853 *Glycine max*
DESCRIPTION: nitrate reductase. mutant.
- 45 CAA58908.1 X84102 *Cichorium intybus*
DESCRIPTION: nitrate reductase (NADH). nia.

CAA40090.1 X56771 *Chlorella vulgaris*
DESCRIPTION: nitrate reductase (NADH).

5

CAA45776.1 X64446 *Zea mays*
DESCRIPTION: nitrate reductase (NAD(P)H). nar.

10 AAD17694.1 AF077372 *Zea mays*
DESCRIPTION: possible reduction of Fe³⁺-chelates. cytochrome b5
reductase. NFR.

15 AAA96242.1 L40147 *Avena strigosa*
DESCRIPTION: nitrate reductase.

20 AAB20155.1 S61885 *Nicotiana plumbaginifolia*
DESCRIPTION: nitrate reductase heme domain. nitrate reductase heme
domain, NR. This sequence comes from fig3; NR.

25 AAA96245.1 L40151 *Hordeum pusillum*
DESCRIPTION: nitrate reductase.

30 AAA96247.1 L40153 *Hordeum stenostachys*
DESCRIPTION: nitrate reductase.

273

35 BAA07395.1 D38220 *Brassica napus*
DESCRIPTION: nitrate reductase.

BAA07394.1 D38219 *Brassica napus*
DESCRIPTION: nitrate reductase.

40 AAA33713.1 L13691 *Petunia x hybrida*
DESCRIPTION: nitrate reductase. putative.

45 CAA32218.1 X14060 *Lycopersicon esculentum*
DESCRIPTION: nitrate reductase.

AAA33712.1 L11563 Petunia x hybrida
DESCRIPTION: nitrate reductase apoenzyme. nia.
5

AAG30576.1 AF314093 Ricinus communis
DESCRIPTION: nitrate reductase. NIA.

10
CAA32217.1 X14059 Nicotiana tabacum
DESCRIPTION: nitrate reductase.

15
CAA32216.1 X14058 Nicotiana tabacum
DESCRIPTION: nitrate reductase.

20
AAA33114.1 M33154 Cucurbita maxima
DESCRIPTION: nitrate reductase.

AAB52786.1 U95317 Solanum tuberosum
DESCRIPTION: NADH nitrate reductase. StNR3.
25

AAB18985.1 U76701 Solanum tuberosum
DESCRIPTION: NADH nitrate reductase. StNR2.

30
AAA34033.1 M32600 Spinacia oleracea
DESCRIPTION: NADH nitrate reductase.

35
BAA13047.1 D86226 Spinacia oleracea
DESCRIPTION: nitrate reductase.

40
CAA38031.1 X54097 Betula pendula
DESCRIPTION: nitrate reductase (NADH). nia1.

45
CAA56696.1 X80670 Lotus japonicus
DESCRIPTION: nitrate reductase (NADH). NIA.

DESCRIPTION: nitrate reductase.

CAA42739.1 X60173 Hordeum vulgare
5 DESCRIPTION: nitrate reductase (NAD(P)H). nar7.

AAF17595.1 AF203033 Chlamydomonas reinhardtii
10 DESCRIPTION: nitrate reductase. NIT1.

CAA45497.1 X64136 Volvox carteri
DESCRIPTION: nitrate reductase (NADH). nitA.

15 AAC49460.1 U39931 Chlorella vulgaris
DESCRIPTION: nitrate reductase.

20 AAC49459.1 U39930 Chlorella vulgaris
DESCRIPTION: nitrate reductase.

CAA29497.1 X06134 Nicotiana tabacum
25 DESCRIPTION: nitrate reductase.

AAA18377.1 U08029 Spinacia oleracea
30 DESCRIPTION: reduces nitrate to nitrite with NADH. NADH:nitrate
reductase.

AAB39553.1 U64308 Agrostemma githago
35 DESCRIPTION: nitrate reductase. agnr1. NADH; similar to agnr2 product
encoded by GenBank Accession Number U64309 and to agnr3 product encoded
by
GenBank Accession Number U64310.

40 AAA03202.1 M27821 Zea mays
DESCRIPTION: NADH:nitrate reductase; (EC 1.6.6.1).

AAA33483.1 M77792 Zea mays
45 DESCRIPTION: enzyme. nitrate reductase. NAR1S.

AAA96245.1 L40151 *Hordeum pusillum*
DESCRIPTION: nitrate reductase.

- 5 AAA96247.1 L40153 *Hordeum stenostachys*
DESCRIPTION: nitrate reductase.

274

- 10 AAC39318.1 AF029858 *Sorghum bicolor*
DESCRIPTION: second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p-hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.

15

BAB40323.1 AB037244 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-1.

20

AAA32913.1 M32885 *Persea americana*
DESCRIPTION: cytochrome P-450LXXIA1 (cyp71A1).

- 25 BAB40324.1 AB037245 *Asparagus officinalis*
DESCRIPTION: cytochrome P450. ASPI-2.

- 30 AAA19701.1 L24438 *Thlaspi arvense*
DESCRIPTION: cytochrome P450.

- 35 CAA71513.1 Y10489 *Glycine max*
DESCRIPTION: putative cytochrome P450.

AAB94589.1 AF022460 *Glycine max*
DESCRIPTION: CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.

40

AAB94588.1 AF022459 *Glycine max*
DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.

- 45 AAB61965.1 U48435 *Solanum chacoense*
DESCRIPTION: putative cytochrome P450.

- CAA70575.1 Y09423 *Nepeta racemosa*
DESCRIPTION: cytochrome P450. CYP71A5.
- 5
- CAA71517.1 Y10493 *Glycine max*
DESCRIPTION: putative cytochrome P450.
- 10
- AAD47832.1 AF166332 *Nicotiana tabacum*
DESCRIPTION: cytochrome P450.
- 15
- AAK38084.1 AF321860 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 20
- AAB94584.1 AF022157 *Glycine max*
DESCRIPTION: capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
- 25
- AAF27282.1 AF122821 *Capsicum annuum*
DESCRIPTION: cytochrome P450. PepCYP.
- 30
- AAK38083.1 AF321859 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.
- 35
- CAA50312.1 X70981 *Solanum melongena*
DESCRIPTION: P450 hydroxylase. CYPEG2.
- 40
- CAB56503.1 AJ238612 *Catharanthus roseus*
DESCRIPTION: cytochrome P450.
- 45
- AAB61964.1 U48434 *Solanum chacoense*
DESCRIPTION: putative cytochrome P450.
- AAK38087.1 AF321863 *Lolium rigidum*
DESCRIPTION: putative cytochrome P450.

CAA71514.1 Y10490 Glycine max
DESCRIPTION: putative cytochrome P450.

5 CAA50645.1 X71654 Solanum melongena
DESCRIPTION: P450 hydroxylase.

10 BAA03635.1 D14990 Solanum melongena
DESCRIPTION: Cytochrome P-450EG4.

15 AAD44151.1 AF124816 Mentha x piperita
DESCRIPTION: cytochrome p450 isoform PM17.

20 AAD44152.1 AF124817 Mentha x piperita
DESCRIPTION: cytochrome p450 isoform PM2.

CAA83941.1 Z33875 Mentha x piperita
DESCRIPTION: cytochrome P-450 oxidase.

25 AAD44150.1 AF124815 Mentha spicata
DESCRIPTION: cytochrome p450.

30 AAB69644.1 AF000403 Lotus japonicus
DESCRIPTION: putative cytochrome P450. LjNP450.

35 BAB40322.1 AB036772 Triticum aestivum
DESCRIPTION: cytochrome P450. N-1.

40 CAC27827.1 AJ295719 Catharanthus roseus
DESCRIPTION: geraniol hydroxylase. cytochrome P450. cyp71.

AAG44132.1 AF218296 Pisum sativum
DESCRIPTION: cytochrome P450. P450 isolog.

45 AAD56282.1 AF155332 Petunia x hybrida

DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

- 5 AAG14963.1 AF214009 Brassica napus
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H3.
- 10 AAD37433.1 AF150881 Lycopersicon esculentum x Lycopersicon peruvianum
DESCRIPTION: catalyzes the hydroxylation of ferulic acid to
5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome
P450-dependent monooxygenase; F5H; FAH1.
- 15 BAB39252.1 AP002968 Oryza sativa
DESCRIPTION: putative cytochrome P450. P0416G11.1.
- 20 AAK38088.1 AF321864 Lolium rigidum
DESCRIPTION: putative cytochrome P450.
- 25 CAA65580.1 X96784 Nicotiana tabacum
DESCRIPTION: cytochrome P450. hsr515.
- AAG14961.1 AF214007 Brassica napus
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H1.
- 30 AAG14962.1 AF214008 Brassica napus
DESCRIPTION: cytochrome p450-dependent monooxygenase. BNF5H2.
- 35 AAB17562.1 U72654 Eustoma grandiflorum
DESCRIPTION: flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
- 279

- 40 AAA34122.1 M84466 Nicotiana tabacum
DESCRIPTION: phenylalanine ammonia lyase. tpa1.
- 45 BAA22948.1 AB008200 Nicotiana tabacum
DESCRIPTION: phenylalanine ammonia-lyase. palB.

AAA34176.1 M90692 *Lycopersicon esculentum*
DESCRIPTION: phenylalanine ammonia-lyase. PAL5.

5 AAF40224.1 AF237955 *Rubus idaeus*
DESCRIPTION: phenylalanine ammonia-lyase 2. PAL2. PAL;
phenylpropanoid;
multigene; flavonoid.

10 CAA37129.1 X52953 *Glycine max*
DESCRIPTION: phenylalanine ammonia-lyase. PAL1.

15 CAA68036.1 X99705 *Triticum aestivum*
DESCRIPTION: phenylalanine ammonia-lyase. PAL.

20 AAA33389.1 M29232 *Ipomoea batatas*
DESCRIPTION: phenylalanine ammonia-lyase.

25 AAA34179.2 M83314 *Lycopersicon esculentum*
DESCRIPTION: deamination of phenylalanine to coumarate. phenylalanine
ammonia lyase. pal.

30 BAA21643.1 D30656 *Populus kitakamiensis*
DESCRIPTION: phenylalanine ammonia-lyase.

AAB67733.1 U43338 *Citrus limon*
DESCRIPTION: phenylalanine ammonia-lyase. pal6.

35 BAA95629.1 AB042520 *Catharanthus roseus*
DESCRIPTION: phenylalanine ammonia lyase.

40 BAA05643.1 D26596 *Camellia sinensis*
DESCRIPTION: phenylalanine ammonia-lyase.

45 CAA73065.1 Y12461 *Helianthus annuus*
DESCRIPTION: phenylalanine ammonia lyase. PAL.

BAA24929.1 D83076 Lithospermum erythrorhizon
DESCRIPTION: phenylalanine ammonia-lyase.

5

BAA24928.1 D83075 Lithospermum erythrorhizon
DESCRIPTION: phenylalanine ammonia-lyase.

10 BAA00885.1 D10001 Pisum sativum
DESCRIPTION: phenylalanine ammonia-lyase.

15 AAA84889.1 U39792 Pinus taeda
DESCRIPTION: phenylalanine ammonia-lyase. lpPAL.

20 CAA61198.1 X87946 Oryza sativa
DESCRIPTION: phenylalanine ammonia-lyase. ZB8.

CAA41169.1 X58180 Medicago sativa
DESCRIPTION: phenylalanine ammonia-lyase. PAL.

25 BAA00887.1 D10003 Pisum sativum
DESCRIPTION: phenylalanine ammonia-lyase. PAL2.

30 BAA00886.1 D10002 Pisum sativum
DESCRIPTION: phenylalanine ammonia-lyase. PAL1.

35 AAA17993.1 M91192 Trifolium subterraneum
DESCRIPTION: phenylalanine ammonia-lyase. PAL1.

40 AAA33805.1 L11747 Populus x generosa
DESCRIPTION: phenylalanine ammonia lyase. PAL.

AAC78457.1 AF036948 Prunus avium
DESCRIPTION: phenylalanine ammonia-lyase. PAL1.

45

BAA23367.1 D85850 Daucus carota

DESCRIPTION: phenylalanine ammonia-lyase. gDcPAL1.

5 CAB42793.1 AJ238753 Citrus clementina x Citrus reticulata
DESCRIPTION: phenylalanine-ammonia lyase. pal1.

10 AAA99500.1 L36822 Stylosanthes humilis
DESCRIPTION: phenylalanine ammonia lyase. PAL17.1.

CAA55075.1 X78269 Nicotiana tabacum
DESCRIPTION: phenylalanine ammonia-lyase.

15 BAA22963.1 D17467 Nicotiana tabacum
DESCRIPTION: phenylalanine ammonia-lyase. TOBPAL1.

20 BAA22947.1 AB008199 Nicotiana tabacum
DESCRIPTION: phenylalanine ammonia-lyase. palA.

25 CAA57057.1 X81159 Petroselinum crispum
DESCRIPTION: phenylalanine ammonia-lyase 3. PAL3. tetramere subunit.

30 AAG49585.1 AF325496 Ipomoea nil
DESCRIPTION: phenylalanine ammonia-lyase.

CAA57056.1 X81158 Petroselinum crispum
DESCRIPTION: phenylalanine ammonia-lyase 2. PAL2. deaminase subunit.

35 CAB42794.1 AJ238754 Citrus clementina x Citrus reticulata
DESCRIPTION: phenylalanine-ammonia lyase. pal2.

40 CAA05251.1 AJ002221 Digitalis lanata
DESCRIPTION: phenylalanine ammonia lyase.

45 BAA07860.1 D43802 Populus kitakamiensis
DESCRIPTION: phenylalanine ammonia-lyase.

- CAB60719.1 AJ250836 *Cicer arietinum*
DESCRIPTION: phenylpropanoid pathway. phenylalanine ammonia-lyase. pal.
- 5 CAA68256.1 X99997 *Bromheadia finlaysoniana*
DESCRIPTION: phenylalanine ammonia-lyase. pal.
- 10 AAK15640.1 AF326116 *Agastache rugosa*
DESCRIPTION: phenylalanine ammonia-lyase. PAL.
- 15 CAA34226.1 X16099 *Oryza sativa* subsp. japonica
DESCRIPTION: phenylalanine ammonia-lyase.
- 20 AAF40223.1 AF237954 *Rubus idaeus*
DESCRIPTION: phenylalanine ammonia-lyase 1. PAL1. PAL;
phenylpropanoid;
multigene; flavonoid.
- 25 BAA11459.1 D78640 *Ipomoea batatas*
DESCRIPTION: Phenylalanine Ammonia-Lyase.
- 30 BAA06337.1 D30657 *Populus kitakamiensis*
DESCRIPTION: phenylalanine ammonia-lyase.
- 35 AAD45384.1 AF165998 *Vigna unguiculata*
DESCRIPTION: phenylalanine ammonia-lyase.
- CAA53733.1 X76130 *Cucumis melo*
DESCRIPTION: phenylalanine ammonia-lyase. pal.
- 40 AAA51873.1 U16130 *Persea americana*
DESCRIPTION: phenylalanine ammonia lyase. PAL.
- 45 BAB19128.1 AB041361 *Dianthus caryophyllus*
DESCRIPTION: phenylalanine ammonia-lyase. Dcpal1.

CAA34715.1 X16772 Petroselinum crispum
DESCRIPTION: phenylalanine ammonia-lyase (AA 137 - 716) (1 is 3rd base in
codon).

5

BAA07861.1 D43803 Populus kitakamiensis
DESCRIPTION: phenylalanine ammonia-lyase.

10 280

AAG43550.1 AF211532 Nicotiana tabacum
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to
RING finger proteins.

15

AAK00436.1 AC060755 Oryza sativa
DESCRIPTION: putative zinc finger protein. OSJNBa0003O19.23.

20

BAA78746.1 AB023482 Oryza sativa
DESCRIPTION: Similar to Arabidopsis thaliana RING-H2 finger protein
RHX1a
mRNA, partial cds.(AF079184).

25

CAA74911.1 Y14573 Hordeum vulgare
DESCRIPTION: ring finger protein. putative.

30

AAG46117.1 AC073166 Oryza sativa
DESCRIPTION: putative ring finger protein. OSJNBb0064P21.7.

35

BAA96875.1 AB045121 Oryza sativa
DESCRIPTION: RING finger 1. RRF1.

40

BAA90357.1 AP001080 Oryza sativa
DESCRIPTION: EST AU070319(S10788) corresponds to a region of the
predicted gene. Similar to RING-H2 finger protein RHA2b (AC006200).

45

BAA90806.1 AP001168 Oryza sativa
DESCRIPTION: ESTs C26000(C11448),AU082130(C11448) correspond to a
region

of the predicted gene.; Similar to mRNA for zinc-finger protein (Z36749).

286

5 AAG14454.1 AF283706 Tulipa gesneriana
DESCRIPTION: auxin-induced protein TGSAUR12. SAUR12. small auxin
upregulated RNA.

10 AAG14456.1 AF283708 Tulipa gesneriana
DESCRIPTION: auxin-induced protein TGSAUR22. SAUR22. small auxin
upregulated RNA.

15 AAG14455.1 AF283707 Tulipa gesneriana
DESCRIPTION: auxin-induced protein TGSAUR21. SAUR21. small auxin
upregulated RNA.

20 AAC08401.1 AF053564 Mesembryanthemum crystallinum
DESCRIPTION: auxin-induced protein. similar to auxin-induced proteins
from soybean.

290

25 AAB65498.1 U73856 Chlamydomonas reinhardtii
DESCRIPTION: carbonic anhydrase, alpha type. CAH3.

30 AAC49983.1 U40871 Chlamydomonas reinhardtii
DESCRIPTION: intracellular carbonic anhydrase, alpha type. CAH3.

35 AAF04292.2 AF190735 Dunaliella salina
DESCRIPTION: carbonic anhydrase. CA.

40 AAC49378.1 U53811 Dunaliella salina
DESCRIPTION: carbonic anhydrase. dca.

45 AAF22644.1 AF183939 Dunaliella salina
DESCRIPTION: duplicated carbonic anhydrase. DCA1. DCA; carbonic
anhydrase
gene family member; salt-inducible; intra-duplicated.

AAD51633.1 AF170173 *Acetabularia acetabulum*
DESCRIPTION: putative carbonic anhydrase 2. CA2. AaCA2.

5

AAD51634.1 AF170174 *Acetabularia acetabulum*
DESCRIPTION: putative carbonic anhydrase 1. CA1. AaCA1.

10 AAD51635.1 AF170175 *Acetabularia acetabulum*
DESCRIPTION: putative carbonic anhydrase 1. CA1. AaCA1.

15 BAA14232.1 D90206 *Chlamydomonas reinhardtii*
DESCRIPTION: carbonic anhydrase.

20 BAA28217.1 AB013804 *Chlorella sorokiniana*
DESCRIPTION: soluble carbonic anhydrase precursor. CAH1.

301

25 AAG03089.2 AC073405 *Oryza sativa*
DESCRIPTION: similar to an Arabidopsis putative P-type transporting
ATPase (AC010926).

30 BAA89544.1 AP001072 *Oryza sativa*
DESCRIPTION: Similar to chromaffin granule ATPase II homolog. (U75321).

35 BAA88191.1 AP000836 *Oryza sativa*
DESCRIPTION: Similar to chromaffin granule ATPase II homolog (U75321).

BAA90510.2 AP001111 *Oryza sativa*
DESCRIPTION: rice EST AU030811, similar to rice Ca²⁺-ATPase (U82966).

40 AAD11618.1 AF050496 *Lycopersicon esculentum*
DESCRIPTION: Ca²⁺-ATPase. LCA1B; alternative transcript.

45 AAA34138.1 M96324 *Lycopersicon esculentum*
DESCRIPTION: The calcium ATPase is a calcium ion pump. Ca²⁺-ATPase.
LCA1.

5 AAD11617.1 AF050495 *Lycopersicon esculentum*
DESCRIPTION: Ca²⁺-ATPase. LCA1A; alternative transcript.

AAF73985.1 AF096871 *Zea mays*
DESCRIPTION: calcium pump. calcium ATPase. cap1.

10 AAD31896.1 AF145478 *Mesembryanthemum crystallinum*
DESCRIPTION: calcium ATPase.

15 AAG28436.1 AF195029 *Glycine max*
DESCRIPTION: plasma membrane Ca²⁺-ATPase. SCA2.

20 CAA63790.1 X93592 *Dunaliella bioculata*
DESCRIPTION: P-type ATPase. cal. calcium pumping; CA1.

25 AAG28435.1 AF195028 *Glycine max*
DESCRIPTION: plasma membrane Ca²⁺-ATPase. SCA1.

CAA68234.1 X99972 *Brassica oleracea*
DESCRIPTION: calmodulin-stimulated calcium-ATPase.

30 AAB58910.1 U82966 *Oryza sativa*
DESCRIPTION: Ca²⁺-ATPase.

35 CAB69824.1 AJ271439 *Prunus persica*
DESCRIPTION: plasma membrane H⁺ ATPase. PPA1.

40 AAB60276.1 U09989 *Zea mays*
DESCRIPTION: H(+)-transporting ATPase. Mha1.

45 BAA01058.1 D10207 *Oryza sativa*
DESCRIPTION: H-ATPase. OSA1.

CAC29435.1 AJ310523 *Vicia faba*
DESCRIPTION: P-type H⁺-ATPase. vha4. predominantly expressed in flowers.

5 AAD20330.1 AF110268 *Oryza sativa*
DESCRIPTION: plasma membrane proton-ATPase gene OSA3.

10 AAA34098.1 M80490 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane H⁺ ATPase. pma3.

15 AAB84203.1 AF029257 *Kosteletzkyia virginica*
DESCRIPTION: plasma membrane H⁺-ATPase.

CAC28224.1 AJ286749 *Sesbania rostrata*
DESCRIPTION: p-type H⁺-ATPase. ha5.

20 AAD46188.1 AF156691 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane proton ATPase. pma9.

25 AAA34173.1 M60166 *Lycopersicon esculentum*
DESCRIPTION: H⁺-ATPase. LHA1.

30 AAA34094.1 M80489 *Nicotiana plumbaginifolia*
DESCRIPTION: plasma membrane H⁺ ATPase. pma1.

35 AAA34052.1 M27888 *Nicotiana plumbaginifolia*
DESCRIPTION: H⁺-translocating ATPase.

CAC28221.1 AJ286746 *Sesbania rostrata*
DESCRIPTION: p-type H⁺-ATPase. ha2.

40 CAA54045.1 X76535 *Solanum tuberosum*
DESCRIPTION: H(+)-transporting ATPase. PHA2.

45 BAA06629.1 D31843 *Oryza sativa*
DESCRIPTION: plasma membrane H⁺-ATPase. OSA2.

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- 785 -

CAA71513.1 Y10489 Glycine max
DESCRIPTION: putative cytochrome P450.

5

AAB94584.1 AF022157 Glycine max
DESCRIPTION: capable of catalyzing the metabolism of phenylurea
herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.

10

AAB61965.1 U48435 Solanum chacoense
DESCRIPTION: putative cytochrome P450.

15

AAB69644.1 AF000403 Lotus japonicus
DESCRIPTION: putative cytochrome P450. LjNP450.

20

BAB40324.1 AB037245 Asparagus officinalis
DESCRIPTION: cytochrome P450. ASPI-2.

25

AAD47832.1 AF166332 Nicotiana tabacum
DESCRIPTION: cytochrome P450.

30

AAB61964.1 U48434 Solanum chacoense
DESCRIPTION: putative cytochrome P450.

35

BAB40323.1 AB037244 Asparagus officinalis
DESCRIPTION: cytochrome P450. ASPI-1.

CAA71514.1 Y10490 Glycine max
DESCRIPTION: putative cytochrome P450.

40

AAB94588.1 AF022459 Glycine max
DESCRIPTION: CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.

45

AAF27282.1 AF122821 Capsicum annuum
DESCRIPTION: cytochrome P450. PepCYP.

CAA50313.1 X70982 Solanum melongena
DESCRIPTION: P450 hydroxylase. CYPEG3.

5 AAA19701.1 L24438 Thlaspi arvense
DESCRIPTION: cytochrome P450.

10 BAA12159.1 D83968 Glycine max
DESCRIPTION: Cytochrome P-450 (CYP93A1).

15 AAK38082.1 AF321858 Lolium rigidum
DESCRIPTION: putative cytochrome P450.

BAB40322.1 AB036772 Triticum aestivum
DESCRIPTION: cytochrome P450. N-1.

20 CAA71516.1 Y10492 Glycine max
DESCRIPTION: putative cytochrome P450.

25 CAA65580.1 X96784 Nicotiana tabacum
DESCRIPTION: cytochrome P450. hsr515.

30 AAK38083.1 AF321859 Lolium rigidum
DESCRIPTION: putative cytochrome P450.

35 AAK38084.1 AF321860 Lolium rigidum
DESCRIPTION: putative cytochrome P450.

CAA71517.1 Y10493 Glycine max
DESCRIPTION: putative cytochrome P450.

40 CAA72196.1 Y11368 Zea mays
DESCRIPTION: cytochrome p450. cyp71c4.

45 CAA57425.1 X81831 Zea mays

DESCRIPTION: cytochrome P-50. CYP71C4. family CYP71, subfamily CYP71C.

- 5 AAC39318.1 AF029858 Sorghum bicolor
DESCRIPTION: second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p-hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.
- 10 AAD56282.1 AF155332 Petunia x hybrida
DESCRIPTION: flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
- 15 CAB56503.1 AJ238612 Catharanthus roseus
DESCRIPTION: cytochrome P450.
- 20 AAK38087.1 AF321863 Lolium rigidum
DESCRIPTION: putative cytochrome P450.
- 25 CAA57421.1 X81827 Zea mays
DESCRIPTION: cytochrome P450. CYP71C1. family CYP71, subfamily CYP71C.
- 30 CAA57422.1 X81828 Zea mays
DESCRIPTION: cytochrome P450. CYP71C1. family CYP71, subfamily CYP71C.
- 35 BAB39252.1 AP002968 Oryza sativa
DESCRIPTION: putative cytochrome P450. P0416G11.1.
- 40 BAA13076.1 D86351 Glycine max
DESCRIPTION: cytochrome P-450 (CYP93A2).
- AAB94589.1 AF022460 Glycine max
DESCRIPTION: CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.
- 45 AAD38930.1 AF135485 Glycine max

DESCRIPTION: cytochrome P450 monooxygenase CYP93D1. CYP93E1.

CAA57423.1 X81829 Zea mays

5 DESCRIPTION: cytochrome P450. CYP71C2. family CYP71, subfamily CYP71C.

CAA72208.1 Y11404 Zea mays

10 DESCRIPTION: cytochrome p450. cyp71c2.

AAG44132.1 AF218296 Pisum sativum

15 DESCRIPTION: cytochrome P450. P450 isolog.

AAK38088.1 AF321864 Lolium rigidum

20 DESCRIPTION: putative cytochrome P450.

CAA64635.1 X95342 Nicotiana tabacum

DESCRIPTION: cytochrome P450. hsr515. hypersensitivity-related gene.

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AAC49826.1 U71604 Catharanthus roseus

DESCRIPTION: involved in the second to last step in vindoline biosynthesis. desacetoxyvindoline 4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase.

30

AAB97311.1 AF008597 Catharanthus roseus

35 DESCRIPTION: desacetoxyvindoline-4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase; involved in the second to last step in vindoline biosynthesis.

AAC49827.1 U71605 Catharanthus roseus

40 DESCRIPTION: involved in the second to last step in vindoline biosynthesis. desacetoxyvindoline 4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase.

BAA95828.1 AP002069 Oryza sativa

45 DESCRIPTION: ESTs D47168(S12332),D46350(S10967) correspond to a region of

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WASHINGTON, D. C.

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DESCRIPTION: UDP-glucose:anthocynin 5-O-glucosyltransferase. PF3R4.

BAB07962.1 AP002524 *Oryza sativa*

5 DESCRIPTION: putative anthocyanin 5-O-glucosyltransferase. P0406H10.16.
contains ESTs AU067881(C10481),AU067882(C10481).

AAK16178.1 AC079887 *Oryza sativa*

10 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.5.

BAA93039.1 AB033758 *Citrus unshiu*

15 DESCRIPTION: limonoid UDP-glucosyltransferase. LGTase.

AAK16172.1 AC079887 *Oryza sativa*

20 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.14.

BAA36422.1 AB013597 *Perilla frutescens*

25 DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue.
PF3R6.

BAB17182.1 AP002843 *Oryza sativa*

30 DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.19.

BAA12737.1 D85186 *Gentiana triflora*

35 DESCRIPTION: UDP-glucose:flavonoid-3-glucosyltransferase.

AAG25643.1 AF303396 *Phaseolus vulgaris*

40 DESCRIPTION: UDP-glucosyltransferase HRA25. putative; defense associated.

AAB48444.1 U82367 *Solanum tuberosum*

45 DESCRIPTION: UDP-glucose glucosyltransferase.

BAA19659.1 AB002818 *Perilla frutescens*

DESCRIPTION: flavonoid 3-O-glucosyltransferase. UDP glucose.

CAA54612.1 X77462 *Manihot esculenta*

DESCRIPTION: UTP-glucose glucosyltransferase. CGT5.

BAA89008.1 AB027454 *Petunia x hybrida*

5 DESCRIPTION: anthocyanidin 3-O-glucosyltransferase. PGT8.

AAK16175.1 AC079887 *Oryza sativa*

10 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.15.

BAA83484.1 AB031274 *Scutellaria baicalensis*

DESCRIPTION: UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

15 AAB36652.1 U32643 *Nicotiana tabacum*

DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS10a.

20 AAK28304.1 AF346432 *Nicotiana tabacum*

DESCRIPTION: phenylpropanoid:glucosyltransferase 2. togt2.
glucosyltransferase.

25 AAB36653.1 U32644 *Nicotiana tabacum*

DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS5a.

30 AAD04166.1 AF101972 *Phaseolus lunatus*

DESCRIPTION: catalyzes formation of O-glucosylzeatin from zeatin and
UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin
O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.

35 AAD21086.1 AF127218 *Forsythia x intermedia*

DESCRIPTION: adds glucose residue to position 3 of flavonoid compounds.
flavonoid 3-O-glucosyltransferase. UFGT.

40 CAA54611.1 X77461 *Manihot esculenta*

DESCRIPTION: UTP-glucose glucosyltransferase. CGT2.

45 AAK28303.1 AF346431 *Nicotiana tabacum*

DESCRIPTION: phenylpropanoid:glucosyltransferase 1. togt1.
glucosyltransferase.

5 CAA54609.1 X77459 Manihot esculenta
DESCRIPTION: UTP-glucose glucosyltransferase. CGT1.

10 CAA54613.1 X77463 Manihot esculenta
DESCRIPTION: UTP-glucose glucosyltransferase. CGT6.

15 BAB41026.1 AB047099 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.

BAB41024.1 AB047097 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.

20 BAB41022.1 AB047095 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.

25 BAB41017.1 AB047090 Vitis labrusca x Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1.
The
gene was derived from one of the parents V. labruscana cv. Ishiharawase.

30 BAB41020.1 AB047093 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.

35 CAA59450.1 X85138 Lycopersicon esculentum
DESCRIPTION: twi1. homologous to glucosyltransferases.

40 BAB41025.1 AB047098 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.

45 BAB41023.1 AB047096 Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.

BAB41018.1 AB047091 Vitis labrusca x Vitis vinifera
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2.
The
gene originated in one of the parents V. vinifera cv. Centennial.

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306

AAB06458.1 U64806 Brassica napus
DESCRIPTION: pathogenesis-related protein PR1. Ypr1.

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AAB01666.1 U21849 Brassica napus
DESCRIPTION: PR-1a. LSC94.

15

AAB09587.1 U70666 Brassica napus
DESCRIPTION: pathogenesis-related protein PR1. Ypr1.

20

CAA47374.1 X66942 Nicotiana tabacum
DESCRIPTION: prb-1b. PRB-1B.

25

AAK30143.1 AF348141 Capsicum annuum
DESCRIPTION: pathogenesis-related protein PR-1 precursor.

30

CAA36790.1 X52555 Nicotiana tabacum
DESCRIPTION: PR-1 protein (AA 1-184).

35

CAA35666.1 X17681 Nicotiana tabacum
DESCRIPTION: pathogenesis-related protein 1b (AA 1-168).

40

CAA31010.1 X12487 Nicotiana tabacum
DESCRIPTION: PR1c preprotein.

CAA29023.1 X05454 Nicotiana tabacum
DESCRIPTION: PR-1c protein.

45

CAA32228.1 X14065 Nicotiana tabacum
DESCRIPTION: PRP 1 precursor (AA -23 to 154).

BAA14220.1 D90196 *Nicotiana tabacum*
DESCRIPTION: PR1a protein precursor.

5

CAA31233.1 X12737 *Nicotiana tabacum*
DESCRIPTION: PR-1a protein (AA 1 - 168).

10 CAA29392.1 X05959 *Nicotiana tabacum*
DESCRIPTION: PR-1a precursor (AA -30 to 138).

15 CAA29660.1 X06361 *Nicotiana tabacum*
DESCRIPTION: PR1a precursor (AA -30 to -1).

20 CAA09671.1 AJ011520 *Lycopersicon esculentum*
DESCRIPTION: pathogenesis-related protein PR1a (P4). pr1a (P4).

25 AAA03615.1 M69247 *Lycopersicon esculentum*
DESCRIPTION: pathogenesis-related protein P4. P4.

CAA30017.1 X06930 *Nicotiana tabacum*
DESCRIPTION: PR-1a protein (AA 1 - 168).

30 CAA31008.1 X12485 *Nicotiana tabacum*
DESCRIPTION: PR1a preprotein.

35 CAA52893.1 X74939 *Hordeum vulgare*
DESCRIPTION: PR-1a pathogenesis related protein (Hv-1a).

40 CAB58263.1 AJ250136 *Solanum tuberosum*
DESCRIPTION: pathogenesis related protein PR-1. pr1-1.

45 AAB49685.1 U89895 *Oryza sativa*
DESCRIPTION: pathogenesis-related protein class 1. PR-1. induced by
pathogen attack in plants.

CAA27183.1 X03465 *Nicotiana tabacum*
DESCRIPTION: PR-1b precursor; (aa -30-138).

5 CAA35665.1 X17680 *Nicotiana tabacum*
DESCRIPTION: pathogenesis-related protein 1b (AA 1-168).

10 BAA14221.1 D90197 *Nicotiana tabacum*
DESCRIPTION: PR1b protein precursor.

15 CAA48672.1 X68738 *Lycopersicon esculentum*
DESCRIPTION: P1(p14) protein. pTE28.1.

20 CAA81229.1 Z26320 *Hordeum vulgare*
DESCRIPTION: pathogenesis-related protein. pathogenesis-related protein.

25 AAA03616.1 M69248 *Lycopersicon esculentum*
DESCRIPTION: pathogenesis-related protein P6. P6.

30 CAA70042.1 Y08804 *Lycopersicon esculentum*
DESCRIPTION: PR protein. PR1b1.

35 AAB05225.1 U49241 *Nicotiana glutinosa*
DESCRIPTION: pathogenesis-related protein-1.

40 CAA31009.1 X12486 *Nicotiana tabacum*
DESCRIPTION: PR1b preprotein.

45 AAC25629.1 U82200 *Zea mays*
DESCRIPTION: pathogenesis related protein-1. PR-1.

50 AAF78528.1 AF195237 *Pyrus pyrifolia*
DESCRIPTION: pathogenesis-related protein. PR-1b.

55 AAD33696.1 AF136636 *Glycine max*
DESCRIPTION: PR1a precursor. PR1a.

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AAAF78527.1 AF195236 *Pyrus pyrifolia*
DESCRIPTION: pathogenesis-related proteins. PR-1a.

CAC03571.1 AJ278436 *Oryza sativa*
DESCRIPTION: defence response. PR1a protein. Pr1a.

5 AAG44566.1 AF251277 *Oryza sativa* subsp. *japonica*
DESCRIPTION: acidic PR-1 type pathogenesis-related protein PR-1a. PR-1a.
induced by pathogen attack.

10 AAC06244.1 AF053343 *Capsicum annuum*
DESCRIPTION: PR-1 protein precursor. pathogen-induced PR1 protein.

15 CAA56174.1 X79778 *Medicago truncatula*
DESCRIPTION: PR-1.

307

20 AAF06347.1 AF195654 *Vitis vinifera*
DESCRIPTION: SCUTL2. thaumatin-like protein.

25 BAA28872.1 AB006009 *Pyrus pyrifolia*
DESCRIPTION: thaumatin-like protein precursor. PsTL1.

AAB38064.1 U32440 *Prunus avium*
DESCRIPTION: thaumatin-like protein precursor.

30 BAA95017.1 AB031870 *Cestrum elegans*
DESCRIPTION: thaumatin-like protein. CETLP.

35 BAA74546.2 AB000834 *Nicotiana tabacum*
DESCRIPTION: thaumatin-like protein SE39b.

40 AAC36740.1 AF090143 *Malus x domestica*
DESCRIPTION: thaumatin-like protein precursor Mdtl1. MDTL1.
pathogenesis-related.

45 CAC10270.1 AJ243427 *Malus x domestica*
DESCRIPTION: thaumatin-like protein. tl. allergen, pathogenesis-related.

- 5 AAB95118.1 U71244 *Brassica rapa*
DESCRIPTION: pathogenesis-related group 5 protein. BFTP. thaumatin-like protein; PR-5.
- 10 CAC09477.1 AL442113 *Oryza sativa*
DESCRIPTION: thaumatin-like protein. H0806H05.10.
- 15 CAB62167.1 AJ242828 *Castanea sativa*
DESCRIPTION: antifungal. thaumatin-like protein. tl1.
- 20 CAA06927.1 AJ006233 *Nicotiana tabacum*
DESCRIPTION: putative thaumatin-like protein precursor.
- 25 AAF06346.1 AF195653 *Vitis vinifera*
DESCRIPTION: SCUTL1. thaumatin-like protein.
- 30 AAB02259.1 U57787 *Avena sativa*
DESCRIPTION: permartin precursor. thaumatin-like protein.
- 35 AAD55090.1 AF178653 *Vitis riparia*
DESCRIPTION: thaumatin. osmotin; pathogenesis-related protein.
- 40 CAA10492.1 AJ131731 *Pseudotsuga menziesii*
DESCRIPTION: Thaumatin-like protein. 5A1A.16.
- 45 CAA09228.1 AJ010501 *Cicer arietinum*
DESCRIPTION: thaumatin-like protein PR-5b.
- BAA95165.1 AB029918 *Nicotiana tabacum*
DESCRIPTION: pistil transmitting tissue specific thaumatin (SE39b)-like protein. SE39b.
- AAF82264.1 AF227324 *Vitis vinifera*
DESCRIPTION: thaumatin-like protein.

CAB85636.1 AJ237998 *Vitis vinifera*
DESCRIPTION: putative thaumatin-like protein. T12.

5

AAB53368.1 U77657 *Oryza sativa*
DESCRIPTION: pathogenesis-related thaumatin-like protein.

10 AAB61590.1 AF003007 *Vitis vinifera*
DESCRIPTION: VVTL1. osmotin-like protein, PR-5 protein; thaumatin-like protein.

15 AAB53367.1 U77656 *Oryza sativa*
DESCRIPTION: pathogenesis-related thaumatin-like protein.

20 CAB85637.1 AJ237999 *Vitis vinifera*
DESCRIPTION: putative thaumatin-like protein. T11. alternative name grip 51.

308

25 BAA14143.1 D90115 *Armoracia rusticana*
DESCRIPTION: peroxidase isozyme.

30 BAA14144.1 D90116 *Armoracia rusticana*
DESCRIPTION: peroxidase isozyme.

35 BAA11853.1 D83225 *Populus nigra*
DESCRIPTION: peroxidase.

CAA66035.1 X97349 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.

40

CAA66036.1 X97350 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.

45 BAA11852.1 D83224 *Populus nigra*
DESCRIPTION: peroxidase.

- CAA66034.1 X97348 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.
5
- CAA66037.1 X97351 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: signal for ER. peroxidase.
10
- BAA07241.1 D38051 *Populus kitakamiensis*
DESCRIPTION: peroxidase. prxA4a.
15
- AAB47602.1 L07554 *Linum usitatissimum*
DESCRIPTION: peroxidase. FLXPER1.
20
- BAA06334.1 D30652 *Populus kitakamiensis*
DESCRIPTION: peroxidase.
25
- AAC98519.1 AF007211 *Glycine max*
DESCRIPTION: peroxidase precursor. GMIPER1. pathogen-induced.
30
- AAB97734.1 AF014502 *Glycine max*
DESCRIPTION: seed coat peroxidase precursor. Ep. H2O2 oxidoreductase;
class III plant peroxidase.
35
- BAA06335.1 D30653 *Populus kitakamiensis*
DESCRIPTION: peroxidase.
40
- AAD37427.1 AF149277 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 1 precursor. FBP1. secretory peroxidase.
45
- CAA62226.1 X90693 *Medicago sativa*.
DESCRIPTION: peroxidase1B. prx1B.
- CAA62227.1 X90694 *Medicago sativa*
DESCRIPTION: peroxidase1C. prx1C.

- 5 AAB41811.1 L36157 *Medicago sativa*
DESCRIPTION: peroxidase. pxdC. amino acid feature: conserved domains, aa
123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 ..
73.
- 10 CAA62225.1 X90692 *Medicago sativa*
DESCRIPTION: peroxidase1A. prx1A.
- 15 AAB41810.1 L36156 *Medicago sativa*
DESCRIPTION: peroxidase. pxdA. amino acid feature: conserved motifs, aa
181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
- 20 AAD37430.1 AF149280 *Phaseolus vulgaris*
DESCRIPTION: peroxidase 5 precursor. FBP5. secretory peroxidase.
- 25 CAB94692.1 AJ242742 *Ipomoea batatas*
DESCRIPTION: Removal of H₂O₂, oxidation of toxic reductants, defence
response toward wounding. peroxidase. pod.
- 30 AAA34108.1 J02979 *Nicotiana tabacum*
DESCRIPTION: lignin-forming peroxidase precursor (EC 1.11.1.7).
- 35 CAA40796.1 X57564 *Armoracia rusticana*
DESCRIPTION: peroxidase. peroxidase precursor.
- 40 BAA01877.1 D11102 *Populus kitakamiensis*
DESCRIPTION: peroxidase. prxA1.
- 45 BAA01992.1 D11396 *Nicotiana tabacum*
DESCRIPTION: 'peroxidase'.
- CAB67121.1 Y19023 *Lycopersicon esculentum*
DESCRIPTION: peroxidase. cevi-1.
- CAA50597.1 X71593 *Lycopersicon esculentum*

DESCRIPTION: peroxidase. CEVI-1.

- 5 AAD43561.1 AF155124 *Gossypium hirsutum*
DESCRIPTION: bacterial-induced peroxidase precursor. Perx_Goshiko.
- 10 BAA92500.1 AP001383 *Oryza sativa*
DESCRIPTION: ESTs D39300(R3292),AU030751(E60187) correspond to a
region
of the predicted gene. Similar to peroxidase ATP6a. (X98774).
- 15 AAF63027.1 AF244924 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx15 precursor.
type III peroxidase.
- 20 AAB02554.1 L37790 *Stylosanthes humilis*
DESCRIPTION: cationic peroxidase.
- 25 AAB06183.1 M37636 *Arachis hypogaea*
DESCRIPTION: cationic peroxidase. PNC1.
- 30 CAA59487.1 X85230 *Triticum aestivum*
DESCRIPTION: peroxidase. pox4.
- BAA94962.1 AB042103 *Asparagus officinalis*
DESCRIPTION: peroxidase. AspPOX1.
- 35 AAF63026.1 AF244923 *Spinacia oleracea*
DESCRIPTION: hydrogen peroxide catabolism. peroxidase prx14 precursor.
type III peroxidase.
- 40 CAB99487.1 AJ276227 *Hordeum vulgare*
DESCRIPTION: defence against plant pathogens. peroxidase. prx8.
- 45 CAA71492.1 Y10466 *Spinacia oleracea*
DESCRIPTION: peroxidase. prxr5.

[illegible]

AAA33121.1 M32742 Cucumis sativus
DESCRIPTION: peroxidase (CuPer2).

15

BAA92422.1 AP001366 *Oryza sativa*
 DESCRIPTION: ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to *A.thaliana* mRNA for peroxidase ATP18a. (X98804).

BAA92497.1 AP001383 *Oryza sativa*
DESCRIPTION: ESTs AU081576(R0541),AU032412(R4029) correspond to a
region
of the predicted gene. Similar to peroxidase ATP18a. (X98804).

CAA59485.1 X85228 Triticum aestivum
DESCRIPTION: peroxidase. POX2.

CAA76680.1 Y17192 Cucurbita pepo
DESCRIPTION: peroxidase. aprx. type III peroxidase.

35

BAA85400.1 AP000615 *Oryza sativa*
DESCRIPTION: similar to OsMlo-h1. (Z95353).

40 CAB06083.1 Z83834 *Hordeum vulgare*
DESCRIPTION: Mlo. Mlo.

CAA74909.1 Y14573 Hordeum vulgare
45 DESCRIPTION: Mlo protein. Mlo.

AAG46114.1 AC073166 *Oryza sativa*
DESCRIPTION: putative Mlo (pathogen resistance) protein.
OSJNBb0064P21.5.

5

CAA06487.1 AJ005341 *Linum usitatissimum*
DESCRIPTION: MLO. homolog.

10 310

AAC63113.1 AF000307 *Brassica napus*
DESCRIPTION: steroid sulfotransferase 3. BnST3.

15

AAC63112.1 AF000306 *Brassica napus*
DESCRIPTION: steroid sulfotransferase 2. BnST2.

20

AAC63111.1 AF000305 *Brassica napus*
DESCRIPTION: steroid sulfotransferase 1. BnST1.

25

AAA61638.1 U10275 *Flaveria bidentis*
DESCRIPTION: O-sulfation of position 3 of flavonols. flavonol
3-sulfotransferase.

30

AAA33342.2 M84135 *Flaveria chloraefolia*
DESCRIPTION: flavonol 3-sulfotransferase.

35

AAA87399.1 U10277 *Flaveria bidentis*
DESCRIPTION: transfers sulfate group into flavonol. sulfotransferase-like
flavonol.

40

AAA33343.1 M84136 *Flaveria chloraefolia*
DESCRIPTION: O-sulfation of position 4' of flavonol. flavonol
4'-sulfotransferase.

312

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AAD22970.1 AF124148 *Glycine max*
DESCRIPTION: trehalase 1 GMTRE1. expressed constitutively in many tissues
of soybean at a low level; similar to the *Arabidopsis thaliana* trehalase

precursor encoded by GenBank Accession Number AC002343.

5 AAG13442.1 AC051634 *Oryza sativa*
DESCRIPTION: putative trehalase. OSJNBb0018B10.19.

10 CAB50901.1 AJ238651 *Medicago truncatula*
DESCRIPTION: trehalase. TRE1 protein. tre1.
313

15 BAA19928.1 AB003491 *Oryza sativa*
DESCRIPTION: tryptophan synthase B. trpB.

20 AAA33491.1 M76685 *Zea mays*
DESCRIPTION: tryptophan synthase beta-subunit. TSB2.

AAB97526.1 AF042321 *Camptotheca acuminata*
DESCRIPTION: tryptophan synthase beta. TSB.

25 AAB97087.1 AF042320 *Camptotheca acuminata*
DESCRIPTION: tryptophan synthase beta subunit.

30 AAA33490.1 M76684 *Zea mays*
DESCRIPTION: tryptophan synthase beta-subunit. TSB1.

AAC25986.1 AF047024 *Chlamydomonas reinhardtii*
DESCRIPTION: tryptophan synthase beta. MAA7.

35 314

40 AAG42689.1 AF271384 *Zea mays*
DESCRIPTION: putative tryptophan synthase alpha. TSAlike.

CAA54131.1 X76713 *Zea mays*
DESCRIPTION: tryptophan synthase, alpha subunit. trpA.

45 AAG42688.1 AF271383 *Zea mays*

DESCRIPTION: putative tryptophan synthase alpha. TSAlike.

315

5 AAB97526.1 AF042321 *Camptotheca acuminata*
DESCRIPTION: tryptophan synthase beta. TSB.

10 AAB97087.1 AF042320 *Camptotheca acuminata*
DESCRIPTION: tryptophan synthase beta subunit.

15 BAA19928.1 AB003491 *Oryza sativa*
DESCRIPTION: tryptophan synthase B. trpB.

AAA33491.1 M76685 *Zea mays*
DESCRIPTION: tryptophan synthase beta-subunit. TSB2.

20 AAA33490.1 M76684 *Zea mays*
DESCRIPTION: tryptophan synthase beta-subunit. TSB1.

25 AAC25986.1 AF047024 *Chlamydomonas reinhardtii*
DESCRIPTION: tryptophan synthase beta. MAA7.

316

30 AAA33967.1 M76981 *Glycine max*
DESCRIPTION: vegetative storage protein. vspA.

35 BAA23563.1 D50094 *Phaseolus vulgaris*
DESCRIPTION: pod storage protein.

40 BAA19152.1 AB000585 *Phaseolus vulgaris*
DESCRIPTION: pod storage protein. PSP.

AAA34020.1 M20037 *Glycine max*
DESCRIPTION: vegetative storage protein.

45 AAA34022.1 M76980 *Glycine max*

DESCRIPTION: vegetative storage protein. vspB.

5 AAA34021.1 M20038 Glycine max
DESCRIPTION: vegetative storage protein.

321

10 BAA87043.1 AB035183 Ipomoea batatas
DESCRIPTION: N-hydroxycinnamoyl/benzoyltransferase. hcbt.

15 CAB06427.1 Z84383 Dianthus caryophyllus
DESCRIPTION: phytoalexin biosynthesis. anthranilate
N-hydroxycinnamoyl/benzoyltransferase.

20 CAB06429.1 Z84385 Dianthus caryophyllus
DESCRIPTION: phytoalexin biosynthesis. anthranilate
N-hydroxycinnamoyl/benzoyltransferase.

25 CAB06430.1 Z84386 Dianthus caryophyllus
DESCRIPTION: phytoalexin biosynthesis. anthranilate
N-hydroxycinnamoyl/benzoyltransferase.

30 CAB11466.1 Z98758 Dianthus caryophyllus
DESCRIPTION: carnation phytoalexin biosynthesis. anthranilate
N-hydroxycinnamoyl/benzoyltransferase.

35 CAB06538.1 Z84571 Dianthus caryophyllus
DESCRIPTION: phytoalexin biosynthesis. anthranilate
N-hydroxycinnamoyl/benzoyltransferase.

40 CAB06428.1 Z84384 Dianthus caryophyllus
DESCRIPTION: phytoalexin biosynthesis. anthranilate
N-hydroxycinnamoyl/benzoyltransferase.

323

45 BAB12694.1 AP002746 Oryza sativa
DESCRIPTION: putative zinc finger transcription factor. P0671B11.10.
contains ESTs AU098331(E31537),C91783(E31537).

DESCRIPTION: ESTs C96615(C10106),C26336(C12127),D21959(C10106) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* DNA chromosome 4, BAC clone T6K21; NAM (no apical meristem) - like protein (AL021889).

DESCRIPTION: ESTs C96615(C10106),C26336(C12127),D21959(C10106) correspond to a region of the predicted gene. Similar to NAM (AL021889).

DESCRIPTION: putative NAM protein. P0436E04.18. contains ESTs E10793(C19698),E10793(C99379).

DESCRIPTION: putative NAM protein. P0436E04.11. contains ESTs R4069(AU032425),R4069(AU082730).

DESCRIPTION: apical meristem formation. NAM.

DESCRIPTION: apical meristem formation. NAM.

DESCRIPTION: putative NAM (no apical meristem) protein.
OSJNBa0026O12.6.

DESCRIPTION: putative NAM (no apical meristem) protein. P0679C08.4.

DESCRIPTION: Similar to NAM like protein (AC005310).

CAB51836.1 AJ243961 Oryza sativa

5 DESCRIPTION: Putative Ser/Thr protein kinase. 11332.7.

BAB18292.1 AP002860 Oryza sativa

10 DESCRIPTION: putative receptor-like protein kinase. P0409B08.19.

BAB39873.1 AP002882 Oryza sativa

15 DESCRIPTION: putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

BAB21240.1 AP002953 Oryza sativa

20 DESCRIPTION: Putative protein kinase. P0426D06.20. contains ESTs
C22359(C11461),C22360(C11461).

AAA33000.1 M76647 Brassica oleracea

25 DESCRIPTION: receptor protein kinase. SKR6.

CAA74661.1 Y14285 Brassica oleracea

30 DESCRIPTION: SFR1. extracellular S domain: 8-1342; transmembrane domain:
1343-1411; intracellular kinase domain: 1412-2554.

CAB89179.1 AJ245479 Brassica napus subsp. napus

35 DESCRIPTION: ser /thr kinase. S-locus receptor kinase. srk.

AAA33008.1 M97667 Brassica napus

40 DESCRIPTION: serine/threonine kinase receptor.

AAA62232.1 U00443 Brassica napus

45 DESCRIPTION: S-receptor kinase. protein contains an immunoglobulin-like
domain.

BAA87853.1 AP000816 Oryza sativa

45 DESCRIPTION: EST AU030604(E51294) corresponds to a region of the
predicted gene. Similar to putative NAK-like Ser/Thr protein kinase.

(AF001308).

- CAA73134.1 Y12531 Brassica oleracea
5 DESCRIPTION: serine/threonine kinase. BRLK.
- BAA92836.1 AB032473 Brassica oleracea
10 DESCRIPTION: S18 S-locus receptor kinase. SRK18.
- AAK21965.1 AY028699 Brassica napus
DESCRIPTION: receptor protein kinase PERK1.
- 15 BAA23676.1 AB000970 Brassica rapa
DESCRIPTION: receptor kinase 1. BcRK1.
- 20 CAA73133.1 Y12530 Brassica oleracea
DESCRIPTION: serine /threonine kinase. ARLK.
- CAA67145.1 X98520 Brassica oleracea
25 DESCRIPTION: receptor-like kinase. SFR2.
- AAK00425.1 AC069324 Oryza sativa
30 DESCRIPTION: Putative protein kinase. OSJNBa0071K19.11.
- AAG03090.1 AC073405 Oryza sativa
DESCRIPTION: Similar to an Arabidopsis somatic embryogenesis
35 receptor-like kinase (AC007504).
- CAB41878.1 Y18259 Brassica oleracea
DESCRIPTION: SRK5 protein. SRK5. receptor-like kinase.
- 40 AAD21872.1 AF078082 Phaseolus vulgaris
DESCRIPTION: receptor-like protein kinase homolog RK20-1.
- 45 BAA21132.1 D88193 Brassica rapa
DESCRIPTION: S-receptor kinase. SRK9 (B.c).

- 5
BAA06285.1 D30049 Brassica rapa
DESCRIPTION: S-receptor kinase SRK9.
- 10
AAB61708.1 U93048 Daucus carota
DESCRIPTION: somatic embryogenesis receptor-like kinase. SERK.
- 15
BAB16871.1 AP002537 Oryza sativa
DESCRIPTION: putative protein kinase APK1A Arabidopsis thaliana.
P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
- 20
AAC23542.1 U20948 Ipomoea trifida
DESCRIPTION: receptor protein kinase. IRK1.
- 25
CAB41879.1 Y18260 Brassica oleracea
DESCRIPTION: SRK15 protein. SRK15. receptor-like kinase.
- 30
AAB93834.1 U82481 Zea mays
DESCRIPTION: KI domain interacting kinase 1. KIK1. receptor-like protein
kinase; serine/threonine protein kinase.
- 35
BAB39409.1 AP002901 Oryza sativa
DESCRIPTION: putative protein kinase. P0456F08.9. contains EST
C23560(R0290).
- 40
CAA74662.1 Y14286 Brassica oleracea
DESCRIPTION: SFR3. extracellular S domain: 123-1346; transmembrane
domain: 1347-1412; intracellular kinase domain: from 1413.
- 45
CAA79355.1 Z18921 Brassica oleracea
DESCRIPTION: S-receptor kinase-like protein.
- 50
BAA92837.1 AB032474 Brassica oleracea
DESCRIPTION: S60 S-locus receptor kinase. SRK60.

- AAK09327.1 AF320614 *Zea mays*
 DESCRIPTION: activates anthocyanin transcription. anthocyanin regulatory
 C1. cl. transcription factor.
- AAA82943.1 U39448 *Picea mariana*
 DESCRIPTION: MYB-like transcriptional factor MBF1. putative DNA binding
 region highly similar to the maize C1.
- AAK19618.1 AF336285 *Gossypium hirsutum*
 DESCRIPTION: GHMYB38. ghmyb38. similar to myb.
- CAA64614.1 X95296 *Lycopersicon esculentum*
 DESCRIPTION: transcription factor. THM27. myb-related.
- AAK19619.1 AF336286 *Gossypium hirsutum*
 DESCRIPTION: GHMYB9. ghmyb9. similar to myb.
- AAC04720.1 AF034134 *Gossypium hirsutum*
 DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-
 binding
 domain protein. Cmy-O. similar to MYB A encoded by GenBank Accession
 Number L04497.
- AAC04718.1 AF034132 *Gossypium hirsutum*
 DESCRIPTION: putative MYB-like transcription factor. MYB-like DNA-
 binding
 domain protein. Cmy-J. similar to MYB A encoded by GenBank Accession
 Number L04497.
-
- CAB93939.1 AJ238739 *Catharanthus roseus*
 DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
 protein. orca1.
- AAF76898.1 AF274033 *Atriplex hortensis*
 DESCRIPTION: apetala2 domain-containing protein.

AAG43545.1 AF211527 *Nicotiana tabacum*
 DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to
 5 EREBP transcription factors.

CAC12822.1 AJ299252 *Nicotiana tabacum*
 DESCRIPTION: AP2 domain-containing transcription factor. ap2.
 10

BAA78738.1 AB023482 *Oryza sativa*
 DESCRIPTION: EST AU055776(S20048) corresponds to a region of the
 predicted gene.; Similar to *Arabidopsis thaliana* AP2 domain containing
 15 protein RAP2.10 mRNA, partial cds.(AF003103).

AAC14323.1 AF058827 *Nicotiana tabacum*
 DESCRIPTION: TSI1. Tsi1. contains putative AP2 DNA-binding domain;
 20 similar to Pti6.

BAA97122.1 AB016264 *Nicotiana sylvestris*
 DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for
 25 basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive
 element binding factor. nserf2.

CAB93940.1 AJ238740 *Catharanthus roseus*
 DESCRIPTION: putative transcription factor. AP2-domain DNA-binding
 30 protein. orca2.

BAA76734.1 AB024575 *Nicotiana tabacum*
 DESCRIPTION: ethylene responsive element binding factor.
 35

CAB96900.1 AJ251250 *Catharanthus roseus*
 DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.
 40

CAB96899.1 AJ251249 *Catharanthus roseus*
 DESCRIPTION: transcription factor. AP2-domain DNA-binding protein. orca3.
 45

AAF63205.1 AF245119 *Mesembryanthemum crystallinum*

DESCRIPTION: AP2-related transcription factor. CDBP. stress induced transcription factor.

- 5 AAC24587.1 AF071893 *Prunus armeniaca*
DESCRIPTION: AP2 domain containing protein. AP2DCP.
- 10 BAA94514.2 AP001800 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome 4, BAC clone F9D16; putative Ap2 domain protein (AL035394).
- 15 BAA97124.1 AB016266 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
- 20 BAA07321.1 D38123 *Nicotiana tabacum*
DESCRIPTION: ERF1. ethylene-responsive transcription factor.
- 25 BAB16083.1 AB036883 *Oryza sativa*
DESCRIPTION: transcriptional repressor. osERF3. osERF3. ERF protein family ERF3 associated repression domain.
- 30 BAB03248.1 AB037183 *Oryza sativa*
DESCRIPTION: ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
- 35 BAA97123.1 AB016265 *Nicotiana sylvestris*
DESCRIPTION: ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
- 40 AAF23899.1 AF193803 *Oryza sativa*
DESCRIPTION: transcription factor EREBP1. EREBP/AP2-like transcription factor.
- 45 AAK31271.1 AC079890 *Oryza sativa*
DESCRIPTION: putative transcriptional factor. OSJNBb0089A17.22.

AAC62619.1 AF057373 *Nicotiana tabacum*
DESCRIPTION: transcription factor. ethylene response element binding
5 protein 1. EREBP1.

AAG43548.1 AF211530 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar
10 to EREBP transcription factors.

BAA90812.1 AP001168 *Oryza sativa*
DESCRIPTION: Similar to mRNA for DREB1A (AB007787).
15

AAG43549.1 AF211531 *Nicotiana tabacum*
DESCRIPTION: Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar
20 to EREBP transcription factors.

BAA99376.1 AP002526 *Oryza sativa*
DESCRIPTION: ESTs AU093391(E60370),AU091593(C60458),
AU093392(E60370)
25 correspond to a region of the predicted gene. Similar to Arabidopsis
thaliana BAC F21J9; AP2 domain protein. (AC000103).

AAK01089.1 AF298231 *Hordeum vulgare*
30 DESCRIPTION: CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE
binding factor.

AAG59618.1 AF239616 *Hordeum vulgare*
35 DESCRIPTION: CRT/DRE-binding factor. CBF.

AAG59619.1 AF243384 *Oryza sativa*
DESCRIPTION: CRT/DRE binding factor. CBF. DREB.
40

AAK01088.1 AF298230 *Hordeum vulgare*
DESCRIPTION: CBF1-like protein BCBF1. BCBF1. AP2 domain protein;
putative
45 DRE binding factor.

AAC49567.1 U41466 Zea mays

DESCRIPTION: Glossy15. Glossy15. AP2 DNA-binding domain protein; similar

- 5 to the Arabidopsis floral homeotic gene APETALA2; maize AP2-domain regulator of leaf epidermal traits; homeotic regulator of leaf epidermal cell identity; allele: W64A; putative transcription factor.

330

10

AAC67571.1 AF060884 Brassica napus

DESCRIPTION: desiccation protein. Cdes. induced by dehydration.

- 15 AAA61564.1 U08108 Glycine max

DESCRIPTION: putative desiccation protectant protein, homolog of Lea14, GenBank Accession Number M88321.

- 20 AAA18543.1 M88322 Gossypium hirsutum

DESCRIPTION: probable desiccation protectant. Group 4 late embryogenesis-abundant protein. Lea14-A. This CDS is colinear and 66% identical with that in cDNA clone pcC27-45 from Craterostigma plantagineum desiccated leaves (Piatkowski et al., 1990, Plant Physiol. 94: 1682-1688).; putative.

25

AAA18542.1 M88321 Gossypium hirsutum

DESCRIPTION: probable desiccation protectant. Group 4 late embryogenesis-abundant protein. Lea14-A. putative.

30

AAD25354.1 AF115314 Glycine max

DESCRIPTION: possible desiccation protectant. seed maturation protein PM22. PM22. similar to desiccation protectant protein encoded by GenBank Accession Number U08108; late embryogenesis abundant protein; LEA protein.

35

AAF64451.1 AF239929 Euphorbia esula

DESCRIPTION: late-embryogenesis abundant protein. similar to desiccation protectant protein and late-embryogenesis abundant protein LEA14.

40

AAB96796.1 U77719 Lycopersicon esculentum

DESCRIPTION: ethylene-responsive late embryogenesis-like protein. ER5. LEA-like protein; drought-inducible; ABA-inducible; putative desiccation

45

protectant protein; similar to cotton Le14A product encoded by GenBank
Accession Number M88321.

345

5

AAAF61647.1 AF190634 *Nicotiana tabacum*
DESCRIPTION: UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

10

BAA36423.1 AB013598 *Verbena x hybrida*
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

15

BAA89009.1 AB027455 *Petunia x hybrida*
DESCRIPTION: anthocyanin 5-O-glucosyltransferase. PH1.

20

BAA36421.1 AB013596 *Perilla frutescens*
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.

25

BAA93039.1 AB033758 *Citrus unshiu*
DESCRIPTION: limonoid UDP-glucosyltransferase. LGTase.

BAA36422.1 AB013597 *Perilla frutescens*
DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue.
PF3R6.

30

AAAF98390.1 AF287143 *Brassica napus*
DESCRIPTION: catalyzes the transfer of glucose from UDP-glucose to
sinapate and some other hydroxycinnamates (4-coumarate, caffeate,
ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

35

BAB07962.1 AP002524 *Oryza sativa*
DESCRIPTION: putative anthocyanin 5-O-glucosyltransferase. P0406H10.16.
contains ESTs AU067881(C10481),AU067882(C10481).

40

AAAF17077.1 AF199453 *Sorghum bicolor*
DESCRIPTION: UDP-glucose glucosyltransferase.
UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.

45

AAK16172.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.14.

5 AAB36653.1 U32644 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS5a.

10 AAK28303.1 AF346431 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 1. togt1.
glucosyltransferase.

15 BAA83484.1 AB031274 *Scutellaria baicalensis*
DESCRIPTION: UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

20 AAK16181.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.16.

25 AAD21086.1 AF127218 *Forsythia x intermedia*
DESCRIPTION: adds glucose residue to position 3 of flavonoid compounds.
flavonoid 3-O-glucosyltransferase. UFGT.

30 AAB36652.1 U32643 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS10a.

35 AAK28304.1 AF346432 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 2. togt2.
glucosyltransferase.

40 CAA59450.1 X85138 *Lycopersicon esculentum*
DESCRIPTION: twi1. homologous to glucosyltransferases.

45 AAK16178.1 AC079887 *Oryza sativa*
DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.5.

AAK16175.1 AC079887 *Oryza sativa*

DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.15.

AAK16180.1 AC079887 *Oryza sativa*

5 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.21.

CAB56231.1 Y18871 *Dorotheanthus bellidiformis*

10 DESCRIPTION: betanidin-5-O-glucosyltransferase.

BAA12737.1 D85186 *Gentiana triflora*

DESCRIPTION: UDP-glucose:flavonoid-3-glucosyltransferase.

15

AAG25643.1 AF303396 *Phaseolus vulgaris*

DESCRIPTION: UDP-glucosyltransferase HRA25. putative; defense associated.

20

BAB41017.1 AB047090 *Vitis labrusca* x *Vitis vinifera*

DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1.
The
gene was derived from one of the parents *V. labruscana* cv. Ishiharawase.

25

AAB81683.1 AF000372 *Vitis vinifera*

DESCRIPTION: UDP glucose:flavonoid 3-o-glucosyltransferase.

30

BAB41020.1 AB047093 *Vitis vinifera*

DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.

35

BAB41022.1 AB047095 *Vitis vinifera*

DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.

BAB41019.1 AB047092 *Vitis vinifera*

40 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.

AAB81682.1 AF000371 *Vitis vinifera*

DESCRIPTION: UDP glucose:flavonoid 3-o-glucosyltransferase.

45

BAB41025.1 AB047098 *Vitis vinifera*

DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.

BAB41023.1 AB047096 *Vitis vinifera*

5 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.

BAB41021.1 AB047094 *Vitis vinifera*

10 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.

BAB41026.1 AB047099 *Vitis vinifera*

15 DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.

BAB41024.1 AB047097 *Vitis vinifera*

DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.

20 BAB41018.1 AB047091 *Vitis labrusca* x *Vitis vinifera*

DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2.
The
gene originated in one of the parents *V. vinifera* cv. Centennial.

25 BAB17182.1 AP002843 *Oryza sativa*

DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.19.

30 BAA19659.1 AB002818 *Perilla frutescens*

DESCRIPTION: flavonoid 3-O-glucosyltransferase. UDP glucose.

BAA89008.1 AB027454 *Petunia x hybrida*

35 DESCRIPTION: anthocyanidin 3-O-glucosyltransferase. PGT8.

BAB17176.1 AP002843 *Oryza sativa*

40 DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.13.

AAB86473.1 AF028237 *Ipomoea purpurea*

DESCRIPTION: UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.

45 350

CAA44216.1 X62343 *Nicotiana tabacum*
DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD14.

5 BAA03099.1 D13991 *Aralia cordata*
DESCRIPTION: cinnamyl alcohol dehydrogenase. cadac1.

10 CAA79622.1 Z19568 *Populus deltoides*
DESCRIPTION: lignin biosynthesis. cinnamyl alcohol dehydrogenase.

15 CAC07423.1 AJ295837 *Populus balsamifera* subsp. *trichocarpa*
DESCRIPTION: lignin monomer biosynthesis. cinnamyl alcohol dehydrogenase.
cad.

20 AAF43140.1 AF217957 *Populus tremuloides*
DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.

25 CAA44217.1 X62344 *Nicotiana tabacum*
DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD19.

CAA79625.1 Z19573 *Medicago sativa*
DESCRIPTION: lignin biosynthesis. cinnamyl alcohol dehydrogenase.

30 AAC35845.1 AF083332 *Medicago sativa*
DESCRIPTION: cinnamyl-alcohol dehydrogenase. MsaCad2.

35 AAC07987.1 AF038561 *Eucalyptus globulus*
DESCRIPTION: catalyses the reduction of cinnamaldehydes to the
corresponding cinnamyl alcohols as the last step in the production of
lignin monomers. cinnamyl alcohol dehydrogenase. CAD.

40 CAA46585.1 X65631 *Eucalyptus gunnii*
DESCRIPTION: cinnamyl-alcohol dehydrogenase. cad.

45 AAG15553.1 AF294793 *Eucalyptus saligna*
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad. CAD.

CAA53211.1 X75480 Eucalyptus gunnii
DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD.

5

AAB70908.1 AF010290 Lolium perenne
DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.

10 CAA74070.1 Y13733 Zea mays
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad.

CAA06687.1 AJ005702 Zea mays
15 DESCRIPTION: cinnamyl alcohol dehydrogenase. cad.

CAA13177.1 AJ231135 Saccharum officinarum
20 DESCRIPTION: lignin biosynthesis. cinnamyl alcohol dehydrogenase. cad.

BAA19487.1 D86590 Zinnia elegans
DESCRIPTION: cinnamyl alcohol dehydrogenase. ZCAD1.

25

CAA51226.1 X72675 Picea abies
DESCRIPTION: cinnamyl-alcohol dehydrogenase.

30 CAA05097.1 AJ001926 Picea abies
DESCRIPTION: cinnamyl alcohol dehydrogenase. cad8.

CAA05096.1 AJ001925 Picea abies
35 DESCRIPTION: cinnamyl alcohol dehydrogenase. cad7.

CAA05095.1 AJ001924 Picea abies
40 DESCRIPTION: cinnamyl alcohol dehydrogenase. cad2.

AAB38774.1 U62394 Pinus radiata
DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.

45

AAC31166.1 AF060491 Pinus radiata

DESCRIPTION: cinnamyl alcohol dehydrogenase. CAD.

CAA86073.1 Z37992 Pinus taeda
5 DESCRIPTION: cinnamyl alcohol dehydrogenase.

CAA86072.1 Z37991 Pinus taeda
10 DESCRIPTION: cinnamyl alcohol dehydrogenase.

BAA04046.1 D16624 Eucalyptus botryoides
DESCRIPTION: cinnamyl alcohol dehydrogenase. Cad1:Eb:1.

15 AAD10327.1 U63534 Fragaria x ananassa
DESCRIPTION: catalyzes the reduction of cinnamylaldehydes leading to
monolignols. cinnamyl alcohol dehydrogenase. CAD. involved with lignin
biosynthesis.

20 AAK28509.1 AF320110 Fragaria x ananassa
DESCRIPTION: cinnamyl alcohol dehydrogenase.

25 AAB38503.1 U79770 Mesembryanthemum crystallinum
DESCRIPTION: cinnamyl-alcohol dehydrogenase Eli3.

30 AAC35846.1 AF083333 Medicago sativa
DESCRIPTION: cinnamyl-alcohol dehydrogenase. MsaCad1.

35 AAA74882.1 L36823 Stylosanthes humilis
DESCRIPTION: cinnamyl-alcohol dehydrogenase. CAD1.

AAF23409.1 AF207552 Brassica napus
40 DESCRIPTION: cinnamyl alcohol dehydrogenase. CADa-1.

AAC15467.1 U24561 Apium graveolens
DESCRIPTION: converts mannitol to mannose. mannitol dehydrogenase. Mtd.
1-oxidoreductase; induced with sodium salicylate; similar to the plant
45 defense gene ELI3 in Arabidopsis thaliana, PIR Accession Number S28044; EC
number unassigned; MTD.

DESCRIPTION: caleosin. 27 kDa calcium-binding protein.

CAA61981.1 X89891 *Oryza sativa*

5 DESCRIPTION: EFA27 for EF hand, abscisic acid, 27kD. efa27.

CAB71337.1 AJ250283 *Hordeum vulgare*

10 DESCRIPTION: putative calcium binding EF-hand protein. bci-4.

CAB42585.1 AJ238627 *Chlorella protothecoides*

DESCRIPTION: putative Ca⁺⁺ binding protein. dee112.

15 353

AAF60316.1 AF236108 *Glycine max*

20 DESCRIPTION: putative purple acid phosphatase precursor. PAP. type 5 acid phosphatase.

AAF60315.1 AF236107 *Ipomoea batatas*

25 DESCRIPTION: putative purple acid phosphatase precursor. PAP. type 5 acid phosphatase.

AAF60317.1 AF236109 *Phaseolus vulgaris*

30 DESCRIPTION: putative purple acid phosphatase precursor. PAP. type 5 acid phosphatase.

359

CAA55039.1 X78203 *Hyoscyamus muticus*

35 DESCRIPTION: glutathione transferase.

AAB65163.1 AF002692 *Solanum commersonii*

40 DESCRIPTION: glutathione S-transferase, class-phi. GST1. low temperature induced.

CAA96431.1 Z71749 *Nicotiana plumbaginifolia*

DESCRIPTION: glutathione S-transferase.

45

BAA01394.1 D10524 *Nicotiana tabacum*

DESCRIPTION: glutathione S-transferase. parB.

5 AAA33930.1 M84968 *Silene vulgaris*
DESCRIPTION: glutathione-S-transferase.

10 AAA33931.1 M84969 *Silene vulgaris*
DESCRIPTION: glutathione-S-transferase.

AAF65767.1 AF242309 *Euphorbia esula*
DESCRIPTION: glutathione S-transferase. putative auxin-binding GST.

15 AAF61392.1 AF133894 *Persea americana*
DESCRIPTION: glutathione S-transferase. GTH.

20 CAB38119.1 AJ010296 *Zea mays*
DESCRIPTION: Glutathione transferase III(b). gst3b.

25 CAB38118.1 AJ010295 *Zea mays*
DESCRIPTION: Glutathione transferase III(a). gst3a.

30 BAB39935.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.17.

AAG34811.1 AF243376 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 21.

35 BAB39941.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.23.

40 CAA09190.1 AJ010451 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2a.

45 CAA09192.1 AJ010453 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2c.

CAA09193.1 AJ010454 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2d.

5

AAG34814.1 AF243379 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 24.

10 CAA09191.1 AJ010452 *Alopecurus myosuroides*
DESCRIPTION: glutathione transferase. GST2b.

15 BAB39939.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.21.

20 AAG32476.1 AF309383 *Oryza sativa* subsp. *japonica*
DESCRIPTION: putative glutathione S-transferase OsGSTF4.

AAG34812.1 AF243377 *Glycine max*
DESCRIPTION: glutathione S-transferase GST 22.

25

BAB39929.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione transferase. P0493G01.7.

30 CAA39487.1 X56012 *Triticum aestivum*
DESCRIPTION: glutathione transferase. gstA1.

35 AAD56395.1 AF184059 *Triticum aestivum*
DESCRIPTION: glutathione S-transferase. GST1.

40 BAB39940.1 AP002914 *Oryza sativa*
DESCRIPTION: putative glutathione S-transferase. P0493G01.22.

45 CAA68993.1 Y07721 *Petunia x hybrida*
DESCRIPTION: conjugates glutathione to anthocyanin to facilitate
transport to the vacuole. glutathione S-transferase. an9 locus.

AAA33469.1 M16902 Zea mays
DESCRIPTION: glutathione S-transferase I.

5 AAG32477.1 AF309384 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTF3.

10 AAA33470.1 M16901 Zea mays
DESCRIPTION: glutathione S-transferase I.

15 AAA20585.1 U12679 Zea mays
DESCRIPTION: glutathione S-transferase IV. GSTIV.

20 CAA56047.1 X79515 Zea mays
DESCRIPTION: glutathione transferase. GST27.

CAA39480.1 X56004 Triticum aestivum
DESCRIPTION: glutathione transferase. gstA2.

25 AAC64007.1 AF062403 Oryza sativa
DESCRIPTION: glutathione S-transferase II.

30 BAB39927.1 AP002914 Oryza sativa
DESCRIPTION: putative glutathione S-transferase. P0493G01.1. contains
ESTs AU031696(R0596),C97559(C60386),C28218(C60386), D28287(R0596).

35 AAG32475.1 AF309382 Oryza sativa subsp. japonica
DESCRIPTION: putative glutathione S-transferase OsGSTF5.

40 AAG34823.1 AF244680 Zea mays
DESCRIPTION: glutathione S-transferase GST 15.

AAG34817.1 AF244674 Zea mays
DESCRIPTION: glutathione S-transferase GST 9.

45 CAA05354.1 AJ002380 Oryza sativa

DESCRIPTION: glutathione S-transferase. Rgst I.

5 AAG34820.1 AF244677 Zea mays
DESCRIPTION: glutathione S-transferase GST 11.

10 AAG34821.1 AF244678 Zea mays
DESCRIPTION: glutathione S-transferase GST 13.

CAB66333.1 AJ279691 Betula pendula
DESCRIPTION: glutathione-S-transferase. gst.

15 AAG34818.1 AF244675 Zea mays
DESCRIPTION: glutathione S-transferase GST 10.

20 AAG34816.1 AF244673 Zea mays
DESCRIPTION: glutathione S-transferase GST 8.

25 AAG34822.1 AF244679 Zea mays
DESCRIPTION: glutathione S-transferase GST 14.

30 CAA05355.1 AJ002381 Oryza sativa
DESCRIPTION: glutathione S-transferase. Rgst II.
360

35 AAA33710.1 L16977 Petunia x hybrida
DESCRIPTION: glutamate decarboxylase. gad.

AAA33709.1 L16797 Petunia x hybrida
DESCRIPTION: glutamate decarboxylase. gad.

40 AAC24195.1 AF020425 Nicotiana tabacum
DESCRIPTION: calmodulin binding protein. glutamate decarboxylase isozyme
1. NtGAD1. calcium-calmodulin-dependent enzyme.

45 AAB40608.1 U54774 Nicotiana tabacum

098372706201

DESCRIPTION: glutamate decarboxylase. NtGAD1. calmodulin regulated enzyme; calmodulin-binding protein.

- 5 AAK18620.1 AF352732 *Nicotiana tabacum*
DESCRIPTION: converts glutamate to gamma-aminobutyric acid. glutamate decarboxylase isozyme 3. GAD; GAD3; NtGAD3; calcium/calmodulin-dependent enzyme.
- 10
- AAC39483.1 AF020424 *Nicotiana tabacum*
DESCRIPTION: glutamate decarboxylase isozyme 2. NtGAD2. calcium-calmodulin-dependent enzyme.
- 15
- BAB32870.1 AB056062 *Oryza sativa*
DESCRIPTION: glutamate decarboxylase. GAD.
- 20
- BAB32868.1 AB056060 *Oryza sativa*
DESCRIPTION: glutamate decarboxylase. GAD.
- 25
- BAB32869.1 AB056061 *Oryza sativa*
DESCRIPTION: glutamate decarboxylase. GAD.
- 30
- BAB32871.1 AB056063 *Oryza sativa*
DESCRIPTION: glutamate decarboxylase. GAD.
- 35
- CAA56812.1 X80840 *Lycopersicon esculentum*
DESCRIPTION: homology to pyroxidal-5'-phosphate-dependant glutamate decarboxylases; putative start codon.
- 40
- CAA50719.1 X71900 *Lycopersicon esculentum*
DESCRIPTION: histidine decarboxylase. hdc. pyridoxal 5'-phosphate dependant.
- 362
-
- 45 AAG13467.1 AC026758 *Oryza sativa*
DESCRIPTION: putative proline oxidase. OSJNBa0015J15.31.

AAD48490.1 AF171226 Brassica napus
DESCRIPTION: proline dehydrogenase. pdh.

5 363

AAA33967.1 M76981 Glycine max
DESCRIPTION: vegetative storage protein. vspA.

10

AAA34022.1 M76980 Glycine max
DESCRIPTION: vegetative storage protein. vspB.

15 AAA34021.1 M20038 Glycine max
DESCRIPTION: vegetative storage protein.

20 BAA23563.1 D50094 Phaseolus vulgaris
DESCRIPTION: pod storage protein.

25 BAA19152.1 AB000585 Phaseolus vulgaris
DESCRIPTION: pod storage protein. PSP.

AAA34020.1 M20037 Glycine max
DESCRIPTION: vegetative storage protein.

30 364

AAB86939.1 AF030387 Oryza sativa
DESCRIPTION: NOI protein.

35

AAC03022.1 AF045033 Zea mays
DESCRIPTION: nitrate-induced NOI protein.

40 AAB86937.1 AF030385 Zea mays
DESCRIPTION: nitrate-induced NOI protein.

366

45 AAF75824.1 AF101788 Pinus taeda
DESCRIPTION: phytocyanin homolog.

5

DESCRIPTION: putative oxygen activation and/or lignin formation.

Plantacyanins; member of the subfamily of Stellacyanins; similar to Rhus

AC004669; similar to F9D12.16 encoded by GenBank Accession Number

DESCRIPTION: plantacyanin. naturally occurring cupredoxin with a Val residue in the position of the axial ligand Met; member of the

blue copper proteins known as **phyto**cyanins.

35

DESCRIPTION: Ca²⁺-ATPase. LCA1A; alternative transcript.

LCA1.

- 834 -

AAD11618.1 AF050496 *Lycopersicon esculentum*
DESCRIPTION: Ca²⁺-ATPase. LCA1B; alternative transcript.

5 CAA63790.1 X93592 *Dunaliella bioculata*
DESCRIPTION: P-type ATPase. cal. calcium pumping; CA1.

10 AAF73985.1 AF096871 *Zea mays*
DESCRIPTION: calcium pump. calcium ATPase. cap1.

15 AAB58910.1 U82966 *Oryza sativa*
DESCRIPTION: Ca²⁺-ATPase.

AAG28435.1 AF195028 *Glycine max*
DESCRIPTION: plasma membrane Ca²⁺-ATPase. SCA1.

20 AAG28436.1 AF195029 *Glycine max*
DESCRIPTION: plasma membrane Ca²⁺-ATPase. SCA2.

25 AAB49042.1 U54690 *Dunaliella acidophila*
DESCRIPTION: plasma membrane proton ATPase. dha1. DaDHA1; proton pump.

30 AAB35314.2 S79323 *Vicia faba*
DESCRIPTION: plasma membrane H(+)-ATPase precursor. plasma membrane H(+)-ATPase. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication.

35 CAB85495.1 AJ132892 *Medicago truncatula*
DESCRIPTION: proton pump. H⁺-ATPase. ha1.

40 CAB85494.1 AJ132891 *Medicago truncatula*
DESCRIPTION: proton pump. H⁺-ATPase. ha1.

45 AAB17186.1 U72148 *Lycopersicon esculentum*
DESCRIPTION: plasma membrane H⁺-ATPase. LHA4. plasma membrane proton

pumping ATPase.

- 5 CAC29436.1 AJ310524 *Vicia faba*
DESCRIPTION: P-type H⁺-ATPase. ha5. predominantly expressed in guard cells and flowers.
- 10 AAB41898.1 U84891 *Mesembryanthemum crystallinum*
DESCRIPTION: plasma membrane proton pump. H⁺-transporting ATPase. PMA.
- 15 CAC29435.1 AJ310523 *Vicia faba*
DESCRIPTION: P-type H⁺-ATPase. vha4. predominantly expressed in flowers.
- 20 AAF98344.1 AF275745 *Lycopersicon esculentum*
DESCRIPTION: plasma membrane H⁺-ATPase. LHA2. P-type ion pump.
369
- 25 BAB17726.1 AB050900 *Raphanus sativus*
DESCRIPTION: asparagine synthetase. Asn1.
- 30 CAA59138.1 X84448 *Brassica oleracea*
DESCRIPTION: asparagine synthase (glutamine-hydrolysing).
- 35 AAC16325.1 AF061740 *Elaeagnus umbellata*
DESCRIPTION: asparagine synthetase. AS.
- 40 CAA08913.1 AJ009952 *Phaseolus vulgaris*
DESCRIPTION: asparagine synthesis. asparagine synthetase type II. as2.
- 45 AAF02775.1 AF190728 *Helianthus annuus*
DESCRIPTION: asparagine synthetase. HAS1.
- AAC49613.1 U77678 *Glycine max*
DESCRIPTION: catalyzes the ATP-dependent transfer of the amide group of glutamine to aspartate producing asparagine and glutamate. asparagine synthetase 2. AS2.

5 AAB81011.1 U89923 *Medicago sativa*
 DESCRIPTION: asparagine synthetase.

10 AAC09952.1 U55874 *Glycine max*
 DESCRIPTION: asparagine synthetase.

15 AAB48058.1 L40327 *Medicago sativa*
 DESCRIPTION: asparagine synthetase.

20 CAA61589.1 X89409 *Lotus japonicus*
 DESCRIPTION: asparagine synthase (glutamine-hydrolysing). AS.

25 CAA67889.1 X99552 *Asparagus officinalis*
 DESCRIPTION: asparagine synthetase.

30 AAF74755.1 AF263432 *Helianthus annuus*
 DESCRIPTION: asparagine synthetase. HAS1.1.

35 AAD05035.1 AF014057 *Triphysaria versicolor*
 DESCRIPTION: asparagine synthetase. AS. glutamine-hydrolyzing.

40 AAD05034.1 AF014056 *Triphysaria versicolor*
 DESCRIPTION: asparagine synthetase. AS. glutamine-hydrolyzing.

45 AAD05033.1 AF014055 *Triphysaria versicolor*
 DESCRIPTION: asparagine synthetase. AS. glutamine-hydrolyzing.

50 CAA96526.1 Z72354 *Vicia faba*
 DESCRIPTION: synthesis of asparagine from aspartate and glutamine.
 asparagine synthetase. VfAS1.

55 CAA48141.1 X67958 *Asparagus officinalis*
 DESCRIPTION: asparagine synthase (glutamine-hydrolysing).

CAA61590.1 X89410 *Lotus japonicus*
DESCRIPTION: asparagine synthase (glutamine-hydrolysing). AS.

5

CAA36429.1 X52179 *Pisum sativum*
DESCRIPTION: asparagine synthase (glutamine-hydrolysing).

10 BAA96252.1 AB035248 *Astragalus sinicus*
DESCRIPTION: asparagine synthetase. AsAS2.

15 CAA36430.1 X52180 *Pisum sativum*
DESCRIPTION: asparagine synthase (glutamine-hydrolysing).

20 BAA96251.1 AB035247 *Astragalus sinicus*
DESCRIPTION: asparagine synthetase. AsAS1.

CAB57292.1 AJ133522 *Phaseolus vulgaris*
DESCRIPTION: asparagine synthetase (type-I). as1.

25

AAC49614.1 U77679 *Glycine max*
DESCRIPTION: catalyzes the ATP-dependent transfer of the amide group of glutamine to aspartate producing asparagine and glutamate. asparagine synthetase 1. AS1.

30

BAA18951.1 D83378 *Oryza sativa*
DESCRIPTION: asparagine synthetase.

35

AAB03991.1 U55873 *Oryza sativa*
DESCRIPTION: asparagine synthetase.

40 AAF02776.1 AF190729 *Helianthus annuus*
DESCRIPTION: asparagine synthetase. HAS2.

45 AAB71532.1 AF005724 *Sandersonia aurantiaca*
DESCRIPTION: role in flower senescence. asparagine synthetase. SAND1.

- CAA58052.1 X82849 Zea mays
DESCRIPTION: asparragine synthetase. AS.
- 5 AAB91481.1 AF037363 Helianthus annuus
DESCRIPTION: asparagine synthetase.
- 10 CAA73762.1 Y13321 Pisum sativum
DESCRIPTION: asparagine synthetase 1. AS1.
- 15 CAA73763.1 Y13322 Pisum sativum
DESCRIPTION: asparagine synthetase 2. AS2.
- 20 BAA96452.1 AB021793 Pyrus pyrifolia
DESCRIPTION: asparagine synthetase. PPFRU32.
- 25 AAA73943.1 L23833 Glycine max
DESCRIPTION: production of phosphoribosylamine using glutamine and
phosphoribosylpyrophosphate as substrates. glutamine
phosphoribosylpyrophosphate amidotransferase.
- 370
-
- 30 AAG21985.1 AF271636 Zea mays
DESCRIPTION: lysine ketoglutarate reductase/saccharopine dehydrogenase.
LKRSDH. bifunctional enzyme; LKR/SDH; lysine 2-oxoglutarate
reductase/saccharopine dehydrogenase.
- 35 AAC18622.2 AF003551 Zea mays
DESCRIPTION: lysine-ketoglutarate reductase/saccharopine dehydrogenase
bifunctional enzyme.
- 40 AAG28387.1 AF191667 Brassica oleracea
DESCRIPTION: lysine-ketoglutarate reductase/saccharopine dehydrogenase.
- 45 AAG28386.1 AF191666 Brassica napus
DESCRIPTION: lysine-ketoglutarate reductase/saccharopine dehydrogenase.

AAB97685.1 AF042184 Brassica napus
DESCRIPTION: lysine-ketoglutarate reductase/saccharopine dehydrogenase.

5

AAG14462.1 AF293461 Brassica napus
DESCRIPTION: lysine-ketoglutarate reductase. LKR.

371

10

CAB62537.1 AJ012583 *Hevea brasiliensis*
DESCRIPTION: pseudo-hevein.

15

AAA33357.1 M36986 Hevea brasiliensis
DESCRIPTION: hevein (HEV1) precursor.

20

CAA05978.1 AJ003196 *Hevea brasiliensis*
DESCRIPTION: N-acetyl-D-glucosamine/N-acetyl-D-neuraminic acid binding
lectin, prohevein.

25

AAF61435.1 AF137352 Pisum sativum
DESCRIPTION: pre-hevein-like protein. PHLP. stress-induced; the coding region is putative in the 5' end.

372

30

AAG28503.1 AF196966 Citrus sinensis
DESCRIPTION: hexokinase.

35

AA18584.1 AF118132 *Spinacia oleracea*
DESCRIPTION: chloroplast outer envelope hexokinase 1. Hxk1.

40

AA18585.1 AF118133 *Nicotiana tabacum*
DESCRIPTION: chloroplast outer envelope hexokinase 1. Hxk1.

AAF14186.1 AF106068 Solanum tuberosum
DESCRIPTION: hexokinase 2.

45

AAG35735.1 AF208543 *Lycopersicon esculentum*

DESCRIPTION: hexokinase. Hxk2.

CAA63966.1 X94302 Solanum tuberosum
5 DESCRIPTION: hexokinase. hxx.

BAA99425.1 AP002743 Oryza sativa
10 DESCRIPTION: putative chloroplast outer envelope hexokinase 1.
P0710E05.10.

374

AAC83688.2 AF083343 Nicotiana tabacum
15 DESCRIPTION: 101 kDa heat shock protein. HSP101.

AAF01280.1 AF174433 Triticum aestivum
20 DESCRIPTION: heat shock protein 101. HSP101. ClpB family member.

AAD33606.1 AF133840 Zea mays
25 DESCRIPTION: heat shock protein HSP101. HSP101. 101 kDa protein.

AAD25223.1 AF077337 Zea mays
DESCRIPTION: heat shock protein 101. HSP101. ClpB/Hsp100 protein
homolog;
101 kDa heat shock protein.
30

AAF91178.1 AF203700 Phaseolus lunatus
DESCRIPTION: ClpB. clpB. heat shock protein HSP100.

35
AAD22629.1 AF097363 Triticum aestivum
DESCRIPTION: heat shock protein 101. Hsp101a.

40 AAC83689.2 AF083344 Triticum aestivum
DESCRIPTION: 101 kDa heat shock protein. HSP101.

AAD26530.1 AF083327 Zea mays
45 DESCRIPTION: 101 kDa heat shock protein. HSP101. similar to HSP100/ClpB;
HSP104.

375

CAA04611.1 AJ001208 *Brassica juncea*

- 5 DESCRIPTION: APS reductase. apsr8. putative mitochondrial or plastidic transit peptide.

CAA04610.1 AJ001207 *Brassica juncea*

- 10 DESCRIPTION: APS reductase. apsr2. putative mitochondrial or plastidic transit peptide.

AAB05871.2 U63784 *Catharanthus roseus*

- 15 DESCRIPTION: reduction of adenylyl sulfate (APS). PAPS-reductase-like protein. par2neu.

CAB65911.1 AJ249831 *Lemna minor*

- 20 DESCRIPTION: APR reducing enzyme, sulphur assimilation. adenosine 5'-phosphosulphate reductase. lapr.

AAF18999.1 AF212155 *Allium cepa*

- 25 DESCRIPTION: APS-reductase.

AAC26855.1 AF069951 *Enteromorpha intestinalis*

- 30 DESCRIPTION: catalyzes the formation of sulfite and 5'-AMP from APS and reduced glutathione. 5'-adenylylsulfate reductase. EAPR1; sulfate assimilation enzyme; similar to *Escherichia coli* 3'-phosphoadenosine, 5'-phosphosulfate (PAPS) reductase encoded by cysH.

AAD02069.1 AF036939 *Chlamydomonas reinhardtii*

- 35 DESCRIPTION: redox-regulator of 5'UTR psbA mRNA binding complex and translation. protein disulfide isomerase. localized to ER and chloroplast.

AAC49896.1 AF027727 *Chlamydomonas reinhardtii*

- 40 DESCRIPTION: involved in the redox-regulated binding of chloroplast poly(A)-binding protein to the 5'-UTR of psbA mRNA; regulates chloroplast translational activation. protein disulfide isomerase RB60. PDI.

376

AAC62017.1 AF077547 Brassica juncea
DESCRIPTION: arginine decarboxylase.

5 AAF26434.1 AF220097 Brassica juncea
DESCRIPTION: arginine decarboxylase.

10 AAF26435.1 AF220098 Brassica juncea
DESCRIPTION: arginine decarboxylase.

15 AAB60880.1 AF002017 Dianthus caryophyllus
DESCRIPTION: arginine decarboxylase. gCARADC8.

20 AAF42972.1 AF127241 Nicotiana tabacum
DESCRIPTION: arginine decarboxylase 2. ADC2.

25 BAA25685.1 AB012873 Nicotiana sylvestris
DESCRIPTION: arginine decarboxylase. NsADC-1.

30 CAA85773.1 Z37540 Pisum sativum
DESCRIPTION: arginine decarboxylase.

35 CAB64599.1 AJ251898 Datura stramonium
DESCRIPTION: polyamine biosynthesis. arginine decarboxylase 1. adc1.

40 AAD09204.1 U35367 Glycine max
DESCRIPTION: arginine decarboxylase.

45 BAA84799.1 AP000559 Oryza sativa
DESCRIPTION: ESTs C99670(E21043),C99671(E21043),
AU078262(R10938),AU078261(R10938),D15282(C0402) correspond to a
region of
the predicted gene.; Similar to arginine decarboxylase (U52851).

AAB67887.1 U63832 Dianthus caryophyllus
DESCRIPTION: arginine decarboxylase. ADC.

AAF42971.1 AF127240 *Nicotiana tabacum*
DESCRIPTION: arginine decarboxylase 1. ADC1.

5

AAF42970.1 AF127239 *Nicotiana tabacum*
DESCRIPTION: arginine decarboxylase 1. ADC1.

10 AAC68511.1 AF045666 *Theobroma cacao*
DESCRIPTION: arginine decarboxylase. spe2.

15 CAA65585.1 X96791 *Vitis vinifera*
DESCRIPTION: arginine decarboxylase. ADC.

20 AAA61347.1 L16582 *Lycopersicon esculentum*
DESCRIPTION: decarboxylation of L-arginine. arginine decarboxylase.

AAC68530.1 AF045685 *Arabidopsis arenosa*
DESCRIPTION: arginine decarboxylase. spe2.

25 AAC68529.1 AF045684 *Capsella bursa-pastoris*
DESCRIPTION: arginine decarboxylase. spe2.

30 AAC68525.1 AF045680 *Arabis drummondii*
DESCRIPTION: arginine decarboxylase. spe2.

35 AAC68526.1 AF045681 *Barbarea vulgaris*
DESCRIPTION: arginine decarboxylase. spe2.

40 AAC68535.1 AF045690 *Nasturtium officinale*
DESCRIPTION: arginine decarboxylase. spe2.

AAC68534.1 AF045689 *Thellungiella salsuginea*
DESCRIPTION: arginine decarboxylase. spe2.

45 AAC68533.1 AF045688 *Thlaspi arvense*

DESCRIPTION: arginine decarboxylase. spe2.

5 AAC68532.1 AF045687 *Stanleya pinnata*
DESCRIPTION: arginine decarboxylase. spe2.

10 AAC68531.1 AF045686 *Sisymbrium altissimum*
DESCRIPTION: arginine decarboxylase. spe2.

AAC68510.1 AF045665 *Aethionema grandiflora*
DESCRIPTION: arginine decarboxylase. spe2.

15 AAC68528.1 AF045683 *Brassica oleracea*
DESCRIPTION: arginine decarboxylase. spe2.

20 AAC68519.1 AF045674 *Arabidopsis arenosa*
DESCRIPTION: arginine decarboxylase. spe2.

25 AAC68527.1 AF045682 *Brassica nigra*
DESCRIPTION: arginine decarboxylase. spe2.

30 AAC68523.1 AF045678 *Thellungiella salsuginea*
DESCRIPTION: arginine decarboxylase. spe2.

AAC68514.1 AF045669 *Arabis drummondii*
DESCRIPTION: arginine decarboxylase. spe2.

35 AAC68524.1 AF045679 *Nasturtium officinale*
DESCRIPTION: arginine decarboxylase. spe2.

40 AAC68522.1 AF045677 *Thlaspi arvense*
DESCRIPTION: arginine decarboxylase. spe2.

45 AAC68513.1 AF045668 *Polanisia dodecandra*
DESCRIPTION: arginine decarboxylase. spe2.

AAC68518.1 AF045673 *Capsella bursa-pastoris*
DESCRIPTION: arginine decarboxylase. spe2.

5

AAC68515.1 AF045670 *Barbarea vulgaris*
DESCRIPTION: arginine decarboxylase. spe2.

10

AAC68521.1 AF045676 *Stanleya pinnata*
DESCRIPTION: arginine decarboxylase. spe2.

15

AAC68520.1 AF045675 *Sisymbrium altissimum*
DESCRIPTION: arginine decarboxylase. spe2.

20

AAC68517.1 AF045672 *Brassica oleracea*
DESCRIPTION: arginine decarboxylase. spe2.

25

AAC68516.1 AF045671 *Brassica nigra*
DESCRIPTION: arginine decarboxylase. spe2.

AAC68512.1 AF045667 *Carica papaya*
DESCRIPTION: arginine decarboxylase. spe2.

30

CAA40137.1 X56802 *Avena sativa*
DESCRIPTION: arginine decarboxylase. spe1.

35

AAD24801.1 AF132498 *Brassica napus*
DESCRIPTION: arginine decarboxylase. ADC.

40

BAA21617.1 AB005880 *Nicotiana tabacum*
DESCRIPTION: arginine decarboxylase.

AAB82607.1 AF026809 *Ipomoea nil*
DESCRIPTION: arginine decarboxylase. adc.

45

377

AAG22606.1 AF258809 Lycopersicon esculentum

DESCRIPTION: aldehyde oxidase. AO2. molybdenum cofactor-binding enzyme.

5

BAA23226.1 D88451 Zea mays

DESCRIPTION: aldehyde oxidase. zmAO-1.

10 AAG22607.1 AF258810 Lycopersicon esculentum

DESCRIPTION: aldehyde oxidase. AO3. molybdenum cofactor-binding enzyme.

15 AAG22605.1 AF258808 Lycopersicon esculentum

DESCRIPTION: aldehyde oxidase. AO1. molybdenum cofactor-binding enzyme.

20 BAA23227.1 D88452 Zea mays

DESCRIPTION: aldehyde oxidase-2. zmAO-2. putative.

25 AAB41742.1 U82559 Lycopersicon esculentum

DESCRIPTION: aldehyde oxidase 1 homolog. TAO1. has sequence properties of the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a multigene family.

30

AAG22608.1 AF259793 Lycopersicon esculentum

DESCRIPTION: aldehyde oxidase. AO1. molybdenum cofactor-binding enzyme.

35

AAB41741.1 U82558 Lycopersicon esculentum

DESCRIPTION: aldehyde oxidase 1 homolog. TAO1. has sequence properties of the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a multigene family.

40

378

BAB21211.1 AP002913 Oryza sativa

45 DESCRIPTION: putative DNA binding protein RAV2. P0480E02.17.

BAB21218.1 AP002913 *Oryza sativa*
DESCRIPTION: putative DNA binding protein RAV2. P0480E02.24.

5

BAA90643.1 AP001129 *Oryza sativa*
DESCRIPTION: Similar to *Arabidopsis thaliana* chromosome II BAC F11F19
genomic sequence, putative DNA-binding protein RAV2. (AC007017).

10

BAA85426.1 AP000616 *Oryza sativa*
DESCRIPTION: similar to putative DNA-binding protein RAV2 (AC007017).

380

15

CAB65369.1 AJ250832 *Pisum sativum*
DESCRIPTION: germin-like protein. ger1.

20

AAF03355.1 AF132671 *Nicotiana plumbaginifolia*
DESCRIPTION: nectarin I precursor. NEC1. germin-like protein.

25

AAD38298.1 AC007789 *Oryza sativa*
DESCRIPTION: putative oxalate oxidase (germin protein).
OSJNBa0049B20.25.

30

BAB18339.1 AP002865 *Oryza sativa*
DESCRIPTION: putative germin protein. P0034C11.30. contains EST
C97263(C53484).

35

BAA25197.1 AB012138 *Lycopersicon esculentum*
DESCRIPTION: adaptation to Mn-deficiency. germin-like protein. Mdip1.

40

AAC78470.1 AF067731 *Solanum tuberosum*
DESCRIPTION: germin-like protein. OXAOXA. similar to oxalate oxidase.

45

AAC04835.1 AF032974 *Oryza sativa*
DESCRIPTION: germin-like protein 4. GER4. similar to wheat and barley
oxalate oxidase.

BAB39980.1 AP003020 *Oryza sativa*

5

BAB39965.1 AP003018 *Oryza sativa*

DESCRIPTION: probable germin protein 4. OSJNBa0004B13.19. contains ESTs
AU101991(S4037),AU070167(R0031).

10

AAC04833.1 AF032972 Oryza sativa

DESCRIPTION: germin-like protein 2. GER2. similar to wheat and barley oxalate oxidase.

15

AAG00425.1 AF250933 *Hordeum vulgare*

DESCRIPTION: germin A. GerA. apoplasmic protein; contains prepeptide for targeting into the cell wall.

20

AAD43972.1 AF141879 *Oryza sativa*

DESCRIPTION: germin-like protein 2 precursor. RGLP2. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.

25

AAD43973.1 AF141880 *Oryza sativa*

DESCRIPTION: germin-like protein 1 precursor. RGLP1. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.

30

AAD43971.1 AF141878 *Oryza sativa*

DESCRIPTION: germin-like protein 1 precursor. RGLP1. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.

35

CAB55559.1 AJ237943 *Triticum aestivum*

DESCRIPTION: germin-like protein. glp2b.

40

CAB55558.1 AJ237942 *Triticum aestivum*

DESCRIPTION: germin-like protein. glp2a.

45

AAC04837.1 AF032976 *Oryza sativa*

DESCRIPTION: germin-like protein 6. GER6. similar to wheat and barley

oxalate oxidase.

5 AAC04832.1 AF032971 Oryza sativa
DESCRIPTION: germin-like protein 1. GER1. similar to wheat and barley
oxalate oxidase.

10 CAA63659.1 X93171 Hordeum vulgare
DESCRIPTION: oxalate oxidase-like protein or germin-like protein.

15 CAB55394.1 AL117264 Oryza sativa
DESCRIPTION: zwh0010.1. similar to Arabidopsis germin-like protein 6
(AF032976); Method: conceptual translation with partial peptide
sequencing.

20 AAB97470.1 AF042489 Oryza sativa
DESCRIPTION: germin-like protein 16. glp16.

25 AAC25777.1 AF072694 Oryza sativa
DESCRIPTION: germin-like protein 7. GER7. similar to wheat and barley
oxalate oxidase.

30 AAG00427.1 AF250935 Hordeum vulgare
DESCRIPTION: germin F. GerF. apoplastic protein; contains prepeptide for
targeting into the cell wall.

35 AAG00426.1 AF250934 Hordeum vulgare
DESCRIPTION: germin B. GerB. apoplastic protein; contains prepeptide for
targeting into the cell wall.

40 BAA78563.1 AB024338 Atriplex lentiformis
DESCRIPTION: germin-like protein.

AAA20245.1 U01963 Hordeum vulgare
DESCRIPTION: germin subunit.

45 AAG00428.1 AF250936 Hordeum vulgare

DESCRIPTION: germin D. GerD. apoplastic protein; contains prepeptide for targeting into the cell wall.

- 5 AAC99473.1 AF039201 *Pinus caribaea*
DESCRIPTION: germin-like protein. PcGER1.
- 10 AAC04834.1 AF032973 *Oryza sativa*
DESCRIPTION: germin-like protein 3. GER3. similar to wheat and barley oxalate oxidase.
- 15 AAA34271.1 M63224 *Triticum aestivum*
DESCRIPTION: germin. germin 9f-3.8.
- 20 AAC05146.1 AF049065 *Pinus radiata*
DESCRIPTION: germin-like protein. PRGer1.
- 25 AAA34268.1 M21962 *Triticum aestivum*
DESCRIPTION: germin protein precursor.
- 30 AAA34270.1 M63223 *Triticum aestivum*
DESCRIPTION: germin. germin 9f-2.8.
- 35 CAA71052.1 Y09917 *Triticum aestivum*
DESCRIPTION: germin homolog. pSBGer3.
- 40 AAG00429.1 AF250937 *Hordeum vulgare*
DESCRIPTION: germin E. GerE. apoplastic protein.
- 45 BAA86880.1 AB028454 *Barbula unguiculata*
DESCRIPTION: germin-like protein.
- CAB65370.1 AJ250833 *Pisum sativum*
DESCRIPTION: germin-like protein. ger2a. 1st variant of this clone.
- AAA33030.1 M93041 *Mesembryanthemum crystallinum*

DESCRIPTION: germin-like protein. germin-like protein.

CAB65371.1 AJ250834 Pisum sativum

5 DESCRIPTION: germin-like protein. ger2b. 2nd variant of the clone PsGER2.

CAA71050.1 Y09915 Triticum aestivum

10 DESCRIPTION: germin homolog. pSBGer1.

CAA71051.1 Y09916 Triticum aestivum

DESCRIPTION: germin homolog. pSBGer2.

15 AAA86365.1 U21743 Brassica napus

DESCRIPTION: germin-like protein. similar to product encoded by GenBank
Accession Number X84786.

20 CAC34417.1 AJ311624 Pisum sativum

DESCRIPTION: Germin-like protein. glp3.

389

25

CAA04703.1 AJ001370 Olea europaea

DESCRIPTION: cytochrome b5. cytb5-2.

30 AAA32990.1 M87514 Brassica oleracea

DESCRIPTION: cytochrome b-5. cytochrome b-5.

CAA50575.1 X71441 Nicotiana tabacum

35 DESCRIPTION: cytochrome b5.

CAA53366.1 X75670 Oryza sativa

40 DESCRIPTION: cytochrome b5.

CAA04702.1 AJ001369 Olea europaea

DESCRIPTION: cytochrome b5. cytb5-1.

45

AAA62621.1 L22209 Cuscuta reflexa

DESCRIPTION: associated with cytokinin-induced haustoria formation in
Cuscuta reflexa. cytochrome b5.

5 AAC49701.1 U79011 *Borago officinalis*
DESCRIPTION: haem-binding protein. cytochrome b5.

10 CAA56318.1 X80008 *Nicotiana tabacum*
DESCRIPTION: cytochrome b5.

15 CAA48240.1 X68140 *Nicotiana tabacum*
DESCRIPTION: cytochrome b5.

20 AAD10774.1 AF098510 *Petunia x hybrida*
DESCRIPTION: involved in anthocyanin biosynthesis. cytochrome b5 DIF-F.
diff. required for full activity of flavonoid 3',5' hydroxylase.

25 AAF60299.1 AF233640 *Petunia x hybrida*
DESCRIPTION: involved in anthocyanin biosynthesis. cytochrome b5 DIF-F.
diff.

30 CAA11033.1 AJ222981 *Physcomitrella patens*
DESCRIPTION: delta6-acyl-lipid desaturase. des6. des6 represents a fusion
between a C-terminal desaturase with a cytochrome b5-related part and a
N-terminal extension.

392

35 AAK28303.1 AF346431 *Nicotiana tabacum*
DESCRIPTION: phenylpropanoid:glucosyltransferase 1. togt1.
glucosyltransferase.

40 AAB36653.1 U32644 *Nicotiana tabacum*
DESCRIPTION: immediate-early salicylate-induced glucosyltransferase.
IS5a.

45 BAB17061.1 AP002523 *Oryza sativa*
DESCRIPTION: putative glucosyl transferase. P0013F10.7. contains EST
C73149(E2992).

- AAK16180.1 AC079887 *Oryza sativa*
 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.21.
 5
- AAD51778.1 AF116858 *Phaseolus vulgaris*
 DESCRIPTION: utilizes UDPX as the sugar donor and catalyzes the formation
 of O-xylosylzeatin from zeatin. zeatin O-xylosyltransferase. ZOX1.
 10
- AAD04166.1 AF101972 *Phaseolus lunatus*
 DESCRIPTION: catalyzes formation of O-glucosylzeatin from zeatin and
 UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin
 O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
 15
- BAA89009.1 AB027455 *Petunia x hybrida*
 DESCRIPTION: anthocyanin 5-O-glucosyltransferase. PH1.
 20
- CAC09351.1 AL442007 *Oryza sativa*
 DESCRIPTION: putative glucosyltransferase. H0212B02.7.
 25
- AAB62270.1 AF006081 *Solanum berthaultii*
 DESCRIPTION: UDPG glucosyltransferase. PLGT.
 30
- AAK16172.1 AC079887 *Oryza sativa*
 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.14.
 35
- AAF61647.1 AF190634 *Nicotiana tabacum*
 DESCRIPTION: UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
 40
- CAA54612.1 X77462 *Manihot esculenta*
 DESCRIPTION: UTP-glucose glucosyltransferase. CGT5.
 45
- AAK16181.1 AC079887 *Oryza sativa*
 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.16.
- AAK16178.1 AC079887 *Oryza sativa*

DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.5.

BAA36412.1 AB012116 Vigna mungo

5 DESCRIPTION: UDP-glucose:flavonoid glycosyltransferase. UFGlyT.

AAK16175.1 AC079887 Oryza sativa

10 DESCRIPTION: putative glucosyltransferase. OSJNBa0040E01.15.

AAF98390.1 AF287143 Brassica napus

15 DESCRIPTION: catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.

BAA36423.1 AB013598 Verbena x hybrida

20 DESCRIPTION: UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

AAF17077.1 AF199453 Sorghum bicolor

25 DESCRIPTION: UDP-glucose glucosyltransferase.
UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.

BAA93039.1 AB033758 Citrus unshiu

30 DESCRIPTION: limonoid UDP-glucosyltransferase. LGTase.

BAB17176.1 AP002843 Oryza sativa

DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.13.

35 BAB17182.1 AP002843 Oryza sativa

DESCRIPTION: putative UTP-glucose glucosyltransferase. P0407B12.19.

BAA89008.1 AB027454 Petunia x hybrida

40 DESCRIPTION: anthocyanidin 3-O-glucosyltransferase. PGT8.

CAA54558.1 X77369 Solanum melongena

45 DESCRIPTION: glycosyl transferase. GT.

CAA54611.1 X77461 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT2.

5 CAA54609.1 X77459 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT1.

10 BAA12737.1 D85186 *Gentiana triflora*
DESCRIPTION: UDP-glucose:flavonoid-3-glucosyltransferase.

15 AAD21086.1 AF127218 *Forsythia x intermedia*
DESCRIPTION: adds glucose residue to position 3 of flavonoid compounds.
flavonoid 3-O-glucosyltransferase. UFGT.

20 AAG25643.1 AF303396 *Phaseolus vulgaris*
DESCRIPTION: UDP-glucosyltransferase HRA25. putative; defense associated.

BAA36411.1 AB012115 *Vigna mungo*
DESCRIPTION: UDP-glucose:flavonoid glycosyltransferase. UFGlyT.

25 BAA19155.1 AB000623 *Nicotiana tabacum*
DESCRIPTION: glucosyl transferase. JIGT.

30 AAD55985.1 AF165148 *Petunia x hybrida*
DESCRIPTION: catalyzes the penultimate step of flavonol
glucosylgalactoside biosynthesis from UDP-galactose and flavonol aglycones
in petunia pollen. UDP-galactose:flavonol 3-O-galactosyltransferase.
F3galtase.

35

CAA54613.1 X77463 *Manihot esculenta*
DESCRIPTION: UTP-glucose glucosyltransferase. CGT6.

40

BAA36421.1 AB013596 *Perilla frutescens*
DESCRIPTION: UDP-glucose:anthocynsin 5-O-glucosyltransferase. PF3R4.

45 BAA19659.1 AB002818 *Perilla frutescens*
DESCRIPTION: flavonoid 3-O-glucosyltransferase. UDP glucose.

AAB81683.1 AF000372 *Vitis vinifera*
DESCRIPTION: UDP glucose:flavonoid 3-o-glucosyltransferase.

5

BAB41025.1 AB047098 *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.

10

BAB41023.1 AB047096 *Vitis vinifera*
DESCRIPTION: UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.

393

15

CAB56756.1 AJ011589 *Pisum sativum*
DESCRIPTION: 5,10-methylenetetrahydrofolate dehydrogenase:
5,10-methenyltetrahydrofolate cyclohydrolase. bifunctional enzyme.

20

AAD01907.1 AF030516 *Pisum sativum*
DESCRIPTION: 5,10-methylenetetrahydrofolate
dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase. bifunctional
protein; 31.3 kDa protein.

25

AAG48834.1 AC084218 *Oryza sativa*
DESCRIPTION: similar to *Pisum sativum* methylenetetrahydrofolate
dehydrogenase (NADP+) (EC 1.5.1.5) (AF030516).

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406

AAD46491.1 AF135014 *Zea mays*
DESCRIPTION: dihydrolipoamide S-acetyltransferase. pyruvate dehydrogenase
complex E2 subunit.

35

BAA90623.1 AP001129 *Oryza sativa*
DESCRIPTION: ESTs AU033004(S0924),C74754(E50863) correspond to a
region
of the predicted gene.; Similar to Rat mRNA for dihydrolipoamide
acetyltransferase. (D10655).

40

45 BAA77024.1 AB026124 *Lithospermum erythrorhizon*
DESCRIPTION: dihydrolipoamide acetyltransferase.

407

AAAF69017.1 AF261654 *Dianthus caryophyllus*

5 DESCRIPTION: ethylene-insensitive 3-like protein 1. EIL1. EIN3-like protein.

CAC09582.1 AJ298994 *Fagus sylvatica*

10 DESCRIPTION: gibberellic acid (GA3)-induced. ethylene insensitive (EIN3/EIL)-like transcription regulator. ein11.

AAG00419.1 AF247568 *Nicotiana tabacum*

15 DESCRIPTION: EIN3. component in ethylene signal transduction pathway.

408

AAC15870.1 AF002016 *Cucurbita* sp.

20 DESCRIPTION: acyl CoA oxidase homolog.

AAAF14635.1 AF202987 *Petroselinum crispum*

25 DESCRIPTION: acyl-CoA oxidase. ACO. peroxisomal acyl-CoA oxidase.

AAB67883.1 U66299 *Phalaenopsis* sp. 'True Lady'

DESCRIPTION: acyl-CoA oxidase homolog.

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AAC32108.1 AF051203 *Picea mariana*

DESCRIPTION: acyl-CoA oxidase homolog. Sb06. similar to *Phalaenopsis* sp. acyl-CoA oxidase homolog encoded by GenBank Accession Number U66299.

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CAA04688.1 AJ001341 *Hordeum vulgare*

DESCRIPTION: putative acyl-CoA oxidase.

40 BAB08201.1 AP002539 *Oryza sativa*

DESCRIPTION: ESTs AU056822(S20908),C26441(C12328), C28477(C61243) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* putative acyl-coA dehydrogenase (AF049236).

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BAA96762.1 AP002521 *Oryza sativa*